06-22-00

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Express Mail No.: EK305107157US
Docket No.: 784CIP2

jc848 U.S. PTO 06/20/00

jc829 U.S. PTO 09/598042 06/20/00

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE
PATENT APPLICATION TRANSMITTAL UNDER 37 CFR 1.53

BOX PATENT APPLICATION
Assistant Commissioner for Patents
Washington, D.C. 20231

Sir:

Transmitted herewith for filing is the patent application of

Inventor(s): Y. Tom Tang, Chenghua Liu, Vinod Asundi, Chongjun Xu, Ping Zhou, Yunqing Ma, Jian-Rui Wang, Qing A. Zhao, Feiyan Ren, Rui-hong Chen, Dunrui Wang, Zhiwei Wang, Tom Wehrman, Jie Zhang, Xiaohong B. Qian, John Tillinghast, Radoje T. Drmanac

Title: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

09598042 062000

1. Type of application

☐ This is a new application for a

☐ Utility patent.

☐ Design patent.

☒ This is a continuation-in-part application of prior application no. 09/552,317 filed April 25, 2000, Attorney Docket No. 784CIP, which is a continuation-in-part application of prior application no. 09/488,725 filed January 21, 2000, Attorney Docket No. 784.

2. Application Papers Enclosed

1	Title Page	
115	Pages of Specification (excluding Claims, Abstract, Drawings & Sequence Listing)	
4	Page(s) of Claims	
1	Page(s) of Abstract	
0	Sheet(s) of Drawings (Figs. X-X)	☐ Formal ☐ Informal
984	Page(s) of Sequence Listing	

CERTIFICATION UNDER 37 CFR 1.10

I hereby certify that this Patent Application Transmittal and the documents referred to as enclosed therewith are being deposited with the United States Postal Service on **June 20, 2000,** in an envelope addressed to the Assistant Commissioner for Patents, Washington, D.C. 20231 utilizing the "Express Mail Post Office to Addressee" service of the United States Postal Service under Mailing Label No. **EK305107157US**

Annya Dushine

Annya Dushine

3. Oath or Declaration

☐ Enclosed

- ☐ Executed by (check all applicable boxes)
- ☐ Inventor(s)
- ☐ Legal representative of inventors(s) (37 CFR 1.42 or 1.43)
- ☐ Joint inventor or person showing a proprietary interest on behalf of inventor who refused to sign or cannot be reached
- ☐ The petition required by 37 CFR 1.47 and the statement required by 37 CFR 1.47 are enclosed. See Item 5D below for fee.

☒ Unexecuted – the undersigned attorney or agent is authorized to file this application on behalf of the applicant(s). An executed declaration will follow.

4. Additional Papers Enclosed

- ☐ Preliminary Amendment
- ☐ Information Disclosure Statement
- ☐ Declaration of Biological Deposit
- ☒ Computer readable copy of sequence listing containing nucleotide and/or amino acid sequence
- ☒ Statement Under 37 CFR § 1.821
- ☒ Paper copy of sequence listing identical to computer copy (984 pages)
- ☐ Microfiche computer program
- ☒ Verified statement claiming small entity status under 37 CFR 1.9 and 1.27
- ☐ Associate Power of Attorney
- ☐ Verified translation of a non-English patent application
- ☒ Return receipt postcard
- ☐ Other _____

5. Priority Applications Under 35 USC 119

Certified copies of applications from which priority under 35 USC 119 is claimed are listed below and

- ☐ are attached.
- ☐ will follow.

6. **Filing Fee Calculation (37 CFR 1.16)**

A. ☒ **Utility Application**

CLAIMS AS FILED – INCLUDING PRELIMINARY AMENDMENT (IF ANY)						
			SMALL ENTITY		OTHER THAN A SMALL ENTITY	
	NO. FILED	NO. EXTRA	RATE	FEE	RATE	FEE
BASIC FEE				$345.00		$690.00
TOTAL	28-20	= 8	X 9 =	$72.00	X 18 =	$0.00
INDEP.	3-3	= 0	X 39 =	$0.00	X 78 =	$0.00
☐ First Presentation of Multiple Dependent Claim			+ 130 =	$0.00	+ 260 =	$0.00
			FILING FEE:	**$417.00**	**OR**	$0.00

B. ☐ **Design Application ($155.00/$310.00)** Filing Fee: $_____

C. ☐ **Plant Application ($240.00/$480.00)** Filing Fee: $_____

D. **Other fees**

☐ Recording Assignment [Fee -- **$40.00** per assignment] $_____

☐ Other $_____

TOTAL FEES $ 417.00

7. **Preliminary Amendment**

Please amend the specification by inserting before the first line the sentence: -- This is a continuation–in-part of application Serial No. 09/552,317, filed April 25, 2000, entitled "Novel Nucleic Acids and Polypeptides" which is a continuation–in-part of application Serial No. 09/488,725, filed January 21, 2000, entitled "Novel Contigs Obtained From Various Libraries" both herein incorporated by reference. --

8. **Method of Payments of Fees**

☐ Enclosed check

☒ Charge Deposit Account No. 501169. A duplicate copy of this transmittal is enclosed

☐ Not enclosed

9. **Deposit Account and Refund Authorization**

The Commissioner is hereby authorized to charge payment of any additional fees due or credit any overpayment to Deposit Account No. 501169. A duplicate copy of this transmittal is enclosed.

Please refund any overpayment to Hyseq, Inc. at the address below.

Please direct all future correspondence to Petrina S. Hsi at the address below.

Respectfully submitted,

Date: June 20, 2000 By: Petrina Hsi

Petrina S. Hsi
Attorney for Applicants
Registration No.: 38,496
HYSEQ, INC.
670 Almanor Avenue
Sunnyvale, CA 94086
(408) 524-8100
(408) 524-8145 (Telefacsimile)

PATENT APPLICATION
Express Mail No.: EK305107157US
Docket No.: 784CIP2

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant(s) or Patentee(s):	Y. Tom Tang, Chenghua Liu, Vinod Asundi, Chongjun Xu, Ping Zhou, Yunqing Ma, Jian-Rui Wang, Qing A. Zhao, Feiyan Ren, Rui-hong Chen, Dunrui Wang, Zhiwei Wang, Tom Wehrman, Jie Zhang, Xiaohong B. Qian, John Tillinghast, Radoje T. Drmanac
Application No. or Patent No.:	Not Yet Assigned
Filed or Issued:	Herewith
For:	NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

VERIFIED STATEMENT (DECLARATION) CLAIMING SMALL ENTITY STATUS (37 CFR § 1.9(f) AND 1.27(c)) - SMALL BUSINESS CONCERN

I hereby declare that I am

( ) The owner of the small business concern identified below:
(X) An official of the small business concern empowered to act on behalf of the concern identified below:

NAME OF CONCERN: HYSEQ, INC.
ADDRESS: 670 Almanor Avenue
Sunnyvale, CA 94086

I hereby declare that the above-identified small business concern qualifies as a small business concern as defined in 13 CFR § 121.12, and reproduced in 37 CFR § 1.9(d), for purposes of paying reduced fees under § 41(a) and (b) of Title 35, United States Code, in that the number of employees of the concern, including those of its affiliates, does not exceed 500 persons. For purposes of this statement, (1) the number of employees of the business concern is the average over the previous fiscal year of the concern of the persons employed on a full-time, part-time or temporary basis during each of the pay periods of the fiscal year, and (2) concerns are affiliates of each other when either, directly or indirectly, one concern controls or has the power to control the other, or a third party or parties controls or has the power to control both.

I hereby declare that rights under contract or law have been conveyed to, and remain with, the small business concern identified above with regard to the invention, entitled NOVEL NUCLEIC ACIDS AND POLYPEPTIDES by inventors, Y. Tom Tang, et al. described in

(X) The specification filed herewith.
( ) Application Serial No. [ ], filed [Date].
( ) Patent No. [ ], issued [Date].

If the rights held by the above identified small business concern are not exclusive, each individual, concern or organization having rights to the invention is listed below[1] and no rights to the invention are held by any person, other than the inventor, who could not qualify as a small business concern under 37 CFR § 1.9(c), or by any concern which would not qualify as a small business concern under 37 CFR § 1.9(d) or a nonprofit organization under 37 CFR § 1.9(e).

Full Name: _____

Address: _____

( ) Individual ( ) Small Business Concern ( ) Nonprofit Organization

I acknowledge the duty to file, in this application or patent, notification of any change in status resulting in loss of entitlement to small entity status prior to paying, or at the time of paying, the earliest of the issue fee or any maintenance fee due after the date on which status as a small entity is no longer appropriate (37 CFR § 1.28(b)).

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under § 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application, any patent issuing thereon, or any patent to which this verified statement is directed.

Name of person signing: James N. Fletcher

Title of person other than owner: Sr. Vice President of Administration and General Counsel

Address of person signing: HYSEQ, INC.
670 Almanor Avenue
Sunnyvale, CA 94086

Signature: _____

Date: 6/16/00

[1]NOTE: Separate verified statements are required from each named person, concern or organization having rights to the invention averring to their status as small entities. (37 CFR § 1.27)

Our Ref. No.: 784CIP2

NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

09/09/2003 15:56:00

Express Mail Label No.: EK305107157US

NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

1. TECHNICAL FIELD

The present invention provides novel polynucleotides and proteins encoded by such polynucleotides, along with uses for these polynucleotides and proteins, for example in therapeutic, diagnostic and research methods.

2. BACKGROUND ART

Technology aimed at the discovery of protein factors (including e.g., cytokines, such as lymphokines, interferons, CSFs, chemokines, and interleukins) has matured rapidly over the past decade. The now routine hybridization cloning and expression cloning techniques clone novel polynucleotides "directly" in the sense that they rely on information directly related to the discovered protein (i.e., partial DNA/amino acid sequence of the protein in the case of hybridization cloning; activity of the protein in the case of expression cloning). More recent "indirect" cloning techniques such as signal sequence cloning, which isolates DNA sequences based on the presence of a now well-recognized secretory leader sequence motif, as well as various PCR-based or low stringency hybridization-based cloning techniques, have advanced the state of the art by making available large numbers of DNA/amino acid sequences for proteins that are known to have biological activity, for example, by virtue of their secreted nature in the case of leader sequence cloning, by virtue of their cell or tissue source in the case of PCR-based techniques, or by virtue of structural similarity to other genes of known biological activity.

Identified polynucleotide and polypeptide sequences have numerous applications in, for example, diagnostics, forensics, gene mapping; identification of mutations responsible for genetic disorders or other traits, to assess biodiversity, and to produce many other types of data and products dependent on DNA and amino acid sequences.

3. SUMMARY OF THE INVENTION

The compositions of the present invention include novel isolated polypeptides, novel isolated polynucleotides encoding such polypeptides, including recombinant DNA molecules, cloned genes or degenerate variants thereof, especially naturally occurring variants such as allelic variants, antisense polynucleotide molecules, and antibodies that specifically recognize one or more

epitopes present on such polypeptides, as well as hybridomas producing such antibodies.

The compositions of the present invention additionally include vectors, including expression vectors, containing the polynucleotides of the invention, cells genetically engineered to contain such polynucleotides and cells genetically engineered to express such polynucleotides.

The present invention relates to a collection or library of at least one novel nucleic acid sequences assembled from expressed sequence tags (ESTs) isolated mainly by sequencing by hybridization (SBH), and in some cases, sequences obtained from one or more public databases. The invention relates also to the proteins encoded by such polynucleotides, along with therapeutic, diagnostic and research utilities for these polynucleotides and proteins. These nucleic acid sequences are designated as SEQ ID NO: 1 - 331 and are provided in the Sequence Listing. In the nucleic acids provided in the Sequence Listing, A is adenosine; C is cytosine; G is guanosine; T is thymine; and N is any of the four bases. In the amino acids provided in the Sequence Listing, * corresponds to the stop codon.

The nucleic acid sequences of the present invention also include, nucleic acid sequences that hybridize to the complement of SEQ ID NO: 1 - 331 under stringent hybridization conditions; nucleic acid sequences which are allelic variants or species homologues of any of the nucleic acid sequences recited above, or nucleic acid sequences that encode a peptide comprising a specific domain or truncation of the peptides encoded by SEQ ID NO: 1 - 331. A polynucleotide comprising a nucleotide sequence having at least 90% identity to an identifying sequence of SEQ ID NO: 1 - 331 or a degenerate variant or fragment thereof. The identifying sequence can be 100 base pairs in length.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NO: 1 - 331. The sequence information can be a segment of any one of SEQ ID NO: 1 - 331 that uniquely identifies or represents the sequence information of SEQ ID NO: 1 - 331. One such segment can be a twenty-mer nucleic acid sequence because the probability that a twenty-mer is fully matched in the human genome is 1 in 300. In the human genome, there are three billion base pairs in one set of chromosome. Because there are 4^{20} possible twenty-mers exist, there are 300 times more twenty-mers than there are base

pairs in a set of human chromosome. Using the same analysis, the probability for a seventeen-mer to be fully matched in the human genome is approximately 1 in 5. When these segments are used in arrays for expression studies, fifteen-mer segment can be used. The probability that the fifteen-mer is fully matched in the expressed sequences is also approximately one in five because expressed sequences in one tissue comprise approximately 5% of the entire genome sequence.

Similarly, when using a sequence information for detecting a single mismatch, a segment can be a twenty-five mer. The probability that the twenty-five mer would appear in a human genome with a single mismatch is calculated by multiplying the probability for a full match ($1 \div 4^{25}$) times the increased probability for mismatch at each nucleotide position (3 x 25). The probability that an eighteen mer with a single mismatch can be detected in an array for expression studies is approximately one in five. The probability that a twenty-mer with a single mismatch can be detected in a human genome is approximately one in five.

A collection as used in this application can be a collection of only one polynucleotide. The collection of sequence information or identifying information of each sequence can be provided on a nucleic acid array. In one embodiment, segments of sequence information is provided on a nucleic acid array to detect the polynucleotide that contains the segment. The array can be designed to detect full-match or mismatch to the polynucleotide that contains the segment. The collection can also be provided in a computer-readable format.

This invention also includes the reverse or direct complement of any of the nucleic acid sequences recited above; cloning or expression vectors containing the nucleic acid sequences; and host cells or organisms transformed with these expression vectors. Nucleic acid sequences (or their reverse or direct complements) according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology, such as use as hybridization probes, use as primers for PCR, use in an array, use in computer-readable media, use in sequencing full-length genes, use for chromosome and gene mapping, use in the recombinant production of protein, and use in generation of anti-sense DNA or RNA, their chemical analogs and the like.

In a preferred embodiment, the nucleic acid sequences of SEQ ID NO: 1-331 or novel segments or parts of the contigs of the invention are used as primers in

expression assays that are well known in the art. In a particularly preferred embodiment, the nucleic acid sequences of SEQ ID NO: 1-331 or novel segments or parts of the contigs provided herein are used in diagnostics for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., Science 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

The isolated polynucleotides of the invention include, but are not limited to, a polynucleotide comprising any one of the nucleotide sequences set forth in SEQ ID NO: 1-331; a polynucleotide comprising any of the full length protein coding sequences of SEQ ID NO: 1-331; and a polynucleotide comprising any of the nucleotide sequences of the mature protein coding sequences of SEQ ID NO: 1-331. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent hybridization conditions to (a) the complement of any one of the nucleotide sequences set forth in SEQ ID NO: 1-331; (b) a nucleotide sequence encoding any one of the amino acid sequences set forth in the Sequence Listing; a polynucleotide which is an allelic variant of any polynucleotides recited above; a polynucleotide which encodes a species homolog (e.g. orthologs) of any of the proteins recited above; or a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of any of the polypeptides comprising an amino acid sequence set forth in the Sequence Listing.

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising any of the amino acid sequences set forth in the Sequence Listing. Polypeptides of the invention also include polypeptides with biological activity that are encoded by (a) any of the polynucleotides having a nucleotide sequence set forth in SEQ ID NO: 1-331; or (b) polynucleotides that hybridize to the complement of the polynucleotides of (a) under stringent hybridization conditions. Biologically or immunologically active variants of any of the polypeptide sequences in the Sequence Listing, and "substantial equivalents" thereof (e.g., with at least about 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98% or 99% amino acid sequence identity) that preferably retain biological activity are also contemplated. The polypeptides of the invention may be wholly or partially chemically synthesized but are preferably produced by recombinant means using the genetically engineered cells (e.g. host cells) of the invention.

The invention also provides compositions comprising a polypeptide of the invention. Polypeptide compositions of the invention may further comprise an acceptable carrier, such as a hydrophilic, e.g., pharmaceutically acceptable, carrier.

The invention also provides host cells transformed or transfected with a polynucleotide of the invention.

The invention also relates to methods for producing a polypeptide of the invention comprising growing a culture of the host cells of the invention in a suitable culture medium under conditions permitting expression of the desired polypeptide, and purifying the polypeptide from the culture or from the host cells. Preferred embodiments include those in which the protein produced by such process is a mature form of the protein.

Polynucleotides according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology. These techniques include use as hybridization probes, use as oligomers, or primers, for PCR, use for chromosome and gene mapping, use in the recombinant production of protein, and use in generation of anti-sense DNA or RNA, their chemical analogs and the like. For example, when the expression of an mRNA is largely restricted to a particular cell or tissue type, polynucleotides of the invention can be used as hybridization probes to detect the presence of the particular cell or tissue mRNA in a sample using, *e.g., in situ* hybridization.

In other exemplary embodiments, the polynucleotides are used in diagnostics as expressed sequence tags for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., Science 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

The polypeptides according to the invention can be used in a variety of conventional procedures and methods that are currently applied to other proteins. For example, a polypeptide of the invention can be used to generate an antibody that specifically binds the polypeptide. Such antibodies, particularly monoclonal antibodies, are useful for detecting or quantitating the polypeptide in tissue. The polypeptides of the invention can also be used as molecular weight markers, and as a food supplement.

Methods are also provided for preventing, treating, or ameliorating a medical condition which comprises the step of administering to a mammalian

subject a therapeutically effective amount of a composition comprising a polypeptide of the present invention and a pharmaceutically acceptable carrier.

In particular, the polypeptides and polynucleotides of the invention can be utilized, for example, as part of methods for the prevention and/or treatment of disorders involving aberrant protein expression or biological activity.

The present invention further relates to methods for detecting the presence of the polynucleotides or polypeptides of the invention in a sample. Such methods can, for example, be utilized as part of prognostic and diagnostic evaluation of disorders as recited herein and for the identification of subjects exhibiting a predisposition to such conditions. The invention also provides kits comprising polynucleotide probes and/or monoclonal antibodies, and optionally quantitative standards, for carrying out methods of the invention. Furthermore, the invention provides methods for evaluating the efficacy of drugs, and monitoring the progress of patients, involved in clinical trials for the treatment of disorders as recited above.

The invention also provides methods for the identification of compounds that modulate (i.e., increase or decrease) the expression or activity of the polynucleotides and/or polypeptides of the invention. Such methods can be utilized, for example, for the identification of compounds that can ameliorate symptoms of disorders as recited herein. Such methods can include, but are not limited to, assays for identifying compounds and other substances that interact with (*e.g.*, bind to) the polypeptides of the invention.

The methods of the invention also provides methods for the treatment of disorders as recited herein which may involve the administration of the polynucleotides or polypeptides of the invention to individuals exhibiting symptoms or tendencies related to disorders as recited herein. In addition, the invention encompasses methods for treating diseases or disorders as recited herein comprising the step of administering compounds and other substances that modulate the overall activity of the target gene products. Compounds and other substances can effect such modulation either on the level of target gene/protein expression or target protein activity.

The polypeptides of the present invention and the polynucleotides encoding them are also useful for the same functions known to one of skill in the art as the polypeptides and polynucleotides to which they have the closest homology (set forth

in Table 1). If no homology is set forth for a sequence, then the polypeptides and polynucleotides of the present invention are useful for a variety of applications, as described herein, including use in arrays for detection.

4. DETAILED DESCRIPTION OF THE INVENTION

4.1. DEFINITIONS

The term "primordial germ cells (PGCs)" refers to a small population of cells set aside from other cell lineages particularly from the yolk sac, mesenteries, or gonadal ridges during embryogenesis that have the potential to differentiate in to germ cells and other cells. PGCs are the source from which GSCs and ES cells are derived

The term "germ line stem cells (GSCs)" refers to stem cells derived from primordial stem cells that provide a steady and continuous source of germ cells for the production of gametes.

The term "embryonic stem cells (ES)" refers to a cell which can give rise to many differentiated cell types in an embryo or an adult, including the germ cells. The PGCs, the GSCs and the ES cells are capable of self-renewal. Thus these cells not only populate the germ line and give rise to a plurality of terminally differentiated cells which comprise the adult specialized organs, but are able to regenerate themselves.

The term "totipotent" refers to the capability of a cell to differentiate into all of the cell types of an adult organism.

The term "pluripotent" refers to the capability of a cell to differentiate into a number of differentiated cell types that are present in an adult organism. A pluripotent cell is restricted in its differentiation capability in comparison to a totipotent cell.

The term "nucleotide sequence" refers to a heteropolymer of nucleotides or the sequence of these nucleotides. The terms "nucleic acid" and "polynucleotide" are also used interchangeably herein to refer to a heteropolymer of nucleotides. Generally, nucleic acid segments provided by this invention may be assembled from fragments of the genome and short oligonucleotide linkers, or from a series of oligonucleotides, or from individual nucleotides, to provide a synthetic nucleic acid which is capable of

being expressed in a recombinant transcriptional unit comprising regulatory elements derived from a microbial or viral operon, or a eukaryotic gene.

The terms "oligonucleotide fragment" or a "polynucleotide fragment", "portion," or "segment" is a sequence of nucleotide residues which is long enough to use in polymerase chain reaction (PCR) or various hybridization procedures to identify or amplify identical or related parts of mRNA or DNA molecules. A fragment or segment may uniquely identify each polynucleotide sequence of the present invention.

The terms "oligonucleotides" or "nucleic acid probes" are prepared based on the polynucleotide sequences provided in the present invention. Oligonucleotides comprise portions of such a polynucleotide sequence having at least about 15 nucleotides and usually at least about 20 nucleotides. Nucleic acid probes comprise portions of such a polynucleotide sequence having fewer nucleotides than about 6 kb, usually fewer than about 1 kb. After appropriate testing to eliminate false positives, these probes may, for example, be used to determine whether specific mRNA molecules are present in a cell or tissue or to isolate similar nucleic acid sequences from chromosomal DNA as described by Walsh et al. (Walsh, P.S. et al., 1992, PCR Methods Appl 1:241-250).

The term "probes" includes naturally occurring or recombinant or chemically synthesized single- or double-stranded nucleic acids. They may be labeled by nick translation, Klenow fill-in reaction, PCR, or other methods well known in the art. Probes of the present invention, their preparation and/or labeling are elaborated in Sambrook, J. et al., 1989, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY; or Ausubel, F.M. et al., 1989, Current Protocols in Molecular Biology, John Wiley & Sons, New York NY, both of which are incorporated herein by reference in their entirety.

The term "stringent" is used to refer to conditions that are commonly understood in the art as stringent. Stringent conditions can include highly stringent conditions (i.e., hybridization to filter-bound DNA in 0.5 M $NaHPO_4$, 7% sodium dodecyl sulfate (SDS), 1 mM EDTA at 65° C, and washing in 0.1X SSC/0.1% SDS at 68° C), and moderately stringent conditions (i.e., washing in 0.2X SSC/0.1% SDS at 42° C). Other exemplary hybridization conditions are described herein in the examples.

In instances of hybridization of deoxyoligonucleotides, additional exemplary stringent hybridization conditions include washing in 6X SSC/0.05% sodium pyrophosphate at 37° C (for 14-base oligos), 48° C (for 17-base oligos), 55° C (for 20-base oligos), and 60° C (for 23-base oligos).

The term "recombinant," when used herein to refer to a polypeptide or protein, means that a polypeptide or protein is derived from recombinant (*e.g.*, microbial, insect, or mammalian) expression systems. "Microbial" refers to recombinant polypeptides or proteins made in bacterial or fungal (e.g., yeast) expression systems. As a product, "recombinant microbial" defines a polypeptide or protein essentially free of native endogenous substances and unaccompanied by associated native glycosylation. Polypeptides or proteins expressed in most bacterial cultures, *e.g., E. coli*, will be free of glycosylation modifications; polypeptides or proteins expressed in yeast will have a glycosylation pattern in general different from those expressed in mammalian cells.

The term "recombinant expression vehicle or vector" refers to a plasmid or phage or virus or vector, for expressing a polypeptide from a DNA (RNA) sequence. An expression vehicle can comprise a transcriptional unit comprising an assembly of (1) a genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers, (2) a structural or coding sequence which is transcribed into mRNA and translated into protein, and (3) appropriate transcription initiation and termination sequences. Structural units intended for use in yeast or eukaryotic expression systems preferably include a leader sequence enabling extracellular secretion of translated protein by a host cell. Alternatively, where recombinant protein is expressed without a leader or transport sequence, it may include an amino terminal methionine residue. This residue may or may not be subsequently cleaved from the expressed recombinant protein to provide a final product.

The term "recombinant expression system" means host cells which have stably integrated a recombinant transcriptional unit into chromosomal DNA or carry the recombinant transcriptional unit extrachromosomally. Recombinant expression systems as defined herein will express heterologous polypeptides or proteins upon induction of the regulatory elements linked to the DNA segment or synthetic gene to be expressed. This term also means host cells which have stably integrated a

recombinant genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers. Recombinant expression systems as defined herein will express polypeptides or proteins endogenous to the cell upon induction of the regulatory elements linked to the endogenous DNA segment or gene to be expressed. The cells can be prokaryotic or eukaryotic.

The term "open reading frame," ORF, means a series of nucleotide triplets coding for amino acids without any termination codons and is a sequence translatable into protein.

The term "expression modulating fragment," EMF, means a series of nucleotides which modulates the expression of an operably linked ORF or another EMF.

As used herein, a sequence is said to "modulate the expression of an operably linked sequence" when the expression of the sequence is altered by the presence of the EMF. EMFs include, but are not limited to, promoters, and promoter modulating sequences (inducible elements). One class of EMFs are fragments which induce the expression or an operably linked ORF in response to a specific regulatory factor or physiological event.

As used herein, an "uptake modulating fragment," UMF, means a series of nucleotides which mediate the uptake of a linked DNA fragment into a cell. UMFs can be readily identified using known UMFs as a target sequence or target motif with the computer-based systems described below.

The presence and activity of a UMF can be confirmed by attaching the suspected UMF to a marker sequence. The resulting nucleic acid molecule is then incubated with an appropriate host under appropriate conditions and the uptake of the marker sequence is determined. As described above, a UMF will increase the frequency of uptake of a linked marker sequence.

The term "active" refers to those forms of the polypeptide which retain the biologic and/or immunologic activities of any naturally occurring polypeptide. According to the invention, the term "biologically active" means that the polypeptide retains at least one of the biological activities of the polypeptide of the invention.

The term "naturally occurring polypeptide" refers to polypeptides produced by cells that have not been genetically engineered and specifically contemplates

various polypeptides arising from post-translational modifications of the polypeptide including, but not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation and acylation.

The term "derivative" refers to polypeptides chemically modified by such techniques as ubiquitination, labeling (e.g., with radionuclides or various enzymes), covalent polymer attachment such as pegylation (derivatization with polyethylene glycol) and insertion or substitution by chemical synthesis of amino acids such as ornithine, which do not normally occur in human proteins.

The term "variant"(or "analog") refers to any polypeptide differing from naturally occurring polypeptides by amino acid insertions, deletions, and substitutions, created using, *e g.*, recombinant DNA techniques. Guidance in determining which amino acid residues may be replaced, added or deleted without abolishing activities of interest, may be found by comparing the sequence of the particular polypeptide with that of homologous peptides and minimizing the number of amino acid sequence changes made in regions of high homology (conserved regions) or by replacing amino acids with consensus sequence.

Preferably, amino acid "substitutions" are the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, *i.e.*, conservative amino acid replacements. "Conservative" amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues involved. For example, nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine; polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine; positively charged (basic) amino acids include arginine, lysine, and histidine; and negatively charged (acidic) amino acids include aspartic acid and glutamic acid. "Insertions" or "deletions" are typically in the range of about 1 to 5 amino acids. The variation allowed may be experimentally determined by systematically making insertions, deletions, or substitutions of amino acids in a polypeptide molecule using recombinant DNA techniques and assaying the resulting recombinant variants for activity.

Alternatively, where alteration of function is desired, insertions, deletions or non-conservative alterations can be engineered to produce altered polypeptides.

Such alterations can, for example, alter one or more of the biological functions or biochemical characteristics of the polypeptides of the invention. For example, such alterations may change polypeptide characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate. Further, such alterations can be selected so as to generate polypeptides that are better suited for expression, scale up and the like in the host cells chosen for expression. For example, cysteine residues can be deleted or substituted with another amino acid residue in order to eliminate disulfide bridges.

As used herein, "substantially equivalent" can refer both to nucleotide and amino acid sequences, for example a mutant sequence, that varies from a reference sequence by one or more substitutions, deletions, or additions, the net effect of which does not result in an adverse functional dissimilarity between the reference and subject sequences. Typically, such a substantially equivalent sequence varies from one of those listed herein by no more than about 20% (*i.e.*, the number of individual residue substitutions, additions, and/or deletions in a substantially equivalent sequence, as compared to the corresponding reference sequence, divided by the total number of residues in the substantially equivalent sequence is about 0.2 or less). Such a sequence is said to have 80% sequence identity to the listed sequence. In one embodiment, a substantially equivalent, *e.g.*, mutant, sequence of the invention varies from a listed sequence by no more than 10% (90% sequence identity); in a variation of this embodiment, by no more than 5% (95% sequence identity); and in a further variation of this embodiment, by no more than 2% (98% sequence identity). Substantially equivalent, *e.g.*, mutant, amino acid sequences according to the invention generally have at least 95% sequence identity with a listed amino acid sequence, whereas substantially equivalent nucleotide sequence of the invention can have lower percent sequence identities, taking into account, for example, the redundancy or degeneracy of the genetic code. For the purposes of the present invention, sequences having substantially equivalent biological activity and substantially equivalent expression characteristics are considered substantially equivalent. For the purposes of determining equivalence, truncation of the mature sequence (*e.g.*, via a mutation which creates a spurious stop codon) should be disregarded. Sequence identity may be determined, e.g., using the Jotun Hein method.

Nucleic acid sequences encoding such substantially equivalent sequences, *e.g.*, sequences of the recited percent identities, can routinely be isolated and identified via standard hybridization procedures well known to those of skill in the art.

Where desired, an expression vector may be designed to contain a "signal or leader sequence" which will direct the polypeptide through the membrane of a cell. Such a sequence may be naturally present on the polypeptides of the present invention or provided from heterologous protein sources by recombinant DNA techniques.

A polypeptide "fragment," "portion," or "segment" is a stretch of amino acid residues of at least about 5 amino acids, often at least about 7 amino acids, typically at least about 9 to 13 amino acids, and, in various embodiments, at least about 17 or more amino acids. To be active, any polypeptide must have sufficient length to display biological and/or immunological activity.

Alternatively, recombinant variants encoding these same or similar polypeptides may be synthesized or selected by making use of the "redundancy" in the genetic code. Various codon substitutions, such as the silent changes which produce various restriction sites, may be introduced to optimize cloning into a plasmid or viral vector or expression in a particular prokaryotic or eukaryotic system. Mutations in the polynucleotide sequence may be reflected in the polypeptide or domains of other peptides added to the polypeptide to modify the properties of any part of the polypeptide, to change characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate.

The term "activated" cells as used in this application are those which are engaged in extracellular or intracellular membrane trafficking, including the export of neurosecretory or enzymatic molecules as part of a normal or disease process.

The term "purified" as used herein denotes that the indicated nucleic acid or polypeptide is present in the substantial absence of other biological macromolecules, *e.g.*, polynucleotides, polypeptides, proteins, and the like. In one embodiment, the polynucleotide or polypeptide is purified such that it constitutes at least 95% by weight, more preferably at least 99.8% by weight, of the indicated biological macromolecules present (but water, buffers, and other small molecules, especially molecules having a molecular weight of less than 1000 daltons, can be present).

The term "isolated" as used herein refers to a nucleic acid or polypeptide separated from at least one other component (e.g., nucleic acid or polypeptide) present with the nucleic acid or polypeptide in its natural source. In one embodiment, the nucleic acid or polypeptide is found in the presence of (if anything) only a solvent, buffer, ion, or other component normally present in a solution of the same. The terms "isolated" and "purified" do not encompass nucleic acids or polypeptides present in their natural source.

The term "infection" refers to the introduction of nucleic acids into a suitable host cell by use of a virus or viral vector.

The term "transformation" means introducing DNA into a suitable host cell so that the DNA is replicable, either as an extrachromosomal element, or by chromosomal integration.

The term "transfection" refers to the taking up of an expression vector by a suitable host cell, whether or not any coding sequences are in fact expressed.

The term "intermediate fragment" means a nucleic acid between 5 and 1000 bases in length, and preferably between 10 and 40 bp in length.

The term "secreted" includes a protein that is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence when it is expressed in a suitable host cell. "Secreted" proteins include without limitation proteins secreted wholly (*e.g.*, soluble proteins) or partially (*e.g.*, receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins which are transported across the membrane of the endoplasmic reticulum. "Secreted" proteins are also intended to include proteins containing non-typical signal sequences (e.g. Interleukin-1 Beta, see Krasney, P.A. and Young, P.R. (1992) Cytokine 4(2):134 -143) and factors released from damaged cells (e.g. Interleukin-1 Receptor Antagonist, see Arend, W.P. et. al. (1998) Annu. Rev. Immunol. 16:27-55)

Each of the above terms is meant to encompass all that is described for each, unless the context dictates otherwise.

4.2 NUCLEIC ACIDS AND POLYPEPTIDES OF THE INVENTION

Nucleotide and amino acid sequences of the invention are set forth in the Sequence Listing. Fragments of the polypeptides or proteins of the present

invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the polypeptide or protein may be in linear form or they may be cyclized using known methods, for example, as described in H. U. Saragovi, et al., Bio/Technology 10, 773-778 (1992) and in R. S. McDowell, et al., J. Amer. Chem. Soc. 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding sites. For example, fragments of the polypeptide or protein may be fused through "linker" sequences to the Fc portion of an immunoglobulin. For a bivalent form of the protein, such a fusion could be to the Fc portion of an IgG molecule. Other immunoglobulin isotypes may also be used to generate such fusions. For example, a protein-IgM fusion would generate a decavalent form of the protein of the invention.

The present invention also provides both full-length and mature forms (for example, without a signal sequence or precursor sequence) of the disclosed polypeptides or proteins. The protein coding sequence is identified in the sequence listing by translation of the disclosed nucleotide sequences. The mature form of such protein may be obtained by expression of a full-length polynucleotide in a suitable mammalian cell or other host cell. The sequence of the mature form of the protein is also determinable from the amino acid sequence of the full-length form. Where polypeptides or proteins of the present invention are membrane bound, soluble forms of the polypeptides or proteins are also provided. In such forms, part or all of the regions causing the polypeptides or proteins to be membrane bound are deleted so that the proteins are fully secreted from the cell in which it is expressed.

The polynucleotides of the invention include naturally occurring or wholly or partially synthetic DNA, e.g., cDNA and genomic DNA, and RNA, e.g., mRNA. SEQ ID NO: 1-331 may include all of the coding region of the cDNA or may represent a portion of the coding region of the cDNA. Further 5' and 3' sequence can be obtained using methods known in the art. For example, full length cDNA or genomic DNA that corresponds to any of the polynucleotides of SEQ ID NO: 1-331 can be obtained by screening appropriate cDNA or genomic DNA libraries under suitable hybridization conditions using any of the polynucleotides of SEQ ID NO: 1-331 or a portion thereof as a probe. Alternatively, the

polynucleotides of SEQ ID NO: 1-331 may be used as the basis for suitable primer(s) that allow identification and/or amplification of genes in appropriate genomic DNA or cDNA libraries.

The nucleic acid sequences of the invention, designated as SEQ ID NO: 1-331 can be assembled ESTs and sequences (including cDNA and genomic sequences) obtained from one or more public databases, such as dbEST, gbpri, and UniGene. The sequences falling within the scope of the present invention are not limited to these specific sequences, but also include allelic and species variations thereof. Allelic and species variations can be routinely determined by comparing the sequence provided in SEQ ID NO: 1-331, a representative fragment thereof, or a nucleotide sequence at least 90% identical, preferably 99.9% identical, to SEQ ID NO: 1-331 with a sequence from another isolate of the same species. Furthermore, to accommodate codon variability, the invention includes nucleic acid molecules coding for the same amino acid sequences as do the specific ORFs disclosed herein. In other words, in the coding region of an ORF, substitution of one codon for another which encodes the same amino acid is expressly contemplated.

The nucleic acids of the present invention, designated as SEQ ID NO: 1-331 can be assembled using an EST sequence as a seed. The EST sequence can be extended using programs or algorithms known in the art. Preferably, a recursive algorithm is used to extend the seed EST into an extended assemblage, by pulling additional sequences from different databases (i.e., Hyseq's database containing EST sequences, dbEST version 114, gb pri 114, and UniGene version 101) that belong to this assemblage. The algorithm terminates when there are no additional sequences from the databases that will extend the assemblage. Further, the inclusion of component sequences into the assemblage is preferably based on a BLASTN hit to the extending assemblage with BLAST score greater than 300 and percent identity greater than 95%. BLAST, which stands for Basic Local Alignment Search Tool, is used to search for local sequence alignments (Altschul, S.F., J. Mol. Evol. 36: 290-300 (1993) and Altschul, S.F. et al., J. Mol. Biol., 215: 403-10 (1990)). BLAST produces alignments of both nucleotide and amino acid sequences to determine sequence similarity. Because of the local nature of the alignments, BLAST is especially useful in determining exact matches. The sequences can then be reviewed and edited.

These EST sequences can provide identifying sequence information, representative fragment or segment information, or novel segment information for SEQ ID NO: 1-331.

The nearest neighbor result for SEQ ID NO: 1-331 can be obtained by searching a database using an algorithm or a program. Preferably, a FASTA version 3 search against Genpept, using Fastxy algorithm. The nearest neighbor result shows the closest homologue from Genpept (and contains the translated amino acid sequences for which the nucleic acid sequence encodes).

The present invention also provides genes corresponding to the cDNA sequences disclosed herein. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials.

Species homologs (or orthologs) of the disclosed polynucleotides and polypeptides or proteins are also provided by the present invention. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species.

The invention also encompasses allelic variants of the disclosed polynucleotides or polypeptides; that is, naturally-occurring alternative forms of the isolated polynucleotide which also encode proteins which are identical, homologous or related to that encoded by the polynucleotides.

4.3 NUCLEIC ACIDS OF THE INVENTION

The isolated polynucleotides of the invention include, but are not limited to, a polynucleotide encoding a polypeptide comprising any of the amino acid sequences listed in the Sequence Lisitng; or the mature protein portion thereof. A preferred nucleic acid sequence is set forth as any of the polynucleotides of SEQ ID NO: 1-331.

The isolated polynucleotides of the invention further include, but are not limited to a polynucleotide comprising any of the nucleotide sequence of SEQ ID NO: 1-331; a polynucleotide comprising the full length protein coding sequence of

the polynucleotides of SEQ ID NO: 1-331; and a polynucleotide comprising the nucleotide sequence encoding the mature protein coding sequence of the polynucleotides of SEQ ID NO: 1-331. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that preferably has biological activity and that hybridizes under stringent conditions (a) to the complement of any of the nucleotides sequences of SEQ ID NO: 1-331 (b) to a polynucleotide encoding the polypeptide of any of the amino acid sequences listed in the Sequence Listing; a polynucleotide which is an allelic variant of any polynucleotide recited above; a polynucleotide which encodes a species homolog of any of the polypeptides or proteins recited above; or a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of any of the polypeptides listed in the Sequence Listing. Domains of interest may depend on the nature of the encoded polypeptide; e.g., domains in receptor-like polypeptides include ligand-binding, extracellular, transmembrane, or cytoplasmic domains, or combinations thereof; domains in immunoglobulin-like proteins include the variable immunoglobulin-like domains; domains in enzyme-like polypeptides include catalytic and substrate binding domains; and domains in ligand polypeptides include receptor-binding domains.

Polynucleotides encoding preferred polypeptide truncations of the invention can be used to generate polynucleotides encoding chimeric or fusion proteins comprising one or more domains of the invention and heterologous protein sequences.

The polynucleotides of the invention additionally include the complement of any of the polynucleotides recited above.

The polynucleotides of the invention also provide polynucleotides including nucleotide sequences that are substantially equivalent to the polynucleotides recited above. Polynucleotides according to the invention can have, *e.g.*, at least about 65%, at least about 70%, at least about 75%, at least about 80%, more typically at least about 90%, and even more typically at least about 95%, sequence identity to a polynucleotide recited above. The invention also provides the complement of such polynucleotides. The polynucleotide can be DNA (genomic, cDNA, amplified, or synthetic) or RNA. Methods and algorithms for obtaining such polynucleotides are well known to those of skill in the art and can include, for example, methods for

determining hybridization conditions which can routinely isolate polynucleotides of the desired sequence identities.

A polynucleotide according to the invention can be joined to any of a variety of other nucleotide sequences by well-established recombinant DNA techniques (see Sambrook J et al. (1989) Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY). Useful nucleotide sequences for joining to polynucleotides include an assortment of vectors, e.g., plasmids, cosmids, lambda phage derivatives, phagemids, and the like, that are well known in the art. Accordingly, the invention also provides a vector including a polynucleotide of the invention and a host cell containing the polynucleotide. In general, the vector contains an origin of replication functional in at least one organism, convenient restriction endonuclease sites, and a selectable marker for the host cell. Vectors according to the invention include expression vectors, replication vectors, probe generation vectors, and sequencing vectors. A host cell according to the invention can be a prokaryotic or eukaryotic cell and can be a unicellular organism or part of a multicellular organism.

The sequences falling within the scope of the present invention are not limited to the specific sequences herein described, but also include allelic variations thereof. Allelic variations can be routinely determined by comparing the nucleotide sequences provided in SEQ ID NO: 1-331, a representative fragment thereof, or a nucleotide sequence at least 99.9% identical to any of the nucleotide sequences of SEQ ID NO: 1-331 with a sequence from another isolate of the same species. To accommodate codon variability, the invention includes nucleic acid molecules coding for the same amino acid sequences as do the specific ORFs disclosed herein. In other words, in the coding region of an ORF, substitution of one codon for another which encodes the same amino acid is expressly contemplated. Any specific sequence disclosed herein can be readily screened for errors by resequencing a particular fragment, such as an ORF, in both directions (*i.e.*, sequence both strands).

The present invention further provides recombinant constructs comprising a nucleic acid having any of the nucleotide sequences of SEQ ID NO: 1-331 or a fragment thereof or any other polynucleotides of the invention. In one embodiment, the recombinant constructs of the present invention comprise a vector, such as a

plasmid or viral vector, into which a nucleic acid having any of the nucleotide sequences of SEQ ID NO: 1-331 or a fragment thereof is inserted, in a forward or reverse orientation. In the case of a vector comprising one of the ORFs of the present invention, the vector may further comprise regulatory sequences, including for example, a promoter, operably linked to the ORF. For vectors comprising the EMFs and UMFs of the present invention, the vector may further comprise a marker sequence or heterologous ORF operably linked to the EMF or UMF. Large numbers of suitable vectors and promoters are known to those of skill in the art and are commercially available for generating the recombinant constructs of the present invention. The following vectors are provided by way of example. Bacterial: pBs, phagescript, PsiX174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene); pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia). Eukaryotic: pWLneo, pSV2cat, pOG44, PXTI, pSG (Stratagene) pSVK3, pBPV, pMSG, pSVL (Pharmacia).

The isolated polynucleotide of the invention may be operably linked to an expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman et al., Nucleic Acids Res. 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, Methods in Enzymology 185, 537-566 (1990). As defined herein "operably linked" means that the isolated polynucleotide of the invention and an expression control sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression control sequence.

Promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers. Two appropriate vectors are pKK232-8 and pCM7. Particular named bacterial promoters include lacI, lacZ, T3, T7, gpt, lambda PR, and trc. Eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art. Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transformation of the host cell, *e.g.*, the ampicillin

resistance gene of *E. coli* and *S. cerevisiae* TRP1 gene, and a promoter derived from a highly-expressed gene to direct transcription of a downstream structural sequence. Such promoters can be derived from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK), a-factor, acid phosphatase, or heat shock proteins, among others. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein into the periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an amino terminal identification peptide imparting desired characteristics, *e.g.*, stabilization or simplified purification of expressed recombinant product. Useful expression vectors for bacterial use are constructed by inserting a structural DNA sequence encoding a desired protein together with suitable translation initiation and termination signals in operable reading phase with a functional promoter. The vector will comprise one or more phenotypic selectable markers and an origin of replication to ensure maintenance of the vector and to, if desirable, provide amplification within the host. Suitable prokaryotic hosts for transformation include *E. coli*, *Bacillus subtilis*, *Salmonella typhimurium* and various species within the genera *Pseudomonas*, *Streptomyces*, and *Staphylococcus*, although others may also be employed as a matter of choice.

As a representative but non-limiting example, useful expression vectors for bacterial use can comprise a selectable marker and bacterial origin of replication derived from commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017). Such commercial vectors include, for example, pKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden) and GEM 1 (Promega Biotech, Madison, WI, USA). These pBR322 "backbone" sections are combined with an appropriate promoter and the structural sequence to be expressed. Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter is induced or derepressed by appropriate means (*e.g.*, temperature shift or chemical induction) and cells are cultured for an additional period. Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification.

Included within the scope of the nucleic acid sequences of the invention are nucleic acid sequence fragments that hybridize under stringent conditions to any of the nucleotide sequences of SEQ ID NO: 1-331, or complements thereof, which fragment is greater than about 10 bp, preferably 20 to 50 bp, and even greater than 100 bp, greater than 300 bp, or greater than 500 bp. Fragments of, e.g. 15, 16, or 20 bp or more that are selective for (i.e. specifically hybridize to any one of the polynucleotides of the invention) are contemplated. Probes capable of specifically hybridizing to a polynucleotide can differentiate polynucleotide sequences of the invention from other polynucleotide sequences in the same family of genes or can differentiate human genes from genes of other species, and are preferably based on unique nucleotide sequences.

In accordance with the invention, polynucleotide sequences comprising the mature protein coding sequences corresponding to SEQ ID NO: 1-331, or functional equivalents thereof, may be used to generate recombinant DNA molecules that direct the expression of that nucleic acid, or a functional equivalent thereof, in appropriate host cells. Also included are the cDNA inserts of any of the clones identified herein.

The nucleic acid sequences of the invention are further directed to sequences which encode variants of the described nucleic acids. These amino acid sequence variants may be prepared by methods known in the art by introducing appropriate nucleotide changes into a native or variant polynucleotide. There are two variables in the construction of amino acid sequence variants: the location of the mutation and the nature of the mutation. Nucleic acids encoding the amino acid sequence variants are preferably constructed by mutating the polynucleotide to encode an amino acid sequence that does not occur in nature. These nucleic acid alterations can be made at sites that differ in the nucleic acids from different species (variable positions) or in highly conserved regions (constant regions). Sites at such locations will typically be modified in series, *e.g.*, by substituting first with conservative choices (*e.g.*, hydrophobic amino acid to a different hydrophobic amino acid) and then with more distant choices (*e.g.*, hydrophobic amino acid to a charged amino acid), and then deletions or insertions may be made at the target site. Amino acid sequence deletions generally range from about 1 to 30 residues, preferably about 1 to 10 residues, and are typically contiguous. Amino acid insertions include amino-

and/or carboxyl-terminal fusions ranging in length from one to one hundred or more residues, as well as intrasequence insertions of single or multiple amino acid residues. Intrasequence insertions may range generally from about 1 to 10 amino residues, preferably from 1 to 5 residues. Examples of terminal insertions include the heterologous signal sequences necessary for secretion or for intracellular targeting in different host cells and sequences such as FLAG or poly-histidine sequences useful for purifying the expressed protein.

In a preferred method, polynucleotides encoding the novel amino acid sequences are changed via site-directed mutagenesis. This method uses oligonucleotide sequences to alter a polynucleotide to encode the desired amino acid variant, as well as a sufficient adjacent nucleotides on both sides of the changed amino acid to form a stable duplex on either side of the site of being changed. In general, the techniques of site-directed mutagenesis are well known to those of skill in the art and this technique is exemplified by publications such as, Edelman et al., DNA 2:183 (1983). A versatile and efficient method for producing site-specific changes in a polynucleotide sequence was published by Zoller and Smith, Nucleic Acids Res. 10:6487-6500 (1982). PCR may also be used to create amino acid sequence variants of the novel nucleic acids. When small amounts of template DNA are used as starting material, primer(s) that differs slightly in sequence from the corresponding region in the template DNA can generate the desired amino acid variant. PCR amplification results in a population of product DNA fragments that differ from the polynucleotide template encoding the polypeptide at the position specified by the primer. The product DNA fragments replace the corresponding region in the plasmid and this gives a polynucleotide encoding the desired amino acid variant.

A further technique for generating amino acid variants is the cassette mutagenesis technique described in Wells et al., Gene 34:315 (1985); and other mutagenesis techniques well known in the art, such as, for example, the techniques in Sambrook et al., supra, and Current Protocols in Molecular Biology, Ausubel et al. Due to the inherent degeneracy of the genetic code, other DNA sequences which encode substantially the same or a functionally equivalent amino acid sequence may be used in the practice of the invention for the cloning and expression of these novel nucleic acids. Such DNA sequences include those which are capable

of hybridizing to the appropriate novel nucleic acid sequence under stringent conditions.

Polynucleotides of the invention can also be used to induce immune responses. For example, as described in Fan et al., Nat. Biotech. 17:870-872 (1999), incorporated herein by reference, nucleic acid sequences encoding a polypeptide may be used to generate antibodies against the encoded polypeptide following topical administration of naked plasmid DNA or following injection, and preferably intramuscular injection of the DNA. The nucleic acid sequences are preferably inserted in a recombinant expression vector and may be in the form of naked DNA.

4.4. HOSTS

The present invention further provides host cells genetically engineered to contain the polynucleotides of the invention. For example, such host cells may contain nucleic acids of the invention introduced into the host cell using known transformation, transfection or infection methods. The present invention still further provides host cells genetically engineered to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in the cell.

Knowledge of DNA sequences provided by the invention allows for modification of cells to permit, or increase, expression of endogenous polypeptide. Cells can be modified (e.g., by homologous recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the protein at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the desired protein encoding sequences. See, for example, PCT International Publication No. WO 94/12650, PCT International Publication No. WO 92/20808, and PCT International Publication No. WO 91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (e.g., ada, dhfr, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous

promoter DNA. If linked to the desired protein coding sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the desired protein coding sequences in the cells.

The host cell can be a higher eukaryotic host cell, such as a mammalian cell, a lower eukaryotic host cell, such as a yeast cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. Introduction of the recombinant construct into the host cell can be effected by calcium phosphate transfection, DEAE, dextran mediated transfection, or electroporation (Davis, L. et al., Basic Methods in Molecular Biology (1986)). The host cells containing one of the polynucleotides of the invention, can be used in conventional manners to produce the gene product encoded by the isolated fragment (in the case of an ORF) or can be used to produce a heterologous protein under the control of the EMF.

Any host/vector system can be used to express one or more of the ORFs of the present invention. These include, but are not limited to, eukaryotic hosts such as HeLa cells, Cv-1 cell, COS cells, 293 cells, and Sf9 cells, as well as prokaryotic host such as *E. coli* and *B. subtilis*. The most preferred cells are those which do not normally express the particular polypeptide or protein or which expresses the polypeptide or protein at low natural level. Mature proteins can be expressed in mammalian cells, yeast, bacteria, or other cells under the control of appropriate promoters. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by Sambrook, et al., in Molecular Cloning: A Laboratory Manual, Second Edition, Cold Spring Harbor, New York (1989), the disclosure of which is hereby incorporated by reference.

Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts, described by Gluzman, Cell 23:175 (1981), and other cell lines capable of expressing a compatible vector, for example, the C127, 3T3, CHO, HeLa and BHK cell lines. Mammalian expression vectors will comprise an origin of replication, a suitable promoter and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5′ flanking nontranscribed sequences.

DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early promoter, enhancer, splice, and polyadenylation sites may be used to provide the required nontranscribed genetic elements. Recombinant polypeptides and proteins produced in bacterial culture are usually isolated by initial extraction from cell pellets, followed by one or more salting-out, aqueous ion exchange or size exclusion chromatography steps. Protein refolding steps can be used, as necessary, in completing configuration of the mature protein. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps. Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents.

A number of types of cells may act as suitable host cells for expression of the polypeptide or protein. Mammalian host cells include, for example, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3 cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from *in vitro* culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL-60, U937, HaK or Jurkat cells.

Alternatively, it may be possible to produce the polypeptide or protein in lower eukaryotes such as yeast, insects or in prokaryotes such as bacteria. Potentially suitable yeast strains include *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Kluyveromyces* strains, *Candida*, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include *Escherichia coli, Bacillus subtilis, Salmonella typhimurium*, or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous

recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or polypeptide or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequence include polyadenylation signals, mRNA stability elements, splice sites, leader sequences for enhancing or modifying transport or secretion properties of the polypeptide or protein, or other sequences which alter or improve the function or stability of polypeptide or protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, *e.g.*, inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the host cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (gpt) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

4.5. POLYPEPTIDES OF THE INVENTION

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising: any one of the amino acid sequences set forth in the Sequence Listing; or an amino acid sequence encoded by any one of the nucleotide sequences designated as SEQ ID NO: 1-331; or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides preferably with biological or immunological activity that are encoded by: (a) a polynucleotide having any one of the nucleotide sequences set forth in SEQ ID NO: 1-331; or (b) polynucleotides encoding any of the amino acid sequences set forth in the Sequence Listing; or (c) polynucleotides that hybridize to the complement of the polynucleotides of either (a) or (b) under stringent hybridization conditions. The invention also provides biologically active or immunologically active variants of any of the polypeptide amino acid sequences set forth in the Sequence Listing, or the corresponding full length or mature protein; and "substantial equivalents" thereof (e.g., with at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, typically at least about 95%, more typically at least about 98%, or most typically at least about 99% amino acid identity) that retain biological activity. Polypeptides encoded by allelic variants may have a similar, increased, or decreased activity compared to polypeptides comprising any one of the amino acid sequences set forth in the Sequence Listing.

Polypeptide compositions of the present invention may further comprise an acceptable carrier, such as a hydrophilic, *e.g.*, pharmaceutically acceptable, carrier.

The invention also relates to methods for producing a polypeptide comprising growing a culture of host cells of the invention in a suitable culture medium, and purifying the polypeptide or protein from the cells or the culture in which the cells are grown. For example, the methods of the invention include a

process for producing a polypeptide in which a host cell containing a suitable expression vector that includes a polynucleotide of the invention is cultured under conditions that allow expression of the encoded polypeptide. The polypeptide can be recovered from the culture, conveniently from the culture medium, or from a lysate prepared from the host cells and further purified. Preferred embodiments include those in which the protein produced by such process is a full length or mature form of the protein.

The present invention further provides isolated polypeptides encoded by the nucleic acid fragments of the present invention or by degenerate variants of the nucleic acid fragments of the present invention. By "degenerate variant" is intended nucleotide fragments which differ from a nucleic acid fragment of the present invention (*e.g.*, an ORF) by nucleotide sequence but, due to the degeneracy of the genetic code, encode an identical polypeptide sequence. Preferred nucleic acid fragments of the present invention are the ORFs that encode proteins. A variety of methodologies known in the art can be utilized to obtain any one of the isolated polypeptides or proteins of the present invention. At the simplest level, the amino acid sequence can be synthesized using commercially available peptide synthesizers. This technique is particularly useful in producing small peptides and fragments of larger polypeptides. Fragments are useful, for example, in generating antibodies against the native polypeptide. In an alternative method, the polypeptide or protein is purified from bacterial cells which naturally produce the polypeptide or protein. One skilled in the art can readily follow known methods for isolating polypeptides and proteins in order to obtain one of the isolated polypeptides or proteins of the present invention. These include, but are not limited to, immunochromatography, HPLC, size-exclusion chromatography, ion-exchange chromatography, and immuno-affinity chromatography. See, *e.g.*, Scopes, Protein Purification: Principles and Practice, Springer-Verlag (1994); Sambrook, et al., in Molecular Cloning: A Laboratory Manual; Ausubel et al., Current Protocols in Molecular Biology. Polypeptide fragments that retain biological/immunological activity include fragments encoding greater than about 100 amino acids, or greater than about 200 amino acids, and fragments that encode specific protein domains.

The polypeptides or proteins of the present invention can alternatively be purified from cells which have been altered to express the desired polypeptide or

protein. As used herein, a cell is said to be altered to express a desired polypeptide or protein when the cell, through genetic manipulation, is made to produce a polypeptide or protein which it normally does not produce or which the cell normally produces at a lower level. One skilled in the art can readily adapt procedures for introducing and expressing either recombinant or synthetic sequences into eukaryotic or prokaryotic cells in order to generate a cell which produces one of the polypeptides of the present invention.

The polypeptide or protein of the invention may also be expressed as a product of transgenic animals, *e.g.*, as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the polypeptide.

The polypeptide or protein may also be produced by known conventional chemical synthesis. Methods for constructing the proteins of the present invention by synthetic means are known to those skilled in the art. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

The polypeptides or proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or deliberately engineered. For example, modifications in the peptide or DNA sequences can be made by those skilled in the art using known techniques. Modifications of interest in the polypeptide or protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, *e.g.*, U.S. Pat. No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein. Regions of the protein that are important for the protein function can be

determined by various methods known in the art including the alanine-scanning method which involved systematic substitution of single or strings of amino acids with alanine, followed by testing the resulting alanine-containing variant for biological activity. This type of analysis determines the importance of the substituted amino acid(s) in biological activity.

Other fragments and derivatives of the sequences of polypeptides or proteins which would be expected to retain protein activity in whole or in part and are useful for screening or other immunological methodologies may also be easily made by those skilled in the art given the disclosures herein. Such modifications are encompassed by the present invention.

The polypeptide or protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, *e.g.*, Invitrogen, San Diego, Calif., U.S.A. (the MaxBat™ kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed."

The polypeptide or protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (*i.e.*, from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearl™ or Cibacrom blue 3GA Sepharose™; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

Alternatively, the polypeptide or protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX), or as a His tag. Kits for

expression and purification of such fusion proteins are commercially available from New England BioLab (Beverly, Mass.), Pharmacia (Piscataway, N.J.) and Invitrogen, respectively. The polypeptide or protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("FLAG®") is commercially available from Kodak (New Haven, Conn.).

Finally, one or more reverse-phase high performance liquid chromatography (RP- HPLC) steps employing hydrophobic RP-HPLC media, *e.g.*, silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

The polypeptides of the invention include analogs (variants). Analogs embrace fragments, as well as antagonists which comprise one or more amino acids deleted, inserted, or substituted. Analogs of the invention also embrace fusions of the polypeptide of the invention or modifications of the polypeptide of the invention or analog is fused to another moiety or moieties, *e.g.*, targeting moiety, imaging moiety or another therapeutic agent. Such analogs may exhibit improved properties such as activity and/or stability. Examples of moieties which may be fused to polypeptides of the invention or analogs thereof include, for example, targeting moieties which provide for the delivery of polypeptide to desired cell types. Other moieties which may be fused to the polypeptides of the invention include therapeutic agents which are used for treatment of disorders described herein.

4.5.1 DETERMINING POLYPEPTIDE AND POLYNUCLEOTIDE IDENTITY AND SIMILARITY

Preferred identity and/or similarity are designed to give the largest match between the sequences tested. Methods to determine identity and similarity are codified in publicly available computer programs including, but are not limited to, the GCG program package, including GAP (Devereux, J., et al., Nucleic Acids Research 12(1):387 (1984); Genetics Computer Group, University of Wisconsin, Madison, WI), BLASTP, BLASTN, BLASTX, and FASTA (Atschul, S.F. et al., J.

Molec. Biol. 215:403-410 (1990). The BLAST X program is publicly available from the National Center for Biotechnology Information (NCBI) and other sources (BLAST Manual, Altschul, S., et al. NCB NLM NIH Bethesda, MD 20894; Altschul, S., et al., J. Mol. Biol. 215:403-410 (1990). The preferred computer program is FASTA version 3, specifically the FASTy program within the FASTA program package. Another preferred algorithm is the well-known Smith Waterman algorithm which can also be used to determine identity.

4.6 GENE THERAPY

Mutations in the polynucleotides of the invention gene may result in loss of normal function of the encoded protein. The invention thus provides gene therapy to restore normal activity of the polypeptides of the invention; or to treat disease states involving polypeptides of the invention. Delivery of a functional genes encoding polypeptides of the invention to appropriate cells is effected *ex vivo*, *in situ*, or *in vivo* by use of vectors, and more particularly viral vectors (e.g., adenovirus, adeno-associated virus, or a retrovirus), or ex vivo by use of physical DNA transfer methods (e.g., liposomes or chemical treatments). See, for example, Anderson, Nature, supplement to vol. 392, no. 6679, pp.25-20 (1998). For additional reviews of gene therapy technology see Friedmann, Science, 244: 1275-1281 (1989); Verma, Scientific American: 68-84 (1990); and Miller, Nature, 357: 455-460 (1992). Introduction of any one of the nucleotides of the present invention or a gene encoding the polypeptides of the present invention can also be accomplished with extrachromosomal substrates (transient expression) or artificial chromosomes (stable expression). Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced in vivo for therapeutic purposes. Alternatively, it is contemplated that in other human disease states, preventing the expression of or inhibiting the activity of polypeptides of the invention will be useful in treating the disease states. It is contemplated that antisense therapy or gene therapy could be applied to negatively regulate the expression of polypeptides of the invention.

Other methods inhibiting expression of a protein include the introduction of antisense molecules to the nucleic acids of the present invention, their complements,

or their translated RNA sequences, by methods known in the art, the removal of the nucleic acids of the present invention such as using targeted deletion methods, or the insertion of a negative regulatory element such as a silencer, which is tissue specific. Further, the polypeptides of the present invention can be inhibited by the introduction of antisense molecules that hybridize to nucleic acids that encode for the polypeptides of the present invention and by the removal of a gene that encode for the polypeptides of the present invention.

The present invention still further provides cells genetically engineered *in vivo* to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in the cell. These methods can be used to increase or decrease the expression of the polynucleotides of the present invention.

Knowledge of DNA sequences provided by the invention allows for modification of cells to permit, increase, or decrease, expression of endogenous polypeptide. Cells can be modified (e.g., by homologous recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the protein at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the desired protein encoding sequences. See, for example, PCT International Publication No. WO 94/12650, PCT International Publication No. WO 92/20808, and PCT International Publication No. WO 91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (e.g., ada, dhfr, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the desired protein coding sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the desired protein coding sequences in the cells.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's

existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequence include polyadenylation signals, mRNA stability elements, splice sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, *e.g.*, inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (gpt) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S.

Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

4.7 TRANSGENIC ANIMALS

In preferred methods to determine biological functions of the polypeptides of the invention in vivo, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of a polynucleotides of the invention promoter is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provid for increased protein expression. The homologous promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

4.8. USES AND BIOLOGICAL ACTIVITY

The polynucleotides and polypeptides of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated

with assays cited herein) identified herein. Uses or activities described for polypeptides or proteins of the present invention may be provided by administration or use of such polypeptides or proteins or of polynucleotides encoding such polypeptides or proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA). The mechanism underlying the particular condition or pathology will dictate whether the polypeptides of the invention, the polynucleotides of the invention or modulators (activators or inhibitors) thereof would be beneficial to the subject in need of treatment. Thus, "therapeutic compositions of the invention" include compositions comprising isolated polynucleotides (including recombinant DNA molecules, cloned genes and degenerate variants thereof) or polypeptides of the invention (including full length protein, mature protein and truncations or domains thereof), or compounds and other substances that modulate the overall activity of the target gene products, either at the level of target gene/protein expression or target protein activity. Such modulators include polypeptides, analogs, (variants), including fragments and fusion proteins, antibodies and other binding proteins; chemical compounds that directly or indirectly activate or inhibit the polypeptides of the invention (identified, e.g., via drug screening assays as described herein); antisense polynucleotides and polynucleotides suitable for triple helix formation; and in particular antibodies or other binding partners that specifically recognize one or more epitopes of the polypeptides of the invention.

The polypeptide or protein of the present invention may likewise be involved in cellular activation or in one of the other physiological pathways described herein.

4.8.1. RESEARCH USES AND UTILITIES

The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic

disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., Cell 75:791-803 (1993)) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The polypeptides or proteins provided by the present invention can similarly be used in assays to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the polypeptide or protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding polypeptide or protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Where the protein binds or potentially binds to another polypeptide or protein (such as, for example, in a receptor-ligand interaction), the polypeptide or protein can be used to identify the other polypeptide or protein with which binding occurs or to identify inhibitors of the binding interaction. Polypeptides or proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E. F. Fritsch and T. Maniatis eds., 1989, and

"Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S. L. and A. R. Kimmel eds., 1987.

4.8.2. NUTRITIONAL USES

Polynucleotides and polypeptides or proteins of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the polypeptide or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the polypeptide or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

4.8.3. CYTOKINE AND CELL PROLIFERATION/DIFFERENTIATION ACTIVITY

A polypeptide of the present invention may exhibit activity relating to cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Many polypeptide or protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor-dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of therapeutic compositions of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+(preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e, CMK, HUVEC, and Caco. Therapeutic compositions of the invention can be used in the following:

Assays for T-cell or thymocyte proliferation include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse

Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Bertagnolli et al., J. Immunol. 145:1706-1712, 1990; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Bertagnolli, et al., I. Immunol. 149:3778-3783, 1992; Bowman et al., I. Immunol. 152:1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A. M. and Shevach, E. M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human interleukin-γ, Schreiber, R. D. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L. S. and Lipsky, P. E. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., J. Exp. Med. 173:1205-1211, 1991; Moreau et al., Nature 336:690-692, 1988; Greenberger et al., Proc. Natl. Acad. Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse and human interleukin 6--Nordan, R. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., Proc. Natl. Aced. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11--Bennett, F., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 9--Ciarletta, A., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W Strober, Pub. Greene Publishing

Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

4.8.4 STEM CELL GROWTH FACTOR ACTIVITY

A polypeptide of the present invention may exhibit stem cell growth factor activity and be involved in the proliferation, differentiation and survival of pluripotent and totipotent stem cells including primordial germ cells, embryonic stem cells, hematopoietic stem cells and/or germ line stem cells. Administration of the polypeptide of the invention to stem cells in vivo or ex vivo is expected to maintain and expand cell populations in a totipotential or pluripotential state which would be useful for re-engineering damaged or diseased tissues, transplantation, manufacture of bio-pharmaceuticals and the development of bio-sensors. The ability to produce large quantities of human cells has important working applications for the production of human proteins which currently must be obtained from non-human sources or donors, implantation of cells to treat diseases such as Parkinson's, Alzheimer's and other neurodegenerative diseases; tissues for grafting such as bone marrow, skin, cartilage, tendons, bone, muscle (including cardiac muscle), blood vessels, cornea, neural cells, gastrointestinal cells and others; and organs for transplantation such as kidney, liver, pancreas (including islet cells), heart and lung.

It is contemplated that multiple different exogenous growth factors and/or cytokines may be administered in combination with the polypeptide of the invention to achieve the desired effect, including any of the growth factors listed herein, other stem cell maintenance factors, and specifically including stem cell factor (SCF), leukemia inhibitory factor (LIF), Flt-3 ligand (Flt-3L), any of the interleukins, recombinant soluble IL-6 receptor fused to IL-6, macrophage inflammatory protein 1-alpha (MIP-1-alpha), G-CSF, GM-CSF, thrombopoietin (TPO), platelet factor 4 (PF-4), platelet-derived growth factor (PDGF), neural growth factors and basic fibroblast growth factor (bFGF).

Since totipotent stem cells can give rise to virtually any mature cell type, expansion of these cells in culture will facilitate the production of large quantities of mature cells. Techniques for culturing stem cells are known in the art and administration of polypeptides of the invention, optionally with other growth factors and/or cytokines, is expected to enhance the survival and proliferation of the stem cell populations. This can be accomplished by direct administration of the polypeptide of the invention to the culture medium. Alternatively, stroma cells transfected with a polynucleotide that encodes for the polypeptide of the invention can be used as a feeder layer for the stem cell populations in culture or in vivo. Stromal support cells for feeder layers may include embryonic bone marrow fibroblasts, bone marrow stromal cells, fetal liver cells, or cultured embryonic fibroblasts (see U.S. Patent No.; 5,690,926).

Stem cells themselves can be transfected with a polynucleotide of the invention to induce autocrine expression of the polypeptide of the invention. This will allow for generation of undifferentiated totipotential/pluripotential stem cell lines that are useful as is or that can then be differentiated into the desired mature cell types. These stable cell lines can also serve as a source of undifferentiated totipotential/pluripotential mRNA to create cDNA libraries and templates for polymerase chain reaction experiments. These studies would allow for the isolation and identification of differentially expressed genes in stem cell populations that regulate stem cell proliferation and/or maintenance.

Expansion and maintenance of totipotent stem cell populations will be useful in the treatment of many pathological conditions. For example, polypeptides of the present invention may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease, accidental damage or genetic disorders. The polypeptide of the invention may be useful for inducing the proliferation of neural cells and for the regeneration of nerve and brain tissue, i.e. for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders which involve degeneration, death or trauma to neural cells or nerve tissue. In addition, the expanded stem cell populations can also be genetically altered for gene therapy purposes and to decrease host rejection of replacement tissues after grafting or implantation.

Expression of the polypeptide of the invention and its effect on stem cells can also be manipulated to achieve controlled differentiation of the stem cells into more differentiated cell types. A broadly applicable method of obtaining pure populations of a specific differentiated cell type from undifferentiated stem cell populations involves the use of a cell-type specific promoter driving a selectable marker. The selectable marker allows only cells of the desired type to survive. For example, stem cells can be induced to differentiate into cardiomyocytes (Wobus et al., Differentiation, 48: 173-182 , (1991); Klug et al., J. Clin. Invest., 98(1): 216-224, (1998)) or skeletal muscle cells (Browder, L. W. In: *Principles of Tissue Engineering eds.* Lanza et al., Academic Press (1997)). Alternatively, directed differentiation of stem cells can be accomplished by culturing the stem cells in the presence of a differentiation factor such as retinoic acid and an antagonist of the polypeptide of the invention which would inhibit the effects of endogenous stem cell factor activity and allow differentiation to proceed.

In vitro cultures of stem cells can be used to determine if the polypeptide of the invention exhibits stem cell growth factor activity. Stem cells are isolated from any one of various cell sources (including hematopoietic stem cells and embryonic stem cells) and cultured on a feeder layer, as described by Thompson et al. Proc. Natl. Acad. Sci, U.S.A., 92: 7844-7848 (1995), in the presence of the polypeptide of the invention alone or in combination with other growth factors or cytokines. The ability of the polypeptide of the invention to induce stem cells proliferation is determined by colony formation on semi-solid support e.g. as described by Bernstein et al., Blood, 77: 2316-2321 (1991).

4.8.5. HEMATOPOIESIS REGULATING ACTIVITY

A polypeptide or protein of the present invention may be involved in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell deficiencies. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or

erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either in-vivo or ex-vivo (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

Therapeutic compositions of the invention can be used in the following:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al., Molecular and Cellular Biology 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M. G. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, N.Y. 1994; Hirayama et al., Proc. Natl. Acad. Sci. USA 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I. K. and Briddell, R. A. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, N.Y. 1994; Neben et al., Experimental Hematology 22:353-359, 1994;

Cobblestone area forming cell assay, Ploemacher, R. E. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, N.Y. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, N.Y. 1994; Long term culture initiating cell assay, Sutherland, H. J. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, N.Y. 1994.

4.8.6 IMMUNE STIMULATING OR SUPPRESSING ACTIVITY

Compositions of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A polynucleotide of the invention can encode a polypeptide involved in such activities. A protein or antibody, other binding partner, or other modulator of the invention may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), *e.g.*, in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases caused by viral, bacterial, fungal or other infection may be treatable using a protein, antibody, binding partner, or other modulator of the invention, including infections by HIV, hepatitis viruses, herpesviruses, mycobacteria, Leishmania spp., malaria spp. and various fungal infections such as candidiasis, as well as other conditions where a boost to the immune system generally may be desirable, e.g., in the treatment of cancer.

Autoimmune disorders which may involve a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a polypeptide or protein of the present invention may also to be

involved in allergic reactions and conditions, such as asthma (particularly allergic asthma), bronchitis or other respiratory problems.

Using the polypeptides or proteins, antibody, binding partners, or other modulators of the invention it may also be possible to modulate immune responses, in a number of ways. The immune response may be enhanced or suppressed. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing the immune response, e.g., preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a molecule which inhibits or blocks the immune response (e.g. a receptor fragment, binding partner, or other modulator such as antisense polynucleotides) may act as an immunosuppressant.

The efficacy of particular immune response modulators in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins *in vivo* as described in Lenschow et al., Science 257:789-792 (1992) and Turka et al., Proc. Natl. Acad. Sci USA, 89:11102-11105

(1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of blocking B lymphocyte antigen function *in vivo* on the development of that disease.

Blocking the inflammatory response may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block costimulation of T cells can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythmatosis in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response may be useful in cases of viral infection such as influenza, the common cold, and encephalitis.

Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells *in vitro* and reintroducing the *in vitro* activated T cells into the patient.

The activity of therapeutic compositions of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E.

Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., I. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Bowmanet al., J. Virology 61:1992-1998; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. Immunol. 144:3028-3033, 1990; and Assays for B cell function: *In vitro* antibody production, Mond, J. J. and Brunswick, M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., Journal of Experimental Medicine 173:549-559, 1991; Macatonia et al., Journal of Immunology 154:5071-5079, 1995; Porgador et al., Journal of Experimental Medicine 182:255-260, 1995; Nair et al., Journal of Virology 67:4062-4069, 1993;

Huang et al., Science 264:961-965, 1994; Macatonia et al., Journal of Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation 94:797-807, 1994; and Inaba et al., Journal of Experimental Medicine 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International Journal of Oncology 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad Sci. USA 88:7548-7551, 1991.

4.8.7 TISSUE GROWTH ACTIVITY

A polypeptide or protein of the present invention also may be involved in bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as in wound healing and tissue repair and replacement, and in healing of burns, incisions and ulcers.

For example, induction of cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Compositions of a protein, antibody, binding partner, or other modulator of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A polypeptide or protein of this invention may also be involved in attracting bone-forming cells, stimulating growth of bone-forming cells, or inducing differentiation of progenitors of bone-forming cells. Treatment of osteoporosis, osteoarthritis, bone degenerative disorders, or periodontal disease, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes may also be possible using the composition of the invention.

Another category of tissue regeneration activity that may involve the protein of the present invention is tendon/ligament formation. Induction of tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors *ex vivo* for return *in vivo* to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The compositions of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, i.e. for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or

trauma to neural cells or nerve tissue. More specifically, a composition may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a composition of the invention.

Compositions of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

Compositions of the present invention may also be involved in the generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Inhibition or modulation of fibrotic scarring may allow normal tissue to regenerate.

A composition of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A composition of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

Therapeutic compositions of the invention can be used in the following:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, H. I. and

Rovee, D. T., eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

4.8.8 ACTIVIN/INHIBIN ACTIVITY

A polypeptide or protein of the present invention may also exhibit activin- or inhibin-related activities. A polynucleotide of the invention may encode a polypeptide exhibiting such characteristics. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins and are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a polypeptide or protein of the present invention, alone or in heterodimers with a member of the inhibin family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the polypeptide or protein of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, U.S. Pat. No. 4,798,885. A polypeptide or protein of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as, but not limited to, cows, sheep and pigs.

The activity of a polypeptide or protein of the invention may, among other means, be measured by the following methods.

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., Endocrinology 91:562-572, 1972; Ling et al., Nature 321:779-782, 1986; Vale et al., Nature 321:776-779, 1986; Mason et al., Nature 318:659-663, 1985; Forage et al., Proc. Natl. Acad. Sci. USA 83:3091-3095, 1986.

4.8.9 CHEMOTACTIC/CHEMOKINETIC ACTIVITY

A polypeptide or protein of the present invention may be involved in chemotactic or chemokinetic activity for mammalian cells, including, for example,

monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Chemotactic and chemokinetic receptor activation can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic compositions (e.g. proteins, antibodies, binding partners, or modulators of the invention) provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

Therapeutic compositions of the invention can be used in the following:

Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Marguiles, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25:1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153:1762-1768, 1994.

4.8.10 HEMOSTATIC AND THROMBOLYTIC ACTIVITY

A polypeptide or protein of the invention may also be involved in hemostatis or thrombolysis or thrombosis. A polynucleotide of the invention can encode a

polypeptide exhibiting such attributes. Compositions may be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A composition of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

Therapeutic compositions of the invention can be used in the following:

Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

4.8.11 CANCER DIAGNOSIS AND THERAPY

Polypeptides of the invention may be involved in cancer cell generation, proliferation or metastasis. Detection of the presence or amount of polynucleotides or polypeptides of the invention may be useful for the diagnosis and/or prognosis of one or more types of cancer. For example, the presence or increased expression of a polynucleotide/polypeptide of the invention may indicate a hereditary risk of cancer, a precancerous condition, or an ongoing malignancy. Conversely, a defect in the gene or absence of the polypeptide may be associated with a cancer condition. Identification of single nucleotide polymorphisms associated with cancer or a predisposition to cancer may also be useful for diagnosis or prognosis.

Cancer treatments promote tumor regression by inhibiting tumor cell proliferation, inhibiting angiogenesis (growth of new blood vessels that is necessary to support tumor growth) and/or prohibiting metastasis by reducing tumor cell motility or invasiveness. Therapeutic compositions of the invention may be effective in adult and pediatric oncology including in solid phase tumors/malignancies, locally advanced tumors, human soft tissue sarcomas, metastatic cancer, including lymphatic metastases, blood cell malignancies including multiple myeloma, acute and chronic leukemias, and lymphomas, head and neck cancers including mouth cancer, larynx cancer and thyroid cancer, lung cancers including small cell carcinoma and non-small cell cancers, breast cancers including

small cell carcinoma and ductal carcinoma, gastrointestinal cancers including esophageal cancer, stomach cancer, colon cancer, colorectal cancer and polyps associated with colorectal neoplasia, pancreatic cancers, liver cancer, urologic cancers including bladder cancer and prostate cancer, malignancies of the female genital tract including ovarian carcinoma, uterine (including endometrial) cancers, and solid tumor in the ovarian follicle, kidney cancers including renal cell carcinoma, brain cancers including intrinsic brain tumors, neuroblastoma, astrocytic brain tumors, gliomas, metastatic tumor cell invasion in the central nervous system, bone cancers including osteomas, skin cancers including malignant melanoma, tumor progression of human skin keratinocytes, squamous cell carcinoma, basal cell carcinoma, hemangiopericytoma and Karposi's sarcoma.

Polypeptides, polynucleotides, or modulators of polypeptides of the invention (including inhibitors and stimulators of the biological activity of the polypeptide of the invention) may be administered to treat cancer. Therapeutic compositions can be administered in therapeutically effective dosages alone or in combination with adjuvant cancer therapy such as surgery, chemotherapy, radiotherapy, thermotherapy, and laser therapy, and may provide a beneficial effect, e.g. reducing tumor size, slowing rate of tumor growth, inhibiting metastasis, or otherwise improving overall clinical condition, without necessarily eradicating the cancer.

The composition can also be administered in therapeutically effective amounts as a portion of an anti-cancer cocktail. An anti-cancer cocktail is a mixture of the polypeptide or modulator of the invention with one or more anti-cancer drugs in addition to a pharmaceutically acceptable carrier for delivery. The use of anti-cancer cocktails as a cancer treatment is routine. Anti-cancer drugs that are well known in the art and can be used as a treatment in combination with the polypeptide or modulator of the invention include: Actinomycin D, Aminoglutethimide, Asparaginase, Bleomycin, Busulfan, Carboplatin, Carmustine, Chlorambucil, Cisplatin (cis-DDP), Cyclophosphamide, Cytarabine HCl (Cytosine arabinoside), Dacarbazine, Dactinomycin, Daunorubicin HCl, Doxorubicin HCl, Estramustine phosphate sodium, Etoposide (V16-213), Floxuridine, 5-Fluorouracil (5-Fu), Flutamide, Hydroxyurea (hydroxycarbamide), Ifosfamide, Interferon Alpha-2a, Interferon Alpha-2b, Leuprolide acetate (LHRH-releasing factor analog),

Lomustine, Mechlorethamine HCl (nitrogen mustard), Melphalan, Mercaptopurine, Mesna, Methotrexate (MTX), Mitomycin, Mitoxantrone HCl, Octreotide, Plicamycin, Procarbazine HCl, Streptozocin, Tamoxifen citrate, Thioguanine, Thiotepa, Vinblastine sulfate, Vincristine sulfate, Amsacrine, Azacitidine, Hexamethylmelamine, Interleukin-2, Mitoguazone, Pentostatin, Semustine, Teniposide, and Vindesine sulfate.

In addition, therapeutic compositions of the invention may be used for prophylactic treatment of cancer. There are hereditary conditions and/or environmental situations (e.g. exposure to carcinogens) known in the art that predispose an individual to developing cancers. Under these circumstances, it may be beneficial to treat these individuals with therapeutically effective doses of the polypeptide of the invention to reduce the risk of developing cancers.

In vitro models can be used to determine the effective doses of the polypeptide of the invention as a potential cancer treatment. These in vitro models include proliferation assays of cultured tumor cells, growth of cultured tumor cells in soft agar (see Freshney, (1987) Culture of Animal Cells: A Manual of Basic Technique, Wily-Liss, New York, NY Ch 18 and Ch 21), tumor systems in nude mice as described in Giovanella et al., J. Natl. Can. Inst., 52: 921-30 (1974), mobility and invasive potential of tumor cells in Boyden Chamber assays as described in Pilkington et al., Anticancer Res., 17: 4107-9 (1997), and angiogenesis assays such as induction of vascularization of the chick chorioallantoic membrane or induction of vascular endothelial cell migration as described in Ribatta et al., Intl. J. Dev. Biol., 40: 1189-97 (1999) and Li et al., Clin. Exp. Metastasis, 17:423-9 (1999) respectively. Suitable tumor cells lines are available, e.g. from American Type Tissue Culture Collection catalogs.

4.8.12 RECEPTOR/LIGAND ACTIVITY

A polypeptide or protein of the present invention may also demonstrate activity as receptor, receptor ligand or inhibitor or agonist of receptor/ligand interactions. A polynucleotide of the invention can encode a polypeptide exhibiting such characteristics. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions

and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses. Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A polypeptide or protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a polypeptide or protein of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley- Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1- 7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

By way of example, the polypeptides of the invention may be used as a receptor for a ligand(s) thereby transmitting the biological activity of that ligand(s). Ligands may be identified through binding assays, affinity chromatography, dihybrid screening assays, BIAcore assays, gel overlay assays, or other methods known in the art.

Studies characterizing drugs or proteins as agonist or antagonist or partial agonists or a partial antagonist require the use of other proteins as competing ligands. The polypeptides of the present invention or ligand(s) thereof may be labeled by being coupled to radioisotopes, colorimetric molecules or a toxin molecules by conventional methods. ("Guide to Protein Purification" Murray P. Deutscher (ed) Methods in Enzymology Vol. 182 (1990) Academic Press, Inc. San Diego). Examples of radioisotopes include, but are not limited to, tritium and carbon-14 . Examples of colorimetric molecules include, but are not limited to, fluorescent molecules such as fluorescamine, or rhodamine or other colorimetric molecules. Examples of toxins include, but are not limited, to ricin.

4.8.13 DRUG SCREENING

This invention is particularly useful for screening chemical compounds by using the novel polypeptides or binding fragments thereof in any of a variety of drug screening techniques. The polypeptides or fragments employed in such a test may either be free in solution, affixed to a solid support, borne on a cell surface or located intracellularly. One method of drug screening utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids expressing the polypeptide or fragment. Drugs are screened against such transformed cells in competitive binding assays. Such cells, either in viable or fixed form, can be used for standard binding assays. One may measure, for example, the formation of complexes between polypeptides of the invention or fragments and the agent being tested or examine the diminution in complex formation between the novel polypeptides and an appropriate cell line, which are well known in the art.

Sources for test compounds that may be screened for ability to bind to or modulate (i.e., increase or decrease) the activity of polypeptides of the invention include (1) inorganic and organic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of either random or mimetic peptides, oligonucleotides or organic molecules.

Chemical libraries may be readily synthesized or purchased from a number of commercial sources, and may include structural analogs of known compounds or compounds that are identified as "hits" or "leads" via natural product screening.

The sources of natural product libraries are microorganisms (including bacteria and fungi), animals, plants or other vegetation, or marine organisms, and libraries of mixtures for screening may be created by: (1) fermentation and extraction of broths from soil, plant or marine microorganisms or (2) extraction of the organisms themselves. Natural product libraries include polyketides, non-ribosomal peptides, and (non-naturally occurring) variants thereof. For a review, see *Science 282*:63-68 (1998).

Combinatorial libraries are composed of large numbers of peptides, oligonucleotides or organic compounds and can be readily prepared by traditional automated synthesis methods, PCR, cloning or proprietary synthetic methods. Of particular interest are peptide and oligonucleotide combinatorial libraries. Still

other libraries of interest include peptide, protein, peptidomimetic, multiparallel synthetic collection, recombinatorial, and polypeptide libraries. For a review of combinatorial chemistry and libraries created therefrom, see Myers, *Curr. Opin. Biotechnol.* 8:701-707 (1997). For reviews and examples of peptidomimetic libraries, see Al-Obeidi et al., *Mol. Biotechnol,* 9(3):205-23 (1998); Hruby et al., *Curr Opin Chem Biol,* 1(1):114-19 (1997); Dorner et al., *Bioorg Med Chem,* 4(5):709-15 (1996) (alkylated dipeptides).

Identification of modulators through use of the various libraries described herein permits modification of the candidate "hit" (or "lead") to optimize the capacity of the "hit" to bind a polypeptide of the invention. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

The binding molecules thus identified may be complexed with toxins, e.g., ricin or cholera, or with other compounds that are toxic to cells such as radioisotopes. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for a polypeptide of the invention. Alternatively, the binding molecules may be complexed with imaging agents for targeting and imaging purposes.

4.8.14 ASSAY FOR RECEPTOR ACTIVITY

The invention also provides methods to detect specific binding of a polypeptide e.g. a ligand or a receptor. The art provides numerous assays particularly useful for identifying previously unknown binding partners for receptor polypeptides of the invention. For example, expression cloning using mammalian or bacterial cells, or dihybrid screening assays can be used to identify polynucleotides encoding binding partners. As another example, affinity chromatography with the appropriate immobilized polypeptide of the invention can be used to isolate polypeptides that recognize and bind polypeptides of the invention (represented by the nucleotide or amino acid sequences set forth in the Sequence Listing. There are a number of different libraries used for the identification of compounds, and in particular small molecule, that modulate (*i.e.,* increase or decrease) biological

activity of a polypeptide of the invention. Ligands for receptor polypeptides of the invention can also be identified by adding exogenous ligands, or cocktails of ligands to two cells populations that are genetically identical except for the expression of the receptor of the invention: one cell population expresses the receptor of the invention whereas the other does not. The response of the two cell populations to the addition of ligands(s) are then compared. Alternatively, an expression library can be co-expressed with the polypeptide of the invention in cells and assayed for an autocrine response to identify potential ligand(s). As still another example, BIAcore assays, gel overlay assays, or other methods known in the art can be used to identify binding partner polypeptides, including, (1) organic and inorganic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of random peptides, oligonucleotides or organic molecules.

The role of downstream intracellular signaling molecules in the signaling cascade of the polypeptide of the invention can be determined. For example, a chimeric protein in which the cytoplasmic domain of the polypeptide of the invention is fused to the extracellular portion of a protein, whose ligand has been identified, is produced in a host cell. The cell is then incubated with the ligand specific for the extracellular portion of the chimeric protein, thereby activating the chimeric receptor. Known downstream proteins involved in intracellular signaling can then be assayed for expected modifications i.e. phosphorylation. Other methods known to those in the art can also be used to identify signaling molecules involved in receptor activity.

4.8.15 ANTI-INFLAMMATORY ACTIVITY

Compositions of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Compositions with such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation intimation associated with

infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Compositions of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material. Compositions of this invention may be utilized to prevent or treat condition such as, but not limited to, utilized, for example, as part of methods for the prevention and/or treatment of disorders involving sepsis, acute pancreatitis, endotoxin shock, cytokine induced shock, rheumatoid arthritis, chronic inflammatory arthritis, pancreatic cell damage from diabetes mellitus type 1, graft versus host disease, inflammatory bowel disease, inflamation associated with pulmonary disease, other autoimmune disease or inflammatory disease, an antiproliferative agent such as for acute or chronic mylegenous leukemia or in the prevention of premature labor secondary to intrauterine infections.

4.8.16 LEUKEMIAS

Leukemias and related disorders may be treated or prevented by administration of a therapeutic that promotes or inhibits function of the polynucleotides and/or polypeptides of the invention. Such leukemias and related disorders include but are not limited to acute leukemia, acute lymphocytic leukemia, acute myelocytic leukemia, myeloblastic, promyelocytic, myelomonocytic, monocytic, erythroleukemia, chronic leukemia, chronic myelocytic (granulocytic) leukemia and chronic lymphocytic leukemia (for a review of such disorders, see Fishman et al., 1985, Medicine, 2d Ed., J.B. Lippincott Co., Philadelphia).

4.8.17 NERVOUS SYSTEM DISORDERS

Nervous system disorders, involving cell types which can be tested for efficacy of intervention with compounds that modulate the activity of the polynucleotides and/or polypeptides of the invention, and which can be treated upon thus observing an indication of therapeutic utility, include but are not limited to nervous system injuries, and diseases or disorders which result in either a disconnection of axons, a diminution or degeneration of neurons, or demyelination.

Nervous system lesions which may be treated in a patient (including human and non-human mammalian patients) according to the invention include but are not limited to the following lesions of either the central (including spinal cord, brain) or peripheral nervous systems:

(i) traumatic lesions, including lesions caused by physical injury or associated with surgery, for example, lesions which sever a portion of the nervous system, or compression injuries;

(ii) ischemic lesions, in which a lack of oxygen in a portion of the nervous system results in neuronal injury or death, including cerebral infarction or ischemia, or spinal cord infarction or ischemia;

(iii) infectious lesions, in which a portion of the nervous system is destroyed or injured as a result of infection, for example, by an abscess or associated with infection by human immunodeficiency virus, herpes zoster, or herpes simplex virus or with Lyme disease, tuberculosis, syphilis;

(iv) degenerative lesions, in which a portion of the nervous system is destroyed or injured as a result of a degenerative process including but not limited to degeneration associated with Parkinson's disease, Alzheimer's disease, Huntington's chorea, or amyotrophic lateral sclerosis;

(v) lesions associated with nutritional diseases or disorders, in which a portion of the nervous system is destroyed or injured by a nutritional disorder or disorder of metabolism including but not limited to, vitamin B12 deficiency, folic acid deficiency, Wernicke disease, tobacco-alcohol amblyopia, Marchiafava-Bignami disease (primary degeneration of the corpus callosum), and alcoholic cerebellar degeneration;

(vi) neurological lesions associated with systemic diseases including but not limited to diabetes (diabetic neuropathy, Bell's palsy), systemic lupus erythematosus, carcinoma, or sarcoidosis;

(vii) lesions caused by toxic substances including alcohol, lead, or particular neurotoxins; and

(viii) demyelinated lesions in which a portion of the nervous system is destroyed or injured by a demyelinating disease including but not limited to multiple sclerosis, human immunodeficiency virus-associated myelopathy, transverse

myelopathy or various etiologies, progressive multifocal leukoencephalopathy, and central pontine myelinolysis.

Therapeutics which are useful according to the invention for treatment of a nervous system disorder may be selected by testing for biological activity in promoting the survival or differentiation of neurons. For example, and not by way of limitation, therapeutics which elicit any of the following effects may be useful according to the invention:

(i) increased survival time of neurons in culture;

(ii) increased sprouting of neurons in culture or in vivo;

(iii) increased production of a neuron-associated molecule in culture or *in vivo*, *e.g.*, choline acetyltransferase or acetylcholinesterase with respect to motor neurons; or

(iv) decreased symptoms of neuron dysfunction in vivo.

Such effects may be measured by any method known in the art. In preferred, non-limiting embodiments, increased survival of neurons may be measured by the method set forth in Arakawa et al. (1990, J. Neurosci. 10:3507-3515); increased sprouting of neurons may be detected by methods set forth in Pestronk et al. (1980, Exp. Neurol. 70:65-82) or Brown et al. (1981, Ann. Rev. Neurosci. 4:17-42); increased production of neuron-associated molecules may be measured by bioassay, enzymatic assay, antibody binding, Northern blot assay, *etc.*, depending on the molecule to be measured; and motor neuron dysfunction may be measured by assessing the physical manifestation of motor neuron disorder, *e.g.*, weakness, motor neuron conduction velocity, or functional disability.

In specific embodiments, motor neuron disorders that may be treated according to the invention include but are not limited to disorders such as infarction, infection, exposure to toxin, trauma, surgical damage, degenerative disease or malignancy that may affect motor neurons as well as other components of the nervous system, as well as disorders that selectively affect neurons such as amyotrophic lateral sclerosis, and including but not limited to progressive spinal muscular atrophy, progressive bulbar palsy, primary lateral sclerosis, infantile and juvenile muscular atrophy, progressive bulbar paralysis of childhood (Fazio-Londe syndrome), poliomyelitis and the post polio syndrome, and Hereditary Motorsensory Neuropathy (Charcot-Marie-Tooth Disease).

4.8.18 ARTHRITIS AND INFLAMMATION

The immunosuppressive effects of the compositions of the invention against rheumatoid arthritis is determined in an experimental animal model system. The experimental model system is adjuvant induced arthritis in rats, and the protocol is described by J. Holoshitz, et at., 1983, Science, 219:56, or by B. Waksman et al., 1963, Int. Arch. Allergy Appl. Immunol., 23:129. Induction of the disease can be caused by a single injection, generally intradermally, of a suspension of killed Mycobacterium tuberculosis in complete Freund's adjuvant (CFA). The route of injection can vary, but rats may be injected at the base of the tail with an adjuvant mixture. The inhibitor is administered in phosphate buffered solution (PBS) at a dose of about 1-5 mg/kg. The control consists of administering PBS only.

The procedure for testing the effects of the test compound would consist of intradermally injecting killed Mycobacterium tuberculosis in CFA followed by immediately administering the inhibitor and subsequent treatment every other day until day 24. At 14, 15, 18, 20, 22, and 24 days after injection of Mycobacterium CFA, an overall arthritis score may be obtained as described by J. Holoskitz above. An analysis of the data would reveal that the test compound would have a dramatic affect on the swelling of the joints as measured by a decrease of the arthritis score.

4.8.19 OTHER ACTIVITIES

A polypeptide or protein of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, co-factors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation,

appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

4.8.20 IDENTIFICATION OF POLYMORPHISMS

The demonstration of polymorphisms makes possible the identification of such polymorphisms in human subjects and the pharmacogenetic use of this information for diagnosis and treatment. Such polymorphisms may be associated with, e.g., differential predisposition or susceptibility to various disease states (such as disorders involving inflammation or immune response) or a differential response to drug administration, and this genetic information can be used to tailor preventive or therapeutic treatment appropriately. For example, the existence of a polymorphism associated with a predisposition to inflammation or autoimmune disease makes possible the diagnosis of this condition in humans by identifying the presence of the polymorphism.

Polymorphisms can be identified in a variety of ways known in the art which all generally involve obtaining a sample from a patient, analyzing DNA from the sample, optionally involving isolation or amplification of the DNA, and identifying the presence of the polymorphism in the DNA. For example, PCR may be used to amplify an appropriate fragment of genomic DNA which may then be sequenced. Alternatively, the DNA may be subjected to allele-specific oligonucleotide hybridization (in which appropriate oligonucleotides are hybridized to the DNA under conditions permitting detection of a single base mismatch) or to a single nucleotide extension assay (in which an oligonucleotide that hybridizes immediately adjacent to the position of the polymorphism is extended with one or more labeled nucleotides). In addition, traditional restriction fragment length polymorphism

analysis (using restriction enzymes that provide differential digestion of the genomic DNA depending on the presence or absence of the polymorphism) may be performed. Arrays with nucleotide sequences of the present invention can be used to detect polymorphisms. The array can comprise modified nucleotide sequences of the present invention in order to detect the nucleotide sequences of the present invention. In the alternative, any one of the nucleotide sequences of the present invention can be placed on the array to detect changes from those sequences.

Alternatively a polymorphism resulting in a change in the amino acid sequence could also be detected by detecting a corresponding change in amino acid sequence of the protein, e.g., by an antibody specific to the variant sequence.

4.9 THERAPEUTIC METHODS

The compositions (including polypeptide fragments, analogs, variants and antibodies or other binding partners or modulators including antisense polynucleotides) of the invention have numerous applications in a variety of therapeutic methods. Examples of therapeutic applications include, but are not limited to, those exemplified herein.

4.9.1 EXAMPLES

Another embodiment of the invention is the administration of an effective amount of the polypeptide or other composition of the invention to individuals affected by a disease or disorder which can be modulated by regulating the IgSF member of the invention. While the mode of administration is not particularly important, parenteral administration is preferred. An exemplary mode of administration is to deliver an intravenous bolus. The dosage of the polypeptide or composition of the invention will normally be determined by the prescribing physician. It is to be expected that the dosage will vary according to the age, weight, condition and response of the individual patient. Typically, the amount of protein or other active ingredient administered per dose will be in the range of about 0.1 to 25 mg/kg of body weight, with the preferred dose being about 0.1 to 10 mg/kg of patient body weight. For parenteral administration, the polypeptides or other active ingredient of the invention will be formulated in an injectable form that includes a pharmaceutically acceptable parenteral vehicle. Such vehicles are well known in the art and examples include water, saline, Ringer's solution, dextrose

solution, and solutions consisting of small amounts of the human serum albumin. The vehicle may contain minor amounts of additives that maintain the isotonicity and stability of the polypeptide or other active ingredient. The preparation of such solutions is within the skill of the art. Typically, the cytokine inhibitor will be formulated in such vehicles at a concentration of about 1-8 mg/ml to about 10 mg/ml.

4.10 PHARMACEUTICAL FORMULATIONS AND ROUTES OF ADMINISTRATION

A polypeptide or other composition of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources and including antibodies and other binding partners of the polypeptides of the invention) may be administered to a patient in need, by itself, or in pharmaceutical compositions where it is mixed with suitable carriers or excipient(s) at doses to treat or ameliorate a variety of disorders. Such a composition may optionally contain (in addition to protein or other active ingredient and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF, Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. In further compositions, polypeptides or proteins of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in questions. These agents include various growth factors such as epidermal growth factor (EGF), platelet-derived growth factor (PDGF), transforming growth factors (TGF-α and TGF-β), insulin-like growth factor (IGF), as well as cytokines described herein.

The pharmaceutical composition may further contain other agents which either enhance the activity of the protein or other active ingredient or compliment its activity or use in treatment. Such additional factors and/or agents may be included

in the pharmaceutical composition to produce a synergistic effect with protein or other active ingredient of the invention, or to minimize side effects. Conversely, protein or other active ingredient of the present invention may be included in formulations of the particular cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti- inflammatory agent to minimize side effects of the cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent. A polypeptide or protein of the present invention may be active in multimers (e.g., heterodimers or homodimers) or complexes with itself or other proteins. As a result, pharmaceutical compositions of the invention may comprise a polypeptide or protein of the invention in such multimeric or complexed form.

As an alternative to being included in a pharmaceutical composition of the invention including a first protein, a second protein or a therapeutic agent may be concurrently administered with the first protein (e.g., at the same time, or at differing times provided that therapeutic concentrations of the combination of agents is achieved at the treatment site). Techniques for formulation and administration of the compounds of the instant application may be found in "Remington's Pharmaceutical Sciences," Mack Publishing Co., Easton, PA, latest edition. A therapeutically effective dose further refers to that amount of the compound sufficient to result in amelioration of symptoms, *e.g.*, treatment, healing, prevention or amelioration of the relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient, administered alone, a therapeutically effective dose refers to that ingredient alone. When applied to a combination, a therapeutically effective dose refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously.

In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein or other active ingredient of the present invention is administered to a mammal having a condition to be treated. Polypeptide or other active ingredient of the present invention may be administered in accordance with the method of the invention either alone or in combination with other therapies such as treatments employing cytokines, lymphokines or other hematopoietic factors. When co- administered with one or more cytokines,

lymphokines or other hematopoietic factors, protein or other active ingredient of the present invention may be administered either simultaneously with the cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein or other active ingredient of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

4.10.1. ROUTES OF ADMINISTRATION

Suitable routes of administration may, for example, include oral, rectal, transmucosal, or intestinal administration; parenteral delivery, including intramuscular, subcutaneous, intramedullary injections, as well as intrathecal, direct intraventricular, intravenous, intraperitoneal, intranasal, or intraocular injections. Administration of protein or other active ingredient of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous administration to the patient is preferred.

Alternately, one may administer the compound in a local rather than systemic manner, for example, via injection of the compound directly into a arthritic joints or in fibrotic tissue, often in a depot or sustained release formulation. In order to prevent the scarring process frequently occurring as complication of glaucoma surgery, the compounds may be administered topically, for example, as eye drops. Furthermore, one may administer the drug in a targeted drug delivery system, for example, in a liposome coated with a specific antibody, targeting, for example, arthritic or fibrotic tissue. The liposomes will be targeted to and taken up selectively by the afflicted tissue.

4.10.2. COMPOSITIONS/FORMULATIONS

Pharmaceutical compositions for use in accordance with the present invention thus may be formulated in a conventional manner using one or more physiologically acceptable carriers comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. These pharmaceutical compositions may be manufactured in a

manner that is itself known, *e.g.*, by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping or lyophilizing processes. Proper formulation is dependent upon the route of administration chosen. When a therapeutically effective amount of protein or other active ingredient of the present invention is administered orally, protein or other active ingredient of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein or other active ingredient of the present invention, and preferably from about 25 to 90% protein or other active ingredient of the present invention. When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein or other active ingredient of the present invention, and preferably from about 1 to 50% protein or other active ingredient of the present invention.

When a therapeutically effective amount of protein or other active ingredient of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein or other active ingredient of the present invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein or other active ingredient solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein or other active ingredient of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art. For

injection, the agents of the invention may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks's solution, Ringer's solution, or physiological saline buffer. For transmucosal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

For oral administration, the compounds can be formulated readily by combining the active compounds with pharmaceutically acceptable carriers well known in the art. Such carriers enable the compounds of the invention to be formulated as tablets, pills, dragees, capsules, liquids, gels, syrups, slurries, suspensions and the like, for oral ingestion by a patient to be treated. Pharmaceutical preparations for oral use can be obtained solid excipient, optionally grinding a resulting mixture, and processing the mixture of granules, after adding suitable auxiliaries, if desired, to obtain tablets or dragee cores. Suitable excipients are, in particular, fillers such as sugars, including lactose, sucrose, mannitol, or sorbitol; cellulose preparations such as, for example, maize starch, wheat starch, rice starch, potato starch, gelatin, gum tragacanth, methyl cellulose, hydroxypropylmethyl-cellulose, sodium carboxymethylcellulose, and/or polyvinylpyrrolidone (PVP). If desired, disintegrating agents may be added, such as the cross-linked polyvinyl pyrrolidone, agar, or alginic acid or a salt thereof such as sodium alginate. Dragee cores are provided with suitable coatings. For this purpose, concentrated sugar solutions may be used, which may optionally contain gum arabic, talc, polyvinyl pyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be added to the tablets or dragee coatings for identification or to characterize different combinations of active compound doses.

Pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a plasticizer, such as glycerol or sorbitol. The push-fit capsules can contain the active ingredients in admixture with filler such as lactose, binders such as starches, and/or lubricants such as talc or magnesium stearate and, optionally, stabilizers. In soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid paraffin, or liquid polyethylene glycols. In addition, stabilizers may be added. All formulations for oral administration should be in

dosages suitable for such administration. For buccal administration, the compositions may take the form of tablets or lozenges formulated in conventional manner.

For administration by inhalation, the compounds for use according to the present invention are conveniently delivered in the form of an aerosol spray presentation from pressurized packs or a nebuliser, with the use of a suitable propellant, *e.g.*, dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane, carbon dioxide or other suitable gas. In the case of a pressurized aerosol the dosage unit may be determined by providing a valve to deliver a metered amount. Capsules and cartridges of, *e.g.*, gelatin for use in an inhaler or insufflator may be formulated containing a powder mix of the compound and a suitable powder base such as lactose or starch. The compounds may be formulated for parenteral administration by injection, *e.g.*, by bolus injection or continuous infusion. Formulations for injection may be presented in unit dosage form, *e.g.*, in ampules or in multi-dose containers, with an added preservative. The compositions may take such forms as suspensions, solutions or emulsions in oily or aqueous vehicles, and may contain formulatory agents such as suspending, stabilizing and/or dispersing agents.

Pharmaceutical formulations for parenteral administration include aqueous solutions of the active compounds in water-soluble form. Additionally, suspensions of the active compounds may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate or triglycerides, or liposomes. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Optionally, the suspension may also contain suitable stabilizers or agents which increase the solubility of the compounds to allow for the preparation of highly concentrated solutions. Alternatively, the active ingredient may be in powder form for constitution with a suitable vehicle, *e.g.*, sterile pyrogen-free water, before use.

The compounds may also be formulated in rectal compositions such as suppositories or retention enemas, *e.g.*, containing conventional suppository bases such as cocoa butter or other glycerides. In addition to the formulations described previously, the compounds may also be formulated as a depot preparation. Such

long acting formulations may be administered by implantation (for example subcutaneously or intramuscularly) or by intramuscular injection. Thus, for example, the compounds may be formulated with suitable polymeric or hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, or as sparingly soluble derivatives, for example, as a sparingly soluble salt.

A pharmaceutical carrier for the hydrophobic compounds of the invention is a cosolvent system comprising benzyl alcohol, a nonpolar surfactant, a water-miscible organic polymer, and an aqueous phase. The cosolvent system may be the VPD co-solvent system. VPD is a solution of 3% w/v benzyl alcohol, 8% w/v of the nonpolar surfactant polysorbate 80, and 65% w/v polyethylene glycol 300, made up to volume in absolute ethanol. The VPD co-solvent system (VPD:5W) consists of VPD diluted 1:1 with a 5% dextrose in water solution. This co-solvent system dissolves hydrophobic compounds well, and itself produces low toxicity upon systemic administration. Naturally, the proportions of a co-solvent system may be varied considerably without destroying its solubility and toxicity characteristics. Furthermore, the identity of the co-solvent components may be varied: for example, other low-toxicity nonpolar surfactants may be used instead of polysorbate 80; the fraction size of polyethylene glycol may be varied; other biocompatible polymers may replace polyethylene glycol, e.g. polyvinyl pyrrolidone; and other sugars or polysaccharides may substitute for dextrose. Alternatively, other delivery systems for hydrophobic pharmaceutical compounds may be employed. Liposomes and emulsions are well known examples of delivery vehicles or carriers for hydrophobic drugs. Certain organic solvents such as dimethylsulfoxide also may be employed, although usually at the cost of greater toxicity. Additionally, the compounds may be delivered using a sustained-release system, such as semipermeable matrices of solid hydrophobic polymers containing the therapeutic agent. Various types of sustained-release materials have been established and are well known by those skilled in the art. Sustained-release capsules may, depending on their chemical nature, release the compounds for a few weeks up to over 100 days. Depending on the chemical nature and the biological stability of the therapeutic reagent, additional strategies for protein or other active ingredient stabilization may be employed.

Docket No. 0505.0784

The pharmaceutical compositions also may comprise suitable solid or gel phase carriers or excipients. Examples of such carriers or excipients include but are not limited to calcium carbonate, calcium phosphate, various sugars, starches, cellulose derivatives, gelatin, and polymers such as polyethylene glycols. Many of the active ingredients of the invention may be provided as salts with pharmaceutically compatible counterions. Such pharmaceutically acceptable base addition salts are those salts which retain the biological effectiveness and properties of the free acids and which are obtained by reaction with inorganic or organic bases such as sodium hydroxide, magnesium hydroxide, ammonia, trialkylamine, dialkylamine, monoalkylamine, dibasic amino acids, sodium acetate, potassium benzoate, triethanol amine and the like.

The pharmaceutical composition of the invention may be in the form of a complex of the polypeptide(s) or protein(s) or other active ingredient of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with co-stimulatory molecules that can directly signal T cells. Alternatively antibodies able to bind surface immunoglobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention. The pharmaceutical composition of the invention may be in the form of a liposome in which polypeptide or protein of the present invention is combined, in addition to other pharmaceutically acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable lipids for liposomal formulation include, without limitation, monoglycerides, diglycerides, sulfatides, lysolecithins, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent Nos. 4,235,871;

4,501,728; 4,837,028; and 4,737,323, all of which are incorporated herein by reference.

The amount of protein or other active ingredient of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein or other active ingredient of the present invention with which to treat each individual patient. Initially, the attending physician will administer low doses of protein or other active ingredient of the present invention and observe the patient's response. Larger doses of protein or other active ingredient of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01 μg to about 100 mg (preferably about 0.1 μg to about 10 mg, more preferably about 0.1 μg to about 1 mg) of protein or other active ingredient of the present invention per kg body weight. For compositions of the present invention which are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systematically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein or other active ingredient of the invention which may also optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing or other active ingredient-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical applications.

The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices for the compositions may be biodegradable and chemically defined calcium sulfate, tricalcium phosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such as sintered hydroxyapatite, bioglass, aluminates, or other ceramics. Matrices may be comprised of combinations of any of the above mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalcium phosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability. Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix.

A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropyl-methylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate, poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt %, preferably 1-10 wt % based on total formulation weight, which represents the amount necessary to prevent desorption of the protein from the polymer matrix and to provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the protein the opportunity to assist the osteogenic activity of the progenitor cells. In further compositions, proteins or other active ingredient of the invention may be combined with other agents

beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF-α and TGF-β), and insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to humans, are desired patients for such treatment with proteins or other active ingredient of the present invention. The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue regeneration will be determined by the attending physician considering various factors which modify the action of the proteins, *e.g.*, amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue (*e.g.*, bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

4.10.3. EFFECTIVE DOSAGE

Pharmaceutical compositions suitable for use in the present invention include compositions wherein the active ingredients are contained in an effective amount to achieve its intended purpose. More specifically, a therapeutically effective amount means an amount effective to prevent development of or to alleviate the existing symptoms of the subject being treated. Determination of the effective amount is well within the capability of those skilled in the art, especially in light of the detailed disclosure provided herein. For any compound used in the method of the invention, the therapeutically effective dose can be estimated initially from appropriate in vitro assays. For example, a dose can be formulated in animal models to achieve a circulating concentration range that can be used to more accurately determine useful doses in humans. For example, a dose can be formulated in animal models to achieve a circulating concentration range that includes the IC_{50} as

determined in cell culture (*i.e.*, the concentration of the test compound which achieves a half-maximal inhibition of the protein's biological activity). Such information can be used to more accurately determine useful doses in humans.

A therapeutically effective dose refers to that amount of the compound that results in amelioration of symptoms or a prolongation of survival in a patient. Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, *e.g.*, for determining the LD_{50} (the dose lethal to 50% of the population) and the ED_{50} (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio between LD_{50} and ED_{50}. Compounds which exhibit high therapeutic indices are preferred. The data obtained from these cell culture assays and animal studies can be used in formulating a range of dosage for use in human. The dosage of such compounds lies preferably within a range of circulating concentrations that include the ED_{50} with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. The exact formulation, route of administration and dosage can be chosen by the individual physician in view of the patient's condition. See, *e.g.*, Fingl et al., 1975, in "The Pharmacological Basis of Therapeutics", Ch. 1 p.1. Dosage amount and interval may be adjusted individually to provide plasma levels of the active moiety which are sufficient to maintain the desired effects, or minimal effective concentration (MEC). The MEC will vary for each compound but can be estimated from *in vitro* data. Dosages necessary to achieve the MEC will depend on individual characteristics and route of administration. However, HPLC assays or bioassays can be used to determine plasma concentrations.

Dosage intervals can also be determined using MEC value. Compounds should be administered using a regimen which maintains plasma levels above the MEC for 10-90% of the time, preferably between 30-90% and most preferably between 50-90%. In cases of local administration or selective uptake, the effective local concentration of the drug may not be related to plasma concentration.

An exemplary dosage regimen for polypeptides or other compositions of the invention will be in the range of about 0.01 to 100 mg/kg of body weight daily, with the preferred dose being about 0.1 to 25 mg/kg of patient body weight daily,

varying in adults and children. Dosing may be once daily, or equivalent doses may be delivered at longer or shorter intervals.

The amount of composition administered will, of course, be dependent on the subject being treated, on the subject's age and weight, the severity of the affliction, the manner of administration and the judgment of the prescribing physician.

4.10.4. PACKAGING

The compositions may, if desired, be presented in a pack or dispenser device which may contain one or more unit dosage forms containing the active ingredient. The pack may, for example, comprise metal or plastic foil, such as a blister pack. The pack or dispenser device may be accompanied by instructions for administration. Compositions comprising a compound of the invention formulated in a compatible pharmaceutical carrier may also be prepared, placed in an appropriate container, and labeled for treatment of an indicated condition.

4.11. ANTIBODIES

Another aspect of the invention is an antibody that specifically binds the polypeptide of the invention. Such antibodies include monoclonal and polyclonal antibodies, single chain antibodies, chimeric antibodies, bifunctional/bispecific antibodies, humanized antibodies, human antibodies, and complementary determining region (CDR)-grafted antibodies, including compounds which include CDR and/or antigen-binding sequences, which specifically recognize a polypeptide of the invention. Preferred antibodies of the invention are human antibodies which are produced and identified according to methods described in WO93/11236, published June 20, 1993, which is incorporated herein by reference in its entirety. Antibody fragments, including Fab, Fab´, $F(ab')_2$, and F_v, are also provided by the invention. The term "specific for" indicates that the variable regions of the antibodies of the invention recognize and bind polypeptides of the invention exclusively (*i.e.*, able to distinguish the polypeptide of the invention from other similar polypeptides despite sequence identity, homology, or similarity found in the family of polypeptides), but may also interact with other proteins (for example, *S. aureus* protein A or other antibodies in ELISA techniques) through interactions with sequences outside the variable region of the antibodies, and in particular, in the constant region of the molecule. Screening assays to determine binding specificity

of an antibody of the invention are well known and routinely practiced in the art. For a comprehensive discussion of such assays, see Harlow et al. (Eds), Antibodies A Laboratory Manual; Cold Spring Harbor Laboratory; Cold Spring Harbor, NY (1988), Chapter 6. Antibodies that recognize and bind fragments of the polypeptides of the invention are also contemplated, provided that the antibodies are first and foremost specific for, as defined above, full length polypeptides of the invention. As with antibodies that are specific for full length polypeptides of the invention, antibodies of the invention that recognize fragments are those which can distinguish polypeptides from the same family of polypeptides despite inherent sequence identity, homology, or similarity found in the family of proteins. As with antibodies that are specific for full length polypeptides of the invention, antibodies of the invention that recognize polypeptides of the invention from its the family polypeptides despite inherent sequence identity, homology, or similarity found in the family of proteins. Antibodies of the invention can be produced using any method well known and routinely practiced in the art.

Non-human antibodies may be humanized by any methods known in the art. In one method, the non-human CDRs are inserted into a human antibody or consensus antibody framework sequence. Further changes can then be introduced into the antibody framework to modulate affinity or immunogenicity.

Antibodies of the invention are useful for, for example, therapeutic purposes (by modulating activity of a polypeptide of the invention), diagnostic purposes to detect or quantitate a polypeptide of the invention, as well as purification of a polypeptide of the invention. Kits comprising an antibody of the invention for any of the purposes described herein are also comprehended. In general, a kit of the invention also includes a control antigen for which the antibody is immunospecific. The invention further provides a hybridoma that produces an antibody according to the invention. Antibodies of the invention are useful for detection and/or purification of the polypeptides of the invention.

Polypeptides or proteins of the invention may also be used to immunize animals to obtain polyclonal and monoclonal antibodies which specifically react with the protein. Such antibodies may be obtained using either the entire protein or fragments thereof as an immunogen. The peptide immunogens additionally may contain a cysteine residue at the carboxyl terminus, and are conjugated to a hapten

such as keyhole limpet hemocyanin (KLH). Methods for synthesizing such peptides are known in the art, for example, as in R. P. Merrifield, J. Amer. Chem. Soc. 85, 2149-2154 (1963); J. L. Krstenansky, et al., FEBS Lett. 211, 10 (1987).

Monoclonal antibodies binding to the protein or polypeptide of the invention may be useful diagnostic agents for the immunodetection of the protein or polypeptide. Neutralizing monoclonal antibodies binding to the polypeptide may also be useful therapeutics for both conditions associated with the polypeptide and also in the treatment of some forms of cancer where abnormal expression of the polypeptide is involved. In the case of cancerous cells or leukemic cells, neutralizing monoclonal antibodies against the polypeptide may be useful in detecting and preventing the metastatic spread of the cancerous cells, which may be mediated by the polypeptide. In general, techniques for preparing polyclonal and monoclonal antibodies as well as hybridomas capable of producing the desired antibody are well known in the art (Campbell, A.M., Monoclonal Antibodies Technology: Laboratory Techniques in Biochemistry and Molecular Biology, Elsevier Science Publishers, Amsterdam, The Netherlands (1984); St. Groth et al., J. Immunol. 35:1-21 (1990); Kohler and Milstein, Nature 256:495-497 (1975)), the trioma technique, the human B-cell hybridoma technique (Kozbor et al., Immunology Today 4:72 (1983); Cole et al., in Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, Inc. (1985), pp. 77-96).

Any animal (mouse, rabbit, *etc.*) which is known to produce antibodies can be immunized with a peptide or polypeptide of the invention. Methods for immunization are well known in the art. Such methods include subcutaneous or intraperitoneal injection of the polypeptide. One skilled in the art will recognize that the amount of the protein encoded by the ORF of the present invention used for immunization will vary based on the animal which is immunized, the antigenicity of the peptide and the site of injection. The protein that is used as an immunogen may be modified or administered in an adjuvant in order to increase the protein's antigenicity. Methods of increasing the antigenicity of a protein are well known in the art and include, but are not limited to, coupling the antigen with a heterologous protein (such as globulin or β-galactosidase) or through the inclusion of an adjuvant during immunization.

For monoclonal antibodies, spleen cells from the immunized animals are removed, fused with myeloma cells, such as SP2/0-Ag14 myeloma cells, and allowed to become monoclonal antibody producing hybridoma cells. Any one of a number of methods well known in the art can be used to identify the hybridoma cell which produces an antibody with the desired characteristics. These include screening the hybridomas with an ELISA assay, Western blot analysis, or radioimmunoassay (Lutz et al., Exp. Cell Research. 175:109-124 (1988)). Hybridomas secreting the desired antibodies are cloned and the class and subclass is determined using procedures known in the art (Campbell, A.M., Monoclonal Antibody Technology: Laboratory Techniques in Biochemistry and Molecular Biology, Elsevier Science Publishers, Amsterdam, The Netherlands (1984)). Techniques described for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce single chain antibodies to proteins of the present invention.

For polyclonal antibodies, antibody-containing antiserum is isolated from the immunized animal and is screened for the presence of antibodies with the desired specificity using one of the above-described procedures. The present invention further provides the above- described antibodies in delectably labeled form. Antibodies can be delectably labeled through the use of radioisotopes, affinity labels (such as biotin, avidin, etc.), enzymatic labels (such as horseradish peroxidase, alkaline phosphatase, etc.) fluorescent labels (such as FITC or rhodamine, etc.), paramagnetic atoms, etc. Procedures for accomplishing such labeling are well-known in the art, for example, see (Sternberger, L.A. et al., J. Histochem. Cytochem. 18:315 (1970); Bayer, E.A. et al., Meth. Enzym. 62:308 (1979); Engval, E. et al., Immunol. 109:129 (1972); Goding, J.W. J. Immunol. Meth. 13:215 (1976)).

The labeled antibodies of the present invention can be used for *in vitro*, *in vivo*, and *in situ* assays to identify cells or tissues in which a fragment of the polypeptide of interest is expressed. The antibodies may also be used directly in therapies or other diagnostics. The present invention further provides the above-described antibodies immobilized on a solid support. Examples of such solid supports include plastics such as polycarbonate, complex carbohydrates such as agarose and Sepharose®, acrylic resins and such as polyacrylamide and latex beads.

Techniques for coupling antibodies to such solid supports are well known in the art (Weir, D.M. et al., "Handbook of Experimental Immunology" 4th Ed., Blackwell Scientific Publications, Oxford, England, Chapter 10 (1986); Jacoby, W.D. et al., Meth. Enzym. 34 Academic Press, N.Y. (1974)). The immobilized antibodies of the present invention can be used for *in vitro*, *in vivo*, and *in situ* assays as well as for immuno-affinity purification of the polypeptides or proteins of the present invention.

4.12. COMPUTER READABLE SEQUENCES

In one application of this embodiment, a nucleotide sequence of the present invention can be recorded on computer readable media. As used herein, "computer readable media" refers to any medium which can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media. A skilled artisan can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising computer readable medium having recorded thereon a nucleotide sequence of the present invention. As used herein, "recorded" refers to a process for storing information on computer readable medium. A skilled artisan can readily adopt any of the presently known methods for recording information on computer readable medium to generate manufactures comprising the nucleotide sequence information of the present invention.

A variety of data storage structures are available to a skilled artisan for creating a computer readable medium having recorded thereon a nucleotide sequence of the present invention. The choice of the data storage structure will generally be based on the means chosen to access the stored information. In addition, a variety of data processor programs and formats can be used to store the nucleotide sequence information of the present invention on computer readable medium. The sequence information can be represented in a word processing text file, formatted in commercially-available software such as WordPerfect and Microsoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase, Oracle, or the like. A skilled artisan can readily adapt any number of data processor structuring formats (*e.g.* text file or database) in

order to obtain computer readable medium having recorded thereon the nucleotide sequence information of the present invention.

By providing any of the nucleotide sequences designated as SEQ ID NO: 1-331 or a representative fragment thereof; or a nucleotide sequence at least 99.9% identical to any of the nucleotide sequences of SEQ ID NO: 1-331 in computer readable form, a skilled artisan can routinely access the sequence information for a variety of purposes. Computer software is publicly available which allows a skilled artisan to access sequence information provided in a computer readable medium. The examples which follow demonstrate how software which implements the BLAST (Altschul et al., J. Mol. Biol. 215:403-410 (1990)) and BLAZE (Brutlag et al., Comp. Chem. 17:203-207 (1993)) search algorithms on a Sybase system is used to identify open reading frames (ORFs) within a nucleic acid sequence. Such ORFs may be protein encoding fragments and may be useful in producing commercially important proteins such as enzymes used in fermentation reactions and in the production of commercially useful metabolites.

As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware means of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based systems are suitable for use in the present invention. As stated above, the computer-based systems of the present invention comprise a data storage means having stored therein a nucleotide sequence of the present invention and the necessary hardware means and software means for supporting and implementing a search means. As used herein, "data storage means" refers to memory which can store nucleotide sequence information of the present invention, or a memory access means which can access manufactures having recorded thereon the nucleotide sequence information of the present invention.

As used herein, "search means" refers to one or more programs which are implemented on the computer-based system to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of a known sequence which

match a particular target sequence or target motif. A variety of known algorithms are disclosed publicly and a variety of commercially available software for conducting search means are and can be used in the computer-based systems of the present invention. Examples of such software includes, but is not limited to, Smith-Waterman, MacPattern (EMBL), BLASTN and BLASTA (NPOLYPEPTIDEIA). A skilled artisan can readily recognize that any one of the available algorithms or implementing software packages for conducting homology searches can be adapted for use in the present computer-based systems. As used herein, a "target sequence" can be any nucleic acid or amino acid sequence of six or more nucleotides or two or more amino acids. A skilled artisan can readily recognize that the longer a target sequence is, the less likely a target sequence will be present as a random occurrence in the database. The most preferred sequence length of a target sequence is from about 10 to 100 amino acids or from about 30 to 300 nucleotide residues. However, it is well recognized that searches for commercially important fragments, such as sequence fragments involved in gene expression and protein processing, may be of shorter length.

As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration which is formed upon the folding of the target motif. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzyme active sites and signal sequences. Nucleic acid target motifs include, but are not limited to, promoter sequences, hairpin structures and inducible expression elements (protein binding sequences).

4.13. TRIPLE HELIX FORMATION

In addition, the fragments of the present invention, as broadly described, can be used to control gene expression through triple helix formation or antisense DNA or RNA, both of which methods are based on the binding of a polynucleotide sequence to DNA or RNA. Polynucleotides suitable for use in these methods are usually 20 to 40 bases in length and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 15241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Olmno, J. Neurochem. 56:560

(1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide.

4.14. DIAGNOSTIC ASSAYS AND KITS

The present invention further provides methods to identify the presence or expression of one of the ORFs of the present invention, or homolog thereof, in a test sample, using a nucleic acid probe or antibodies of the present invention, optionally conjugated or otherwise associated with a suitable label.

In general, methods for detecting a polynucleotide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polynucleotide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polynucleotide of the invention is detected in the sample. Such methods can also comprise contacting a sample under stringent hybridization conditions with nucleic acid primers that anneal to a polynucleotide of the invention under such conditions, and amplifying annealed polynucleotides, so that if a polynucleotide is amplified, a polynucleotide of the invention is detected in the sample.

In general, methods for detecting a polypeptide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polypeptide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polypeptide of the invention is detected in the sample.

In detail, such methods comprise incubating a test sample with one or more of the antibodies or one or more of the nucleic acid probes of the present invention and assaying for binding of the nucleic acid probes or antibodies to components within the test sample.

Conditions for incubating a nucleic acid probe or antibody with a test sample vary. Incubation conditions depend on the format employed in the assay, the detection methods employed, and the type and nature of the nucleic acid probe or

antibody used in the assay. One skilled in the art will recognize that any one of the commonly available hybridization, amplification or immunological assay formats can readily be adapted to employ the nucleic acid probes or antibodies of the present invention. Examples of such assays can be found in Chard, T., An Introduction to Radioimmunoassay and Related Techniques, Elsevier Science Publishers, Amsterdam, The Netherlands (1986); Bullock, G.R. et al., Techniques in Immunocytochemistry, Academic Press, Orlando, FL Vol. 1 (1982), Vol. 2 (1983), Vol. 3 (1985); Tijssen, P., Practice and Theory of immunoassays: Laboratory Techniques in Biochemistry and Molecular Biology, Elsevier Science Publishers, Amsterdam, The Netherlands (1985). The test samples of the present invention include cells, protein or membrane extracts of cells, or biological fluids such as sputum, blood, serum, plasma, or urine. The test sample used in the above-described method will vary based on the assay format, nature of the detection method and the tissues, cells or extracts used as the sample to be assayed. Methods for preparing protein extracts or membrane extracts of cells are well known in the art and can be readily be adapted in order to obtain a sample which is compatible with the system utilized.

In another embodiment of the present invention, kits are provided which contain the necessary reagents to carry out the assays of the present invention. Specifically, the invention provides a compartment kit to receive, in close confinement, one or more containers which comprises: (a) a first container comprising one of the probes or antibodies of the present invention; and (b) one or more other containers comprising one or more of the following: wash reagents, reagents capable of detecting presence of a bound probe or antibody.

In detail, a compartment kit includes any kit in which reagents are contained in separate containers. Such containers include small glass containers, plastic containers or strips of plastic or paper. Such containers allows one to efficiently transfer reagents from one compartment to another compartment such that the samples and reagents are not cross-contaminated, and the agents or solutions of each container can be added in a quantitative fashion from one compartment to another. Such containers will include a container which will accept the test sample, a container which contains the antibodies used in the assay, containers which contain wash reagents (such as phosphate buffered saline, Tris-buffers, etc.), and containers

which contain the reagents used to detect the bound antibody or probe. Types of detection reagents include labeled nucleic acid probes, labeled secondary antibodies, or in the alternative, if the primary antibody is labeled, the enzymatic, or antibody binding reagents which are capable of reacting with the labeled antibody. One skilled in the art will readily recognize that the disclosed probes and antibodies of the present invention can be readily incorporated into one of the established kit formats which are well known in the art.

4.15. MEDICAL IMAGING

The novel polypeptides and binding partners of the invention are useful in medical imaging of sites expressing the molecules of the invention (e.g., where the polypeptide of the invention is involved in the immune response, for imaging sites of inflammation or infection). See, e.g., Kunkel et al., U.S. Pat. NO. 5,413,778. Such methods involve chemical attachment of a labeling or imaging agent, administration of the labeled polypeptide to a subject in a pharmaceutically acceptable carrier, and imaging the labeled polypeptide *in vivo* at the target site.

4.16 SCREENING ASSAYS

Using the isolated polypeptides or proteins and polynucleotides of the invention, the present invention further provides methods of obtaining and identifying agents which bind to a polypeptide encoded by an ORF corresponding to any of the nucleotide sequences set forth as SEQ ID NO: 1-331, or bind to a specific domain of the polypeptide encoded by the nucleic acid. In detail, said method comprises the steps of:

(a) contacting an agent with an isolated protein encoded by an ORF of the present invention, or nucleic acid of the invention; and

(b) determining whether the agent binds to said protein or said nucleic acid.

In general, therefore, such methods for identifying compounds that bind to a polynucleotide of the invention can comprise contacting a compound with a polynucleotide of the invention for a time sufficient to form a polynucleotide/compound complex, and detecting the complex, so that if a polynucleotide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Likewise, in general, therefore, such methods for identifying compounds that bind to a polypeptide of the invention can comprise contacting a compound with a polypeptide of the invention for a time sufficient to form a polypeptide/compound complex, and detecting the complex, so that if a polypeptide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Methods for identifying compounds that bind to a polypeptide of the invention can also comprise contacting a compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a receptor gene sequence in the cell, and detecting the complex by detecting reporter gene sequence expression, so that if a polypeptide/compound complex is detected, a compound that binds a polypeptide of the invention is identified.

Compounds identified via such methods can include compounds which modulate the activity of a polypeptide of the invention (that is, increase or decrease its activity, relative to activity observed in the absence of the compound). Alternatively, compounds identified via such methods can include compounds which modulate the expression of a polynucleotide of the invention (that is, increase or decrease expression relative to expression levels observed in the absence of the compound). Compounds, such as compounds identified via the methods of the invention, can be tested using standard assays well known to those of skill in the art for their ability to modulate activity/expression.

The agents screened in the above assay can be, but are not limited to, peptides, carbohydrates, vitamin derivatives, or other pharmaceutical agents. The agents can be selected and screened at random or rationally selected or designed using protein modeling techniques.

For random screening, agents such as peptides, carbohydrates, pharmaceutical agents and the like are selected at random and are assayed for their ability to bind to the protein encoded by the ORF of the present invention. Alternatively, agents may be rationally selected or designed. As used herein, an agent is said to be "rationally selected or designed" when the agent is chosen based on the configuration of the particular protein. For example, one skilled in the art can readily adapt currently available procedures to generate peptides, pharmaceutical agents and the like capable of binding to a specific peptide sequence

in order to generate rationally designed antipeptide peptides, for example see Hurby et al., Application of Synthetic Peptides: Antisense Peptides," In Synthetic Peptides, A User's Guide, W.H. Freeman, NY (1992), pp. 289-307, and Kaspczak et al., Biochemistry 28:9230-8 (1989), or pharmaceutical agents, or the like.

In addition to the foregoing, one class of agents of the present invention, as broadly described, can be used to control gene expression through binding to one of the ORFs or EMFs of the present invention. As described above, such agents can be randomly screened or rationally designed/selected. Targeting the ORF or EMF allows a skilled artisan to design sequence specific or element specific agents, modulating the expression of either a single ORF or multiple ORFs which rely on the same EMF for expression control. One class of DNA binding agents are agents which contain base residues which hybridize or form a triple helix formation by binding to DNA or RNA. Such agents can be based on the classic phosphodiester, ribonucleic acid backbone, or can be a variety of sulfhydryl or polymeric derivatives which have base attachment capacity.

Agents suitable for use in these methods usually contain 20 to 40 bases and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Okano, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide and other DNA binding agents. Agents which bind to a protein encoded by one of the ORFs of the present invention can be used as a diagnostic agent, in the control of bacterial infection by modulating the activity of the protein encoded by the ORF. Agents which bind to a protein encoded by one of the ORFs of the present invention can be formulated using known techniques to generate a pharmaceutical composition.

4.17. USE OF NUCLEIC ACIDS AS PROBES

Another aspect of the subject invention is to provide for polypeptide-specific nucleic acid hybridization probes capable of hybridizing with naturally occurring nucleotide sequences. The hybridization probes of the subject invention may be derived from any of the nucleotide sequences designated as SEQ ID NO: 1-331. Because the corresponding gene is only expressed in a limited number of tissues, a hybridization probe derived from of any of the nucleotide sequences designated as SEQ ID NO: 1-331 can be used as an indicator of the presence of RNA of cell type of such a tissue in a sample.

Any suitable hybridization technique can be employed, such as, for example, in situ hybridization. PCR as described in US Patents Nos. 4,683,195 and 4,965,188 provides additional uses for oligonucleotides based upon the nucleotide sequences. Such probes used in PCR may be of recombinant origin, may be chemically synthesized, or a mixture of both. The probe will comprise a discrete nucleotide sequence for the detection of identical sequences or a degenerate pool of possible sequences for identification of closely related genomic sequences.

Other means for producing specific hybridization probes for nucleic acids include the cloning of nucleic acid sequences into vectors for the production of mRNA probes. Such vectors are known in the art and are commercially available and may be used to synthesize RNA probes in vitro by means of the addition of the appropriate RNA polymerase as T7 or SP6 RNA polymerase and the appropriate radioactively labeled nucleotides. The nucleotide sequences may be used to construct hybridization probes for mapping their respective genomic sequences. The nucleotide sequence provided herein may be mapped to a chromosome or specific regions of a chromosome using well known genetic and/or chromosomal mapping techniques. These techniques include in situ hybridization, linkage analysis against known chromosomal markers, hybridization screening with libraries or flow-sorted chromosomal preparations specific to known chromosomes, and the like. The technique of fluorescent in situ hybridization of chromosome spreads has been described, among other places, in Verma et al (1988) Human Chromosomes: A Manual of Basic Techniques, Pergamon Press, New York NY.

Fluorescent *in situ* hybridization of chromosomal preparations and other physical chromosome mapping techniques may be correlated with additional genetic map data. Examples of genetic map data can be found in the 1994 Genome Issue of

Science (265:1981f). Correlation between the location of a nucleic acid on a physical chromosomal map and a specific disease (or predisposition to a specific disease) may help delimit the region of DNA associated with that genetic disease. The nucleotide sequences of the subject invention may be used to detect differences in gene sequences between normal, carrier or affected individuals. The nucleotide sequence may be used to produce purified polypeptides using well known methods of recombinant DNA technology. Among the many publications that teach methods for the expression of genes after they have been isolated is Goeddel (1990) Gene Expression Technology, Methods and Enzymology, Vol 185, Academic Press, San Diego. Polypeptides may be expressed in a variety of host cells, either prokaryotic or eukaryotic. Host cells may be from the same species from which a particular polypeptide nucleotide sequence was isolated or from a different species. Advantages of producing polypeptides by recombinant DNA technology include obtaining adequate amounts of the protein for purification and the availability of simplified purification procedures.

4.18 Preparation of Sequencing Chips and Arrays

A basic example is using 6-mers attached to 50 micron surfaces to give a chip with dimensions of 3 x 3 mm which can be combined to give an array of 20 x 20 cm. Another example is using 9-mer oligonucleotides attached to 10 x 10 microns surface to create a 9-mer chip, with dimensions of 5 x 5 mm. 4000 units of such chips may be used to create a 30 x 30 cm array. In an array in which 4,000 to 16,000 oligochips are arranged into a square array. A plate, or collection of tubes, as also depicted, may be packaged with the array as part of the sequencing kit.

The arrays may be separated physically from each other or by hydrophobic surfaces. One possible way to utilize the hydrophobic strip separation is to use technology such as the Iso-Grid Microbiology System produced by QA Laboratories, Toronto, Canada.

Hydrophobic grid membrane filters (HGMF) have been in use in analytical food microbiology for about a decade where they exhibit unique attractions of extended numerical range and automated counting of colonies. One commercially-available grid is ISO-GRID™ from QA Laboratories Ltd. (Toronto, Canada) which consists of a square (60 x 60 cm) of polysulfone polymer (Gelman

Tuffryn HT-450, 0.45u pore size) on which is printed a black hydrophobic ink grid consisting of 1600 (40 x 40) square cells. HGMF have previously been inoculated with bacterial suspensions by vacuum filtration and incubated on the differential or selective media of choice.

Because the microbial growth is confined to grid cells of known position and size on the membrane, the HGMF functions more like an MPN apparatus than a conventional plate or membrane filter. Peterkin *et al.* (1987) reported that these HGMFs can be used to propagate and store genomic libraries when used with a HGMF replicator. One such instrument replicates growth from each of the 1600 cells of the ISO-GRID and enables many copies of the master HGMF to be made (Peterkin *et al.*, 1987).

Sharpe *et al.* (1989) also used ISO-GRID HGMF form QA Laboratories and an automated HGMF counter (MI-100 Interpreter) and RP-100 Replicator. They reported a technique for maintaining and screening many microbial cultures.

Peterkin and colleagues later described a method for screening DNA probes using the hydrophobic grid-membrane filter (Peterkin *et al.*, 1989). These authors reported methods for effective colony hybridization directly on HGMFs. Previously, poor results had been obtained due to the low DNA binding capacity of the epoxysulfone polymer on which the HGMFs are printed. However, Peterkin *et al.* (1989) reported that the binding of DNA to the surface of the membrane was improved by treating the replicated and incubated HGMF with polyethyleneimine, a polycation, prior to contact with DNA. Although this early work uses cellular DNA attachment, and has a different objective to the present invention, the methodology described may be readily adapted for Format 3 SBH.

In order to identify useful sequences rapidly, Peterkin *et al.* (1989) used radiolabeled plasmid DNA from various clones and tested its specificity against the DNA on the prepared HGMFs. In this way, DNA from recombinant plasmids was rapidly screened by colony hybridization against 100 organisms on HGMF replicates which can be easily and reproducibly prepared.

Manipulation with small (2-3 mm) chips, and parallel execution of thousands of the reactions. The solution of the invention is to keep the chips and the probes in the corresponding arrays. In one example, chips containing 250,000 9-mers are synthesized on a silicon wafer in the form of 8 x 8 mM plates (15 uM/oligonucleotide,

Pease et al., 1994) arrayed in 8 x 12 format (96 chips) with a 1 mM groove in between. Probes are added either by multichannel pipette or pin array, one probe on one chip. To score all 4000 6-mers, 42 chip arrays have to be used, either using different ones, or by reusing one set of chip arrays several times.

In the above case, using the earlier nomenclature of the application, F=9; P=6; and F + P = 15. Chips may have probes of formula BxNn, where x is a number of specified bases B; and n is a number of non-specified bases, so that x = 4 to 10 and n = 1 to 4. To achieve more efficient hybridization, and to avoid potential influence of any support oligonucleotides, the specified bases can be surrounded by unspecified bases, thus represented by a formula such as (N)nBx(N)m.

4.19 Preparation of Support Bound Oligonucleotides

Oligonucleotides, i.e., small nucleic acid segments, may be readily prepared by, for example, directly synthesizing the oligonucleotide by chemical means, as is commonly practiced using an automated oligonucleotide synthesizer.

Support bound oligonucleotides may be prepared by any of the methods known to those of skill in the art using any suitable support such as glass, polystyrene or Teflon. One strategy is to precisely spot oligonucleotides synthesized by standard synthesizers. Immobilization can be achieved using passive adsorption (Inouye & Hondo, 1990); using UV light (Nagata *et al.*, 1985; Dahlen *et al.*, 1987; Morriey & Collins, 1989) or by covalent binding of base modified DNA (Keller *et al.*, 1988; 1989); all references being specifically incorporated herein.

Another strategy that may be employed is the use of the strong biotin-streptavidin interaction as a linker. For example, Broude *et al.* (1994) describe the use of Biotinylated probes, although these are duplex probes, that are immobilized on streptavidin-coated magnetic beads. Streptavidin-coated beads may be purchased from Dynal, Oslo. Of course, this same linking chemistry is applicable to coating any surface with streptavidin. Biotinylated probes may be purchased from various sources, such as, e.g., Operon Technologies (Alameda, CA).

Nunc Laboratories (Naperville, IL) is also selling suitable material that could be used. Nunc Laboratories have developed a method by which DNA can be covalently bound to the microwell surface termed Covalink NH. CovaLink NH is a polystyrene surface grafted with secondary amino groups (>NH) that serve as

bridge-heads for further covalent coupling. CovaLink Modules may be purchased from Nunc Laboratories. DNA molecules may be bound to CovaLink exclusively at the 5'-end by a phosphoramidate bond, allowing immobilization of more than 1 pmol of DNA (Rasmussen *et al.*, 1991).

The use of CovaLink NH strips for covalent binding of DNA molecules at the 5'-end has been described (Rasmussen et al., 1991). In this technology, a phosphoramidate bond is employed (Chu et al., 1983). This is beneficial as immobilization using only a single covalent bond is preferred. The phosphoramidate bond joins the DNA to the CovaLink NH secondary amino groups that are positioned at the end of spacer arms covalently grafted onto the polystyrene surface through a 2 nm long spacer arm. To link an oligonucleotide to CovaLink NH via an phosphoramidate bond, the oligonucleotide terminus must have a 5'-end phosphate group. It is, perhaps, even possible for biotin to be covalently bound to CovaLink and then streptavidin used to bind the probes.

More specifically, the linkage method includes dissolving DNA in water (7.5 ng/ul) and denaturing for 10 min. at 95°C and cooling on ice for 10 min. Ice-cold 0.1 M 1-methylimidazole, pH 7.0 (1-MeIm_7), is then added to a final concentration of 10 mM 1-MeIm_7. A ss DNA solution is then dispensed into CovaLink NH strips (75 ul/well) standing on ice.

Carbodiimide 0.2 M 1-ethyl-3-(3-dimethylaminopropyl)-carbodiimide (EDC), dissolved in 10 mM 1-MeIm_7, is made fresh and 25 ul added per well. The strips are incubated for 5 hours at 50°C. After incubation the strips are washed using, e.g., Nunc-Immuno Wash; first the wells are washed 3 times, then they are soaked with washing solution for 5 min., and finally they are washed 3 times (where in the washing solution is 0.4 N NaOH, 0.25% SDS heated to 50°C).

It is contemplated that a further suitable method for use with the present invention is that described in PCT Patent Application WO 90/03382 (Southern & Maskos), incorporated herein by reference. This method of preparing an oligonucleotide bound to a support involves attaching a nucleoside 3'-reagent through the phosphate group by a covalent phosphodiester link to aliphatic hydroxyl groups carried by the support. The oligonucleotide is then synthesized on the supported nucleoside and protecting groups removed from the synthetic oligonucleotide chain under standard conditions that do not cleave the oligonucleotide from the support.

Suitable reagents include nucleoside phosphoramidite and nucleoside hydrogen phosphorate.

An on-chip strategy for the preparation of DNA probe for the preparation of DNA probe arrays may be employed. For example, addressable laser-activated photodeprotection may be employed in the chemical synthesis of oligonucleotides directly on a glass surface, as described by Fodor *et al.* (1991), incorporated herein by reference. Probes may also be immobilized on nylon supports as described by Van Ness *et al.* (1991); or linked to Teflon using the method of Duncan & Cavalier (1988); all references being specifically incorporated herein.

To link an oligonucleotide to a nylon support, as described by Van Ness *et al.* (1991), requires activation of the nylon surface via alkylation and selective activation of the 5'-amine of oligonucleotides with cyanuric chloride.

One particular way to prepare support bound oligonucleotides is to utilize the light-generated synthesis described by Pease *et al.*, (1994, incorporated herein by reference). These authors used current photolithographic techniques to generate arrays of immobilized oligonucleotide probes (DNA chips). These methods, in which light is used to direct the synthesis of oligonucleotide probes in high-density, miniaturized arrays, utilize photolabile 5'-protected *N*-acyl-deoxynucleoside phosphoramidites, surface linker chemistry and versatile combinatorial synthesis strategies. A matrix of 256 spatially defined oligonucleotide probes may be generated in this manner and then used in the advantageous Format 3 sequencing, as described in WO 95/09248, incorporated herein by reference.

4.20 Preparation of Nucleic Acid Fragments

The nucleic acids to be sequenced may be obtained from any appropriate source, such as cDNAs, genomic DNA, chromosomal DNA, microdissected chromosome bands, cosmid or YAC inserts, and RNA, including mRNA without any amplification steps. For example, Sambrook *et al.* (1989) describes three protocols for the isolation of high molecular weight DNA from mammalian cells (p. 9.14-9.23).

DNA fragments may be prepared as clones in M13, plasmid or lambda vectors and/or prepared directly from genomic DNA or cDNA by PCR or other amplification methods. Samples may be prepared or dispensed in multiwell plates. About 100-1000 ng of DNA samples may be prepared in 2-500 ml of final volume.

The nucleic acids would then be fragmented by any of the methods known to those of skill in the art including, for example, using restriction enzymes as described at 9.24-9.28 of Sambrook *et al.* (1989), shearing by ultrasound and NaOH treatment.

Low pressure shearing is also appropriate, as described by Schriefer *et al.* (1990, incorporated herein by reference). In this method, DNA samples are passed through a small French pressure cell at a variety of low to intermediate pressures. A lever device allows controlled application of low to intermediate pressures to the cell. The results of these studies indicate that low-pressure shearing is a useful alternative to sonic and enzymatic DNA fragmentation methods.

One particularly suitable way for fragmenting DNA is contemplated to be that using the two base recognition endonuclease, *Cvi*JI, described by Fitzgerald *et al.* (1992). These authors described an approach for the rapid fragmentation and fractionation of DNA into particular sizes that they contemplated to be suitable for shotgun cloning and sequencing. The present inventor envisions that this will also be particularly useful for generating random, but relatively small, fragments of DNA for use in the present sequencing technology.

The restriction endonuclease *Cvi*JI normally cleaves the recognition sequence PuGCPy between the G and C to leave blunt ends. Atypical reaction conditions, which alter the specificity of this enzyme (*Cvi*JI**), yield a quasi-random distribution of DNA fragments form the small molecule pUC19 (2688 base pairs). Fitzgerald *et al.* (1992) quantitatively evaluated the randomness of this fragmentation strategy, using a *Cvi*JI** digest of pUC19 that was size fractionated by a rapid gel filtration method and directly ligated, without end repair, to a lac Z minus M13 cloning vector. Sequence analysis of 76 clones showed that *Cvi*JI** restricts pyGCPy and PuGCPu, in addition to PuGCPy sites, and that new sequence data is accumulated at a rate consistent with random fragmentation.

As reported in the literature, advantages of this approach compared to sonication and agarose gel fractionation include: smaller amounts of DNA are required (0.2-0.5 ug instead of 2-5 ug); and fewer steps are involved (no preligation, end repair, chemical extraction, or agarose gel electrophoresis and elution are needed). These advantages are also proposed to be of use when preparing DNA for sequencing by Format 3.

Irrespective of the manner in which the nucleic acid fragments are obtained or prepared, it is important to denature the DNA to give single stranded pieces available for hybridization. This is achieved by incubating the DNA solution for 2-5 minutes at 80-90°C. The solution is then cooled quickly to 2°C to prevent renaturation of the DNA fragments before they are contacted with the chip. Phosphate groups must also be removed from genomic DNA by methods known in the art.

4.21 Preparation of DNA Arrays

Arrays may be prepared by spotting DNA samples on a support such as a nylon membrane. Spotting may be performed by using arrays of metal pins (the positions of which correspond to an array of wells in a microtiter plate) to repeated by transfer of about 20 nl of a DNA solution to a nylon membrane. By offset printing, a density of dots higher than the density of the wells is achieved. One to 25 dots may be accommodated in 1 mm^2, depending on the type of label used. By avoiding spotting in some preselected number of rows and columns, separate subsets (subarrays) may be formed. Samples in one subarray may be the same genomic segment of DNA (or the same gene) from different individuals, or may be different, overlapped genomic clones. Each of the subarrays may represent replica spotting of the same samples. In one example, a selected gene segment may be amplified from 64 patients. For each patient, the amplified gene segment may be in one 96-well plate (all 96 wells containing the same sample). A plate for each of the 64 patients is prepared. By using a 96-pin device, all samples may be spotted on one 8 x 12 cm membrane. Subarrays may contain 64 samples, one from each patient. Where the 96 subarrays are identical, the dot span may be 1 mm^2 and there may be a 1 mm space between subarrays.

Another approach is to use membranes or plates (available from NUNC, Naperville, Illinois) which may be partitioned by physical spacers e.g. a plastic grid molded over the membrane, the grid being similar to the sort of membrane applied to the bottom of multiwell plates, or hydrophobic strips. A fixed physical spacer is not preferred for imaging by exposure to flat phosphor-storage screens or x-ray films.

The present invention is illustrated in the following examples. Upon consideration of the present disclosure, one of skill in the art will appreciate that many other embodiments and variations may be made in the scope of the present invention. Accordingly, it is intended that the broader aspects of the present invention not be limited to the disclosure of the following examples. The present invention is not to be limited in scope by the exemplified embodiments which are intended as illustrations of single aspects of the invention, and compositions and methods which are functionally equivalent are within the scope of the invention. Indeed, numerous modifications and variations in the practice of the invention are expected to occur to those skilled in the art upon consideration of the present preferred embodiments. Consequently, the only limitations which should be placed upon the scope of the invention are those which appear in the appended claims.

All references cited within the body of the instant specification are hereby incorporated by reference in their entirety.

5. EXAMPLES

5.1 EXAMPLE 1

Novel Nucleic Acid Sequences Obtained From Various Libraries

A plurality of novel nucleic acids were obtained from cDNA libraries prepared from various human tissues and in some cases isolated from a genomic library derived from human chromosome using standard PCR, SBH sequence signature analysis and Sanger sequencing techniques. The inserts of the library were amplified with PCR using primers specific for the vector sequences which flank the inserts. Clones from cDNA libraries were spotted on nylon membrane filters and screened with oligonucleotide probes (e.g., 7-mers) to obtain signature sequences. The clones were clustered into groups of similar or identical sequences. Representative clones were selected for sequencing.

In some cases, the 5' sequence of the amplified inserts was then deduced using a typical Sanger sequencing protocol. PCR products were purified and subjected to fluorescent dye terminator cycle sequencing. Single pass gel sequencing was done using a 377 Applied Biosystems (ABI) sequencer to obtain the novel nucleic acid

sequences. In some cases RACE (Random Amplification of cDNA Ends) was performed to further extend the sequence in the 5' direction.

5.2 EXAMPLE 2

Novel Nucleic Acids

The nucleic acids of the present invention, designated as SEQ ID NO: 1-331 were assembled from sequences that were obtained from a cDNA library by methods described in Example 1 above, and in some cases, sequences obtained from one or more public databases. The nucleic acids were assembled using an EST sequence as a seed. Then a recursive algorithm was used to extend the seed EST into an extended assemblage, by pulling additional sequences from different databases (i.e., Hyseq's database containing EST sequences, dbEST version 114, gb pri 114, and UniGene version 101) that belong to this assemblage. The algorithm terminated when there was no additional sequences from the above databases that would extend the assemblage. Inclusion of component sequences into the assemblage was based on a BLASTN hit to the extending assemblage with BLAST score greater than 300 and percent identity greater than 95%.

The nearest neighbor results for SEQ ID NO: 1-331 were obtained by a FASTA version 3 search against Genpept release 117, using FASTXY algorithm. FASTXY is an improved version of FASTA alignment which allows in-codon frame shifts. The nearest neighbor result showed the closest homologue from Genpept (and contains the translated amino acid sequences for which the nucleic acid sequence encodes). The nearest neighbor results for SEQ ID NO: 1-331 are shown in the Table 1 below.

TABLE 1

SEQ ID NO. OF CURRENT APPLI-CATION	CORRESPONDING SEQ ID NO. IN PRIORITY APPLICATION ATTORNEY DOCKET NO. 784 CIP	ACCESSION NUMBER	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
1	1103	AF082664	Gallus gallus interferon alpha/beta receptor 1	188	27
2	2673	AK000530	Homo sapiens unnamed protein product	904	100.000
3	4117	AF113136	Homo sapiens IL-1 receptor-associated-kinase-M; IRAK-M	3902	100.000
4	5556	AB011102	Homo sapiens KIAA0530 protein	10208	99.936
5	5562	X02761	Homo sapiens fibronectin precursor	15747	98.754
6	5562	X02761	Homo sapiens fibronectin precursor	15747	98.754
7	5562	X02761	Homo sapiens fibronectin precursor	15747	98.754
8	5562	X02761	Homo sapiens fibronectin precursor	15747	98.754
9	5563	AJ011679	Homo sapiens Rab6 GTPase activating protein, GAPCenA	6737	100.000
10	5564	Y17816	Suberites domuncula cytochrome P450	622	28.838
11	5565	AF117754	Homo sapiens thyroid hormone receptor-associated protein complex component TRAP240	14773	99.816
12	5689	Z97630	Homo sapiens dJ466N1.4 (novel protein similar to ANK3 (ankyrin 3, node of Ranvier (ankyrin G)))	1204	98.953
13	5729	Y09615	Homo sapiens mTERF	494	30.060
14	5745	AL133404	Homo sapiens dJ238O23.1 (novel protein similar to PIGR (polymeric immunoglobulin receptor))	801	100.000
15	5777	AB032951	Homo sapiens KIAA1125 protein	5921	99.890
16	5777	AB032951	Homo sapiens KIAA1125 protein	5921	99.890
17	5789	AF201303	Homo sapiens dhfr oribeta-binding protein RIP60	4120	98.413
18	5792	AF064205	Homo sapiens dynactin 1 p150 isoform	8120	100.000

TABLE 1

19	5804	AE003550	Drosophila melanogaster CG14164 gene product	243	31.646
20	5805	AB032903	Homo sapiens guanosine monophosphate reductase isolog	2298	99.713
21	5805	AB032903	Homo sapiens guanosine monophosphate reductase isolog	2298	99.713
22	5844	AF140507	Homo sapiens Ca2+/calmodulin-dependent protein kinase kinase beta	3989	99.830
23	5844	AF140507	Homo sapiens Ca2+/calmodulin-dependent protein kinase kinase beta	3989	99.830
24	5850	AB030378	Mus musculus chondroItin 4-sulfotransferase	731	43.003
25	5867	U33460	Homo sapiens DNA-directed RNA polymerase I, largest subunit	11332	99.361
26	5973	AF192499	Mus musculus putative secreted protein ZSIG37	779	55.656
27	5995	U43701	Homo sapiens ribosomal protein L23a	999	100.000
28	5995	U43701	Homo sapiens ribosomal protein L23a	999	100.000
29	6005	AE003493	Drosophila melanogaster CG11102 gene product	895	30.521
30	6007	AF061739	Homo sapiens unknown	1176	93.939
31	6007	AF061739	Homo sapiens unknown	1213	100.000
32	6009	AF231917	Homo sapiens long-chain 2-hydroxy acid oxidase HAOX2	2315	100.000
33	6012	Z29481	Homo sapiens 3-hydroxyanthranilic acid dioxygenase	1943	99.650
34	6015	AB001451	Homo sapiens Sck	3722	100.000
35	6016	Y00644	Homo sapiens precursor polypeptide (AA -34 to 287)	2122	99.685
36	6016	Y00644	Homo sapiens precursor polypeptide (AA -34 to 287)	2122	99.685
37	6018	AF220152	Homo sapiens TACC2	5711	94.877
38	6018	AF220152	Homo sapiens TACC2	5818	99.888
39	6018	AF220152	Homo sapiens TACC2	5818	99.888
40	6023	AL117496	Homo sapiens hypothetical protein	11197	99.888
41	6070	AF187305	Myxine glutinosa	435	45.578

TABLE 1

			calmodulin		
42	6081	D88769	Mus musculus latexin	1305	85.135
43	6089	AB023147	Homo sapiens KIAA0930 protein	2312	100.000
44	6118	U19617	Mus musculus Elf-1	3456	88.226
45	6118	U19617	Mus musculus Elf-1	3456	88.226
46	6130	AL110267	Homo sapiens hypothetical protein	1946	100.000
47	6177	AF176903	Mus musculus sprouty 1	1920	83.072
48	6189	X59244	Homo sapiens ZNF43	5716	100.000
49	6191	X06026	Homo sapiens T-cell receptor T3 gamma chain	1205	99.451
50	6204	X63547	Homo sapiens oncogene	7604	100.000
51	6204	X63547	Homo sapiens oncogene	7604	100.000
52	6284	M94043	Rattus norvegicus rab-related GTP-binding protein	1393	96.209
53	6367	L31783	Mus musculus uridine kinase	1184	71.984
54	6436	X83973	Homo sapiens transcription factor	4486	98
55	6442	AF224741	Homo sapiens chloride channel protein 7	5287	99.876
56	6445	Z92825	Unknown predicted using Genefinder; Similarity to Yeast low-afinity glucose transporter HXT4 (PS:32	1193	41.597
57	6457	U33005	Mus musculus Tbc1	5648	87.649
58	6458	D79994	Homo sapiens similar to ankyrin of Chromatium vinosum.	8504	99.923
59	6458				
60	6462	AB028991	Homo sapiens KIAA1068 protein	2363	100.000
61	6472	AF149758	Homo sapiens CpG binding protein	3442	96.023
62	6499	AK001651	Homo sapiens unnamed protein product	3008	95.706
63	6499	AK001651	Homo sapiens unnamed protein product	3061	99.787
64	6505	S70011	Rattus sp. tricarboxylate carrier	1170	55.414
65	6534	AB011154	Homo sapiens KIAA0582 protein	3106	100.000
66	6534	AB011154	Homo sapiens KIAA0582 protein	3106	100.000
67	6540	AJ245738	Homo sapiens claudin-15	1546	100.000
68	6550	AB018290	Homo sapiens KIAA0747 protein	7100	100.000
69	6550	AB018290	Homo sapiens KIAA0747 protein	7100	100.000

TABLE 1

70	6592	AB018338	Homo sapiens KIAA0795 protein	3195	100.000
71	6645	AL035541	Homo sapiens dJ718J7.1 (PUTATIVE novel protein similar to Tr:O15168)	1427	100.000
72	6671	AF126426	Homo sapiens neurotrimin	2303	100.000
73	6763	D14592	Rattus norvegicus MAP kinase kinase-related protein	2539	93.750
74	6763	D14592	Rattus norvegicus MAP kinase kinase-related protein	2539	93.750
75	6786	AL157431	Homo sapiens hypothetical protein	3251	100.000
76	6824	AE000406	Escherichia coli putative DNA topoisomerase	1239	100.000
77	6830	D31765	Homo sapiens KIAA0061	6254	100.000
78	6831	AL009191	Unknown /prediction=(method:"" genefinder"", version:""084""); /prediction=(method:"" genscan"", ve	476	30.056
79	6832	AF129756	Homo sapiens G4	2022	99.660
80	6834	AL096768	Homo sapiens dJ858B16.2 (phosphatidylserine decarboxylase (PSSC, EC 4.1.1.65))	2622	100.000
81	6834				
82	6835	X57351	Homo sapiens 1-8D	866	98.485
83	6837	AC005594	Homo sapiens R26984_1	3453	98.641
84	6843	X73113	Homo sapiens fast MyBP-C	7583	99.912
85	6859	AL117424	Homo sapiens hypothetical protein	1671	100.000
86	6915	AB018423	Mus musculus SH2 domain-containing protein	1779	76.744
87	6932	AL008730	Homo sapiens dJ487J7.1.1 (putative protein dJ487J7.1 isoform 1)	4011	99.652
88	6957	AJ010100	Homo sapiens NKp44RG2	194	28.070
89	6961	AC007067	Arabidopsis thaliana T10O24.21	577	29.653
90	6973	AC004990	Homo sapiens supported by Genscan and several ESTs: C83049 (NID:g3062006), AA823760 (NID:g2893628), AA215791	3426	98.643

TABLE 1

			(NID:g1815572), AI095488 (NID:g3434464), and AA969095 (NID:g3144275)		
91	6973	AC004990	Homo sapiens supported by Genscan and several ESTs: C83049 (NID:g3062006), AA823760 (NID:g2893628), AA215791 (NID:g1815572), AI095488 (NID:g3434464), and AA969095 (NID:g3144275)	3426	98.643
92	7001	AC005587	Homo sapiens similar to mouse olfactory receptor 13; similar to P34984 (PID:g464305)	1458	71.711
93	7007	A61971	unidentified MCSP	15081	99.215
94	7018	AB033899	Homo sapiens fatty acid coenzyme A ligase 5	4582	100.000
95	7019	AF151020	Homo sapiens HSPC186	705	58.242
96	7020	AF061944	Homo sapiens kinase deficient protein KDP	4221	99.254
97	7020	AF061944	Homo sapiens kinase deficient protein KDP	4221	99.254
98	7021	AL117567	Homo sapiens hypothetical protein	2042	99.385
99	7023	AL021366	Homo sapiens cICK0721Q.3 (Kinesin related protein)	4398	100.000
100	7027	AC005594	Homo sapiens R26984_1	3417	98.252
101	7028	AB014599	Homo sapiens KIAA0699 protein	5341	100.000
102	7029	AL050069	Homo sapiens hypothetical protein	1789	100.000
103	7031	AJ006267	Homo sapiens ClpX-like protein	4124	100.000
104	7032	AF100753	Homo sapiens ancient ubiquitous 46 kDa protein AUP1	2643	96.585
105	7033	AB015982	Homo sapiens serine/threonine kinase	6054	100.000
106	7035	AF151074	Homo sapiens HSPC240	1070	64.427
107	7036	M35522	Canis familiaris GTP-binding protein (rab7)	458	50.376
108	7039	AB023210	Homo sapiens KIAA0993 protein	2577	100.000
109	7043	AF125533	Homo sapiens NADH-cytochrome b5	1643	93.680

TABLE 1

			reductase isoform		
110	7044	AC005614	Homo sapiens F23269_2	4310	99.836
111	7046	AB018288	Homo sapiens KIAA0745 protein	5809	98.900
112	7054	X52425	Homo sapiens interleukin 4 receptor	5828	100.000
113	7061	AF001533	Mus musculus mitogen-induced	2483	98.172
114	7077	A84423	unidentified unnamed protein product	2535	95.332
115	7092	AE003744	Drosophila melanogaster CG10365 gene product	612	47.573
116	7094	AL049548	Homo sapiens dJ398G3.1 (ortholog of rat CPG2)	4426	99.856
117	7106	AK000790	Homo sapiens unnamed protein product	1539	99.095
118	7107	AJ249753	Lygodactylus picturatus iota-crystallin	583	61.719
119	7111	AC002343	Arabidopsis thaliana Ser/Thr protein kinase isolog	488	33.918
120	7123	Y08915	Homo sapiens alpha 4 protein	2232	100.000
121	7142	AE003538	Drosophila melanogaster CG10191 gene product	769	48.374
122	7142	AL117629	Homo sapiens hypothetical protein	1238	100.000
123	7154	AK000278	Homo sapiens unnamed protein product	3364	99.235
124	7160	AK001218	Homo sapiens unnamed protein product	2692	100.000
125	7169	AF061022	Homo sapiens CTH	343	32.950
126	7185	M63109	Leishmania major glycoprotein 96-92	187	27.128
127	7197	AE003602	Drosophila melanogaster Atu gene product	1195	36.804
128	7219	AE003772	Drosophila melanogaster CG7943 gene product	798	43.273
129	7226	AF095927	Rattus norvegicus protein phosphatase 2C	2469	94.898
130	7229	L41254	Rattus norvegicus transmembrane protein	336	62.637
131	7234	AL031581	Unknown /prediction=(method:"" genefinder"", version:""084"", score:""52.12""); /prediction=(metho	796	44.850
132	7235	X93498	Homo sapiens 21-Glutamic Acid-Rich	1602	100.000

TABLE 1

			Protein		
133	7235	X93498	Homo sapiens 21-Glutamic Acid-Rich Protein	1602	100.000
134	7238	AL078579	Arabidopsis thaliana putative acyl-CoA binding protein	531	38.077
135	7247	AB014589	Homo sapiens KIAA0689 protein	3783	100.000
136	7261	AB028946	Homo sapiens KIAA1023 protein	3587	100.000
137	7262	U72245	Homo sapiens phospholemman chloride channel	252	51.220
138	7267	Z99106	Bacillus subtilis similar to hypothetical proteins	464	32.540
139	7272	AB014601	Homo sapiens KIAA0701 protein	4013	99.683
140	7273	AB007889	Homo sapiens KIAA0429	2432	100.000
141	7282	X81804	Bos taurus ozf	2147	95.223
142	7288	AE003791	Drosophila melanogaster CG11110 gene product	644	58.599
143	7291	Z68493	Caenorhabditis elegans predicted using Genefinder	466	41.379
144	7293	D89937	Homo sapiens follistatin-related protein (FRP)	2146	100.000
145	7294	AF161483	Homo sapiens HSPC134	742	50.617
146	7299	AK000518	Homo sapiens unnamed protein product	608	100.000
147	7300	AB011115	Homo sapiens KIAA0543 protein	7541	100.000
148	7312	AK001360	Homo sapiens unnamed protein product	4013	99.203
149	7313	AE003718	Drosophila melanogaster CG7623 gene product	1199	48.250
150	7315	AF056490	Homo sapiens cAMP-specific phosphodiesterase 8A	4713	99.719
151	7318	AE003543	Drosophila melanogaster CG5906 gene product	382	45.865
152	7321	AK001830	Homo sapiens unnamed protein product	1208	100.000
153	7330	X73478	Homo sapiens phosphotyrosyl phosphatase activator	2196	99.690
154	7331	AL049697	Homo sapiens dJ382I10.5.1 (novel protein similar to arginyl-tRNA synthetase (arginine-	2587	99.500

TABLE 1

			tRNA ligase, EC 6.1.1.19) (isoform 1))		
155	7333	AF169802	Homo sapiens cytochrome b5 reductase b5R.2	1860	99.275
156	7350	Z22642	Homo sapiens PO-GA	7383	100.000
157	7352	AK000996	Homo sapiens unnamed protein product	1880	100.000
158	7384	AK000544	Homo sapiens unnamed protein product	2445	96.875
159	7403	AC002301	Homo sapiens Homolog of rat Zymogen granule membrane protein	270	37.594
160	7431	L02241	Mus musculus protein kinase inhibitor	354	74.359
161	7441	J04970	Homo sapiens carboxypeptidase M precursor	3050	100.000
162	7453	X67325	Homo sapiens p27	318	67.500
163	7467	AL022724	Homo sapiens dJ413H6.1.1 (hamster Androgen-dependent Expressed Protein LIKE PUTATIVE protein) (isoform 1)	1716	100.000
164	7471	AF125535	Homo sapiens pp21 homolog	239	45.536
165	7493	AE003490	Drosophila melanogaster CG2540 gene product	443	42
166	7502	AJ250839	Homo sapiens serine/threonine protein kinase	1852	71.311
167	7511	U23484	Caenorhabditis elegans EEED8.6 gene product	517	33.133
168	7514	AF214680	Homo sapiens C3HC4-like zinc finger protein	1540	99.565
169	7520	AE003458	Drosophila melanogaster CG4207 gene product	264	30.256
170	7541	U46690	Mus musculus ATP-dependent RNA helicase	2643	85.000
171	7570	AK000553	Homo sapiens unnamed protein product	2032	99.664
172	7578	AE003791	Drosophila melanogaster CG10404 gene product	501	59.124
173	7583	D43636	Homo sapiens KIAA0096 gene product is related to a protein kinase.	3491	100.000
174	7592	AC007954	Homo sapiens unknown	1005	100.000
175	7601	D43949	Homo sapiens This gene is novel.	4103	100.000
176	7602	Y07923	Homo sapiens GTP-	1542	100.000

TABLE 1

			binding protein		
177	7608	AB039933	Mus musculus polyposis locus protein 1-like 1 (TB2 protein-like 1)	994	76.410
178	7615	AL133654	Homo sapiens hypothetical protein	1843	92.500
179	7617	AF161462	Homo sapiens HSPC113	1173	98.315
180	7622	X55681	Lycopersicon esculentum extensin (class I)	173	34.524
181	7624	X78925	Homo sapiens zinc finger protein	5133	99.727
182	7626	X03084	Homo sapiens C1q B-chain precursor	1598	100.000
183	7640	U57344	Mus musculus Meis3	2357	89.153
184	7641	U57344	Mus musculus Meis3	2080	81.794
185	7641	U57344	Mus musculus Meis3	2263	86.280
186	7641	U57344	Mus musculus Meis3	2263	86.280
187	7642	AF033120	Homo sapiens p53 regulated PA26-T2 nuclear protein	1765	58.439
188	7649	AF200357	Mus musculus pantothenate kinase 1 beta	2046	82.369
189	7656	D50646	Mus musculus SDF2	905	65.482
190	7657	AX001017	unidentified unnamed protein product	2807	96.652
191	7657	AX001017	unidentified unnamed protein product	2807	96.652
192	7662	X54134	Homo sapiens protein-tyrosine phosphatase	4739	100.000
193	7668	AF117582	Manduca sexta calcyphosine-like protein	775	51.923
194	7673	AF216751	Homo sapiens CDA14	2467	100.000
195	7690	AF169035	Homo sapiens protein kinase	2881	99.534
196	7700	AF084259	Mus musculus bromodomain-containing protein BP75	1138	36.013
197	7709	Y00752	Rattus norvegicus serine dehydratase (AA 1 - 327)	1281	61.562
198	7736	AK000630	Homo sapiens unnamed protein product	3283	99.611
199	7737	AB028859	Homo sapiens hDj9	2425	100.000
200	7744	AB002368	Homo sapiens KIAA0370	5083	100.000
201	7771	M74555	Mus musculus house-keeping protein	1452	53.061
202	7786	AK000657	Homo sapiens unnamed protein product	2904	100.000
203	7791	X54162	Homo sapiens 64 Kd autoantigen	3704	99.650
204	7797	AL110479	Caenorhabditis elegans predicted using	916	47.535

TABLE 1

			Genefinder; cDNA EST yk524f8.5 comes from this gene; cDNA EST yk631e2.5 comes from this gene; cDNA EST EMBL:C08367 comes from this gene; cDNA EST yk524f8.3 comes from this gene		
205	7806	X80199	Homo sapiens MLN 51	3666	100.000
206	7812	J04204	Bos taurus 32 kd accessory protein	2332	100.000
207	7812	J04204	Bos taurus 32 kd accessory protein	2332	100.000
208	7818	AF161254	Homo sapiens 8D6 antigen	1952	100.000
209	7822	AF151835	Homo sapiens CGI-78 protein	973	59.167
210	7827	AE003459	Drosophila melanogaster CG9848 gene product	616	53.797
211	7830	AE003519	Drosophila melanogaster CG6896 gene product	920	41.191
212	7835	AC005067	Homo sapiens Supported by Human EST H08032.1 (NID:g872854), mouse EST AA870042.1 (NID:g2965487), and genscan	2465	100.000
213	7836	D86971	Homo sapiens no similarities to reported gene products	4510	100.000
214	7840	X66295	Mus musculus C1q C chain	1273	73.171
215	7858	Z29328	Homo sapiens Ubiquitin-conjugating enzyme UbcH2	1228	100.000
216	7858	Z29328	Homo sapiens Ubiquitin-conjugating enzyme UbcH2	1228	100.000
217	7861	AJ002030	Homo sapiens progresterone binding protein	1492	100.000
218	7866	X70649	Homo sapiens member of DEAD box protein family	5029	100.000
219	7868	AF072128	Mus musculus claudin-2	1404	91.304
220	7896	AL021453	Homo sapiens dJ821D11.1 (PUTATIVE protein)	335	100.000
221	7898	Y08565	Homo sapiens UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase	4280	99.839
222	7900	AF061023	Gallus gallus ChT1	180	20.879

TABLE 1

223	7906	AL035521	Arabidopsis thaliana putative protein	417	41.772
224	7908	AL117473	Homo sapiens hypothetical protein	2778	100.000
225	7909	AE003678	Drosophila melanogaster CG9615 gene product	1422	63.548
226	7917	D87470	Homo sapiens KIAA0280	1989	100.000
227	7932	AL035659	Homo sapiens dJ979N1.1 (dJ979N1.1)	6710	98.389
228	7940	AB032401	Mus musculus mmDj4	2290	92.090
229	7940	AB032401	Mus musculus mmDj4	2574	92.947
230	7984	AF007170	Homo sapiens unknown	3719	99.822
231	7984	AF007170	Homo sapiens unknown	3719	99.822
232	8001	AF112210	Homo sapiens heat shock protein hsp70-related protein	3247	99.607
233	8021	AB001568	Arabidopsis thaliana phospholipid hydroperoxide glutathione peroxidase-like protein	432	40.244
234	8029	AB027466	Homo sapiens spondin 2	2272	99.698
235	8033	AF125314	Mus musculus XAP89 protein	877	65.560
236	8040	X64588	Cricetulus longicaudatus cyclin B	2445	87.558
237	8052	Z11804	Dictyostelium discoideum ras protein	519	50.303
238	8096	Z50749	Homo sapiens yeast sds22 homolog	2266	100.000
239	8096	Z50749	Homo sapiens yeast sds22 homolog	2266	100.000
240	8113	AB026491	Homo sapiens PICK1	2709	100.000
241	8126	AC018908	Arabidopsis thaliana putative phosphatidylinositol-4-phosphate 5-kinase	237	38.532
242	8132	AB030189	Mus musculus contains transmembrane (TM) region and ATP binding region	1541	93.671
243	8137	AF116865	Mus musculus hedgehog-interacting protein	4660	94.143
244	8137	AF116865	Mus musculus hedgehog-interacting protein	4660	94.143
245	8159	AF155107	Homo sapiens NY-REN-37 antigen	1300	99.425
246	8159	AF155107	Homo sapiens NY-REN-37 antigen	1315	100.000
247	8161	AL031320	Homo sapiens dJ20N2.1 (novel protein similar to yeast and bacterial cytosine deaminase)	1076	99.371
248	8176	U37026	Rattus norvegicus	198	30.769

TABLE 1

			sodium channel beta 2 subunit		
249	8196	AL078599	Homo sapiens dJ991C6.1 (novel protein similar to C. elegans F55A12.9 (Tr:P91086))	3079	98.913
250	8200	AL109630	Drosophila melanogaster BACR7A4.h	735	32.083
251	8212	M89797	Mus musculus Wnt-4	2425	98.860
252	8220	AB029434	Homo sapiens ghrelin precursor	797	100.000
253	8238	AE003628	Drosophila melanogaster CG18626 gene product	625	36.482
254	8254	AB011157	Homo sapiens KIAA0585 protein	2864	100.000
255	8255	AK000562	Homo sapiens unnamed protein product	2400	99.730
256	8288	AB012309	Cyprinus carpio allograft inflammatory factor-1	740	78.169
257	8296	AF065382	Yersinia pestis adenylate kinase	267	30.556
258	8329	AF233322	Mus musculus zinc transporter like 2	2463	95.767
259	8362	AB037886	Homo sapiens NESH	2503	100.000
260	8429	AE003621	Drosophila melanogaster CG13384 gene product	1047	39.752
261	8436	AK001553	Homo sapiens unnamed protein product	1485	100.000
262	8448	AE003584	Drosophila melanogaster CG15362 gene product	296	36.090
263	8472	AE000909	Methanobacterium thermoautotrophicum serine/threonine protein kinase related protein	464	30.032
264	8502	AL050131	Homo sapiens hypothetical protein	1517	100.000
265	8504	AF019661	Mus musculus zeta proteasome chain; PSMA5	1538	100.000
266	8507	U11271	Homo sapiens thromboxane A2 receptor	2393	98.103
267	8508	Z82244	Homo sapiens bK286B10.1 (target of myb1 (chicken) homolog)	288	61.176
268	8509	AL022318	Homo sapiens bK150C2.3 (PUTATIVE novel protein similar to APOBEC1 (Apolipoprotein B mRNA	1457	100.000

TABLE 1

			editing protein) and Phorbolin)		
269	8515	AB034695	Homo sapiens endomucin-2	1583	99.617
270	8519	AL132980	Arabidopsis thaliana putative protein	276	28.500
271	8530	AL034548	Homo sapiens dJ1103G7.3 (novel protein kinase domains containing protein similar to phosphoprotein C8FW)	2443	99.721
272	8532	AF161470	Homo sapiens HSPC121	2478	99.732
273	8532	AF161470	Homo sapiens HSPC121	2478	99.732
274	8539	Y16791	Homo sapiens keratin, type I	2818	99.294
275	8541	AK001623	Homo sapiens unnamed protein product	1191	56.494
276	8543	M32334	Homo sapiens intercellular adhesion molecule 2	1835	100.000
277	8593	U29488	Caenorhabditis elegans C56C10.3 gene product	849	61.333
278	8595	AL117207	Caenorhabditis elegans Y60A3A.20	431	51.786
279	8615	X77858	Human papillomavirus type 59 ORF putative E5	99	31.746
280	8620	AF017807	Homo sapiens Arp2/3 complex 16kDa subunit	685	68.831
281	8621	AF077042	Homo sapiens 30S ribosomal protein S7 homolog	1625	100.000
282	8623	AB018322	Homo sapiens KIAA0779 protein	2019	100.000
283	8625	AF180819	Homo sapiens LAK1 protein	3544	100.000
284	8628	Z75134	Canis familiaris rod transducin	2322	100.000
285	8628	Z75134	Canis familiaris rod transducin	2322	100.000
286	8629	AF249873	Homo sapiens muscle-specific protein	1789	100.000
287	8630	AL050007	Homo sapiens hypothetical protein	506	98.795
288	8631	AK001341	Homo sapiens unnamed protein product	2372	99.419
289	8633	AF156102	Homo sapiens ELL complex EAP30 subunit	1678	99.612
290	8634	Z95114	Homo sapiens bK212A2.1 (TNF-inducible protein CG12-1 (similar to apolipoprotein L))	1201	59.627
291	8635	X89773	Homo sapiens interferon induced	1184	100.000
292	8636	AL050143	Homo sapiens	759	100.000

TABLE 1

			hypothetical protein		
293	8659	AJ011098	Homo sapiens telethonin	742	100.000
294	8660	AE003751	Drosophila melanogaster CG10420 gene product	456	30.933
295	8667	AF034801	Homo sapiens liprin-alpha4	3281	98.228
296	8667	AF034801	Homo sapiens liprin-alpha4	3312	100.000
297	8685	AL049851	Homo sapiens dJ889J22B.1 (novel protein (isoform 1))	2273	100.000
298	8805	AL133100	Homo sapiens hypothetical protein	2206	100.000
299	8896	AB032967	Homo sapiens KIAA1141 protein	6481	99.891
300	8978	AL035423	Homo sapiens dJ20I3.1 (brain mitochondrial carrier protein-1 (BMCP1))	1316	76.981
301	9046	AF198532	Homo sapiens lymphoid enhancer binding factor-1	2802	100.000
302	9048	AK002137	Homo sapiens unnamed protein product	1645	97.571
303	9116	AL050008	Homo sapiens hypothetical protein	1660	100.000
304	9195	AB037836	Homo sapiens KIAA1415 protein	6358	99.685
305	9201	AB014579	Homo sapiens KIAA0679 protein	5141	99.870
306	9307	Z82022	Homo sapiens GlcNac-1-P transferase	2640	99.750
307	9321	U90543	Homo sapiens butyrophilin	333	44.444
308	9397	AJ222644	Arabidopsis thaliana asparaginyl-tRNA synthetase	1266	46.855
309	9405	AF054180	Homo sapiens hematopoietic cell derived zinc finger protein	452	79.121
310	9406	AF209192	Homo sapiens Apobec-1 complementation factor	3873	99.659
311	9422	Z75330	Homo sapiens nuclear protein SA-1	8280	99.921
312	9494	L42324	Homo sapiens G protein-linked receptor	2157	98.792
313	9512	AJ131891	Homo sapiens DNA polymerase mu	3370	100.000
314	9632	AL137523	Homo sapiens hypothetical protein	1766	99.638
315	9661	AK000195	Homo sapiens unnamed protein product	2209	100.000

TABLE 1

316	9664	X57802	Homo sapiens immunoglobulin lambda light chain	1220	81.498
317	9691	Z36715	Homo sapiens Net	2614	98.771
318	9700	AF161532	Homo sapiens HSPC047	939	100.000
319	9716	AB032955	Homo sapiens KIAA1129 protein	4121	99.680
320	9721	D63877	Homo sapiens KIAA0157 gene product is novel.	609	40.271
321	9870	L13687	Homo sapiens ADP-ribosylation factor-like protein 2	419	36.667
322	9887	AJ387747	Homo sapiens sialin	3333	99.798
323	9923	AK001518	Homo sapiens unnamed protein product	1335	65.031
324	9938	AB005541	Rattus rattus PCTAIRE3	2687	87.553
325	9964	AJ238379	Homo sapiens putative TH1 protein	3828	100.000
326	10007	AB033090	Homo sapiens KIAA1264 protein	5081	99.734
327	10009	AF186469	Rattus norvegicus TM6P1	341	26.754
328	10046	X78077	Equus caballus link protein	1289	54.717
329	10156	AE003507	Drosophila melanogaster CG6769 gene product	1053	39.540
330	10276	AF227899	Homo sapiens breast carcinoma-associated antigen isoform I	5616	99.771
331	10283	AF198532	Homo sapiens lymphoid enhancer binding factor-1	2802	100.000

CLAIMS

WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 1 – 331, or the mature protein coding portion thereof, the active domain thereof, or the complement thereof.

2. An isolated polynucleotide encoding a polypeptide with biological activity, said polynucleotide which hybridizes to the polynucleotide of claim 1 under stringent hybridization conditions.

3. An isolated polynucleotide encoding a polypeptide with biological activity, said polynucleotide having greater than about 90% sequence identity with the polynucleotide of claim 1.

4. The polynucleotide of claim 1 which is a DNA.

5. An isolated polynucleotide which comprises the complement of the polynucleotide of claim 1.

6. A vector comprising the polynucleotide of claim 1.

7. An expression vector comprising the polynucleotide of claim 1.

8. A host cell genetically engineered to contain the polynucleotide of claim 1.

9. A host cell genetically engineered to contain the polynucleotide of claim 1 in operative association with a regulatory sequence that controls expression of the polynucleotide in the host cell.

10. A composition comprising a polypeptide, wherein the polypeptide is selected from the group consisting of:

(a) a polypeptide encoded by any one of the polynucleotide of claim 1;

(b) a polypeptide encoded by a polynucleotide hybridizing under stringent conditions with any one of SEQ ID NO: 1 - 331; and

(c) a variant of the protein (a) or (b).

11. A composition comprising the polypeptide of claim 10 and a carrier.

12. An antibody directed against the polypeptide of claim 10.

13. A method for detecting the polynucleotide of claim 1 in a sample, comprising:

a) contacting the sample with a compound that binds to and forms a complex with the polynucleotide of claim 1 for a period sufficient to form the complex; and

b) detecting the complex, so that if a complex is detected, the polynucleotide of claim 1 is detected.

14. A method for detecting the polynucleotide of claim 1 in a sample, comprising:

a) contacting the sample under stringent hybridization conditions with nucleic acid primers that anneal to the polynucleotide of claim 1 under such conditions;

b) amplifying a product comprising at least a portion of the polynucleotide of claim 1; and

c) detecting said product and thereby the polynucleotide of claim 1 in the sample.

15. The method of claim 14, wherein the polynucleotide is an RNA molecule that encodes a polypeptide of claim 10, and the method further comprises reverse transcribing an annealed RNA molecule into a cDNA polynucleotide.

16. A method for detecting the polypeptide of claim 10 in a sample, comprising:

a) contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex; and

b) detecting formation of the complex, so that if a complex formation is detected, the polypeptide of claim 10 is detected.

17. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

a) contacting the compound with the polypeptide of claim 10 under conditions and for a time sufficient to form a polypeptide/compound complex; and

b) detecting the complex, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

18. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

a) contacting the compound with the polypeptide of claim 10, in a cell, for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and

b) detecting the complex by detecting reporter gene sequence expression, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

19. A method of producing the polypeptide of claim 10, comprising,

a) culturing the host cell of claim 8 for a period of time sufficient to express the polypeptide in said cell; and

b) isolating the polypeptide from the cell culture or cells of step (a).

20. An isolated polypeptide comprising an amino acid selected from the group consisting of any one of the polypeptides listed in the Sequence Listing, the mature protein portion thereof, or the active domain thereof.

21. The polypeptide of claim 20 wherein the polypeptide is provided on a polypeptide array.

22. A collection of polynucleotides, wherein the collection comprising the sequence information of at least one of SEQ ID NO: 1 - 331.

23. The collection of claim 22, wherein the collection is provided on a nucleic acid array.

24. The array of claim 23, wherein the array detects full-matches to any one of the polynucleotides in the collection of claim 22.

25. The array of claim 22, wherein the array detects mismatches to any one of the polynucleotides in the collection of claim 22.

26. The collection of claim 22, wherein the collection is provided in a computer-readable format.

27. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

28. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising an antibody that specifically binds to a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

ABSTRACT OF THE INVENTION

The present invention provides novel nucleic acids, novel polypeptide sequences encoded by these nucleic acids and uses thereof.

5

Sequence Listing

Express Mail No.: EK305107157US
Docket No.: 784CIP2

DECLARATION FOR PATENT APPLICATION AND POWER OF ATTORNEY

As [a] below named inventor(s), I/we hereby declare that:

Y. Tom Tang, Chenghua Liu, Vinod Asundi, Chongjun Xu, Ping Zhou, Yunqing Ma, Jian-Rui Wang, Qing A. Zhao, Feiyan Ren, Rui-hong Chen, Dunrui Wang, Zhiwei Wang, Tom Wehrman, Jie Zhang, Xiaohong B. Qian, John Tillinghast, Radoje T. Drmanac

My/our residence, post office address and citizenship is/are as stated below next to my/our name(s).

I/we believe I/we am/are an/the original, first and sole/joint inventor of the subject matter which is claimed and for which a patent is sought on the invention entitled: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES, the specification of which

_X_ is attached hereto.

____ was filed on [date] as Application Serial Number [ ] and was amended on [date].

I/We hereby state that I/we have reviewed and understand the contents of the above-identified specification, including the claims as amended by any amendment referred to above.

I/We acknowledge the duty to disclose information which is material to the examination of this application in accordance with Title 37, Code of Federal Regulations, Section 1.56(a).

I/We hereby claim foreign priority benefits under Title 35, United States Code, § 119 of any foreign application(s) for patent or inventor's certificate, listed below and so identified, and I/we have also identified below any foreign application for patent or inventor's certificate on this invention filed by me or my legal representatives or assigns and having a filing date before that of the application on which priority is claimed:

NUMBER	COUNTRY	DAY/MONTH/ YEAR FILED	PRIORITY CLAIMED - YES OR NO

I/We hereby claim the benefit under Title 35, United States Code, § 120 of any United States application(s) listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States application in the manner provided by the first paragraph of Title 35, United States Code, § 112, I/we acknowledge the duty to disclose material information as defined in Title 37, Code of Federal Regulations, § 1.56(a) which occurred between the filing date of the prior application and the national or PCT international filing date of this application.

SERIAL NUMBER	FILING DATE	STATUS
09/552,317	April 25, 2000	Pending
09/488,725	January 21, 2000	Pending

I/We hereby declare that all statements made herein of my/our own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under § 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

I/We hereby appoint the following attorneys and agents, with full power of substitution and revocation, to prosecute this application and to transact all business in the United States Patent and Trademark Office connected therewith and request that all correspondence and telephone calls with respect to this application be directed to Petrina S. Hsi, HYSEQ, INC., 670 Almanor Avenue, Sunnyvale, CA 94086, Telephone No. (408) 524-8100:

ATTORNEY	REGISTRATION NO.
Petrina S. Hsi	38,496

Full name of first joint inventor: Y. Tom Tang

Inventor's signature: _____ Date: _____

Residence and Post Office Address: 4230 Ranwick Court, San Jose, CA 95118

Citizenship: People's Republic of China

Full name of second joint inventor: Chenghua Liu

Inventor's signature: _____ Date: _____

Residence and Post Office Address: 1125 Ranchero Way, Apt. # 14, San Jose, CA 95117

Citizenship: People's Republic of China

Full name of third joint inventor: Vinod Asundi

Inventor's signature: _____ Date: _____

Residence and Post Office Address: 709 Foster City Blvd., Foster City, CA 94404

Citizenship: United States of America

Full name of fourth joint inventor: Chongjun Xu

Inventor's signature: _____ Date: _____

Residence and Post Office Address: 2918 Manitoba Drive, San Jose, CA 95130

Citizenship: People's Republic of China

Full name of fifth joint inventor: Ping Zhou

Inventor's signature: _____ Date: _____

Residence and Post Office Address: 1461 Japaur Lane, San Jose, CA 95132

Citizenship: People's Republic of China

Full name of sixth joint inventor: Yunqing Ma

Inventor's signature: _____ Date: _____

Residence and Post Office Address: 280 West California Avenue, Apt. 206, Sunnyvale, CA 94086

Citizenship: People's Republic of China

Full name of
seventh joint inventor: Jian-Rui Wang

Inventor's signature: _____ Date: _____

Residence and Post
Office Address: 744 Stendhal Lane, Cupertino, CA 95014

Citizenship: People's Republic of China

Full name of
eighth joint inventor: Qing A. Zhao

Inventor's signature: _____ Date: _____

Residence and Post
Office Address: 1028 S. de Anza Blvd., Apt. B-210, San Jose, CA 95129

Citizenship: People's Republic of China

Full name of
ninth joint inventor: Feiyan Ren

Inventor's signature: _____ Date: _____

Residence and Post
Office Address: 20685 Garden Manor Court, Cupertino, CA 95014

Citizenship: United States of America

Full name of
tenth joint inventor: Rui-hong Chen

Inventor's signature: _____ Date: _____

Residence and Post
Office Address: 1031 Flying Fish Street, Foster City, CA 94404

Citizenship: United States of America

Full name of eleventh joint inventor: Dunrui Wang

Inventor's signature: _____ Date: _____

Residence and Post Office Address: 932 La Palma Place, Milpitas, CA 95035

Citizenship: People's Republic of China

Full name of twelfth joint inventor: Zhiwei Wang

Inventor's signature: _____ Date: _____

Residence and Post Office Address: 936 Alturas Avenue, #B36, Sunnyvale, CA 94085

Citizenship: People's Republic of China

Full name of thirteenth joint inventor: Tom Wehrman

Inventor's signature: _____ Date: _____

Residence and Post Office Address: 300 Pasteur Drive, Edwards R314, Stanford University Medical Center, Stanford, CA 94305

Citizenship: United States of America

Full name of fourteenth joint inventor: Jie Zhang

Inventor's signature: _____ Date: _____

Residence and Post Office Address: 20800 Homestead Road, #38B, Cupertino, CA 95014

Citizenship: People's Republic of China

Full name of
fifteenth joint inventor: Xiaohong B. Qian

Inventor's signature: _____ Date: _____

Residence and Post
Office Address: 3662 Tumble Way, San Jose, CA 95132

Citizenship: People's Republic of China

Full name of
sixteenth joint inventor: John Tillinghast

Inventor's signature: _____ Date: _____

Residence and Post
Office Address: 269 Santa Margarita Avenue, Menlo Park, CA 94025

Citizenship: United States of America

Full name of
seventeenth joint inventor: Radoje T. Drmanac

Inventor's signature: _____ Date: _____

Residence and Post
Office Address: 850 East Greenwich Place, Palo Alto, CA 94303

Citizenship: Yugoslavia

SEQUENCE LISTING

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Liu, Chenghua
Asundi, Vinod
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Zhao, Qing A.
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US 2005/0260750 A1

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Met His Ala Arg Ala Ala Arg Gln Cys Asp Gly Tyr Leu Gln
1 5 10

aat tcg ccc ttt tcc cgg gtc gac gat ttc gtc gcg ctg ctc gga gag 96
Asn Ser Pro Phe Ser Arg Val Asp Asp Phe Val Ala Leu Leu Gly Glu
15 20 25 30

ctc tgc gct gtt ctg gac agc tgc gac ggc gcg ctg ggc tgg cgc ggc 144
Leu Cys Ala Val Leu Asp Ser Cys Asp Gly Ala Leu Gly Trp Arg Gly
31 36 41 46

ctg gca gag aga ctt tca agc agc tgg ctg gat gtt cgt cat att gaa 192
Leu Ala Glu Arg Leu Ser Ser Ser Trp Leu Asp Val Arg His Ile Glu
47 52 57 62

aag tat gta gac caa ggt aaa agt gga aca aga gaa tta ctt tgg tcc 240
Lys Tyr Val Asp Gln Gly Lys Ser Gly Thr Arg Glu Leu Leu Trp Ser

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 63                  68                  73                  78

tgg gca cag aaa aac aag acc atc ggt gac ctt tta cag gtc ctc cag      288
Trp Ala Gln Lys Asn Lys Thr Ile Gly Asp Leu Leu Gln Val Leu Gln
 79                  84                  89                  94

gag atg gga cat cgt cga gct att cat tta att aca aac tat gga gca      336
Glu Met Gly His Arg Arg Ala Ile His Leu Ile Thr Asn Tyr Gly Ala
 95                 100                 105                 110

gtg ttg agt cct tca gag aag agt tat cag gaa ggt gga ttt cca aat      384
Val Leu Ser Pro Ser Glu Lys Ser Tyr Gln Glu Gly Gly Phe Pro Asn
111                 116                 121                 126

ata tta ttc aag gaa aca gcc aat gtc acc gtg gat aat gtt ctt att      432
Ile Leu Phe Lys Glu Thr Ala Asn Val Thr Val Asp Asn Val Leu Ile
127                 132                 137                 142

cct gaa cat aat gaa aaa gga gta ctg ctt aaa tct tcc atc agc ttt      480
Pro Glu His Asn Glu Lys Gly Val Leu Leu Lys Ser Ser Ile Ser Phe
143                 148                 153                 158

caa aat atc ata gaa gga act aga aat ttc cac aaa gac ttc cta att      528
Gln Asn Ile Ile Glu Gly Thr Arg Asn Phe His Lys Asp Phe Leu Ile
159                 164                 169                 174

gga gaa gga gag att ttt gag gta tac aga gtg gag att caa aac cta      576
Gly Glu Gly Glu Ile Phe Glu Val Tyr Arg Val Glu Ile Gln Asn Leu
175                 180                 185                 190

aca tat gct gtc aaa tta ttt aaa cag gag aaa aaa atg cag tgt aag      624
Thr Tyr Ala Val Lys Leu Phe Lys Gln Glu Lys Lys Met Gln Cys Lys
191                 196                 201                 206

aag cat tgg aag agg ttt tta tct gag ctt gaa gtt tta cta ctg ttt      672
Lys His Trp Lys Arg Phe Leu Ser Glu Leu Glu Val Leu Leu Leu Phe
207                 212                 217                 222

cat cac cca aac ata cta gag ttg gct gca tat ttt aca gag act gag      720
His His Pro Asn Ile Leu Glu Leu Ala Ala Tyr Phe Thr Glu Thr Glu
223                 228                 233                 238

aag ttc tgt ctg att tat cca tac atg aga aat gga aca ctt ttt gac      768
Lys Phe Cys Leu Ile Tyr Pro Tyr Met Arg Asn Gly Thr Leu Phe Asp
239                 244                 249                 254

aga ttg cag tgt gta ggt gac acg gcc cca ctc cct tgg cac att cga      816
Arg Leu Gln Cys Val Gly Asp Thr Ala Pro Leu Pro Trp His Ile Arg
255                 260                 265                 270

atc ggt ata tta ata gga ata tcc aaa gcc att cac tac ctg cac aac      864
Ile Gly Ile Leu Ile Gly Ile Ser Lys Ala Ile His Tyr Leu His Asn
271                 276                 281                 286

gtt caa cca tgc tcg gtc atc tgt ggc agt ata tca agt gca aac atc      912
Val Gln Pro Cys Ser Val Ile Cys Gly Ser Ile Ser Ser Ala Asn Ile
287                 292                 297                 302
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ctt ttg gat gat cag ttt caa ccc aaa cta act gat ttt gcc atg gca      960
Leu Leu Asp Asp Gln Phe Gln Pro Lys Leu Thr Asp Phe Ala Met Ala
303                 308                 313                 318

cac ttc cgg tcc cac cta gaa cat cag agt tgt acc ata aat atg acc     1008
His Phe Arg Ser His Leu Glu His Gln Ser Cys Thr Ile Asn Met Thr
319                 324                 329                 334

agc agc agc agt aaa cat ctg tgg tac atg cca gaa gag tac atc aga     1056
Ser Ser Ser Ser Lys His Leu Trp Tyr Met Pro Glu Glu Tyr Ile Arg
335                 340                 345                 350

cag ggg aaa ctt tcc att aaa aca gat gtc tac agc ttt gga att gta     1104
Gln Gly Lys Leu Ser Ile Lys Thr Asp Val Tyr Ser Phe Gly Ile Val
351                 356                 361                 366

ata atg gaa gtt cta aca gga tgt aga gta gtg tta gat gat cca aaa     1152
Ile Met Glu Val Leu Thr Gly Cys Arg Val Val Leu Asp Asp Pro Lys
367                 372                 377                 382

cat atc cag ctg cgg gat ctc ctt aga gaa ttg atg gag aag aga ggc     1200
His Ile Gln Leu Arg Asp Leu Leu Arg Glu Leu Met Glu Lys Arg Gly
383                 388                 393                 398

ctg gat tca tgt ctc tca ttt cta gat aag aaa gtg cct ccc tgc cct     1248
Leu Asp Ser Cys Leu Ser Phe Leu Asp Lys Lys Val Pro Pro Cys Pro
399                 404                 409                 414

cgg aat ttc tct gcc aag ctc ttc tgt ttg gca ggc cgg tgt gct gca     1296
Arg Asn Phe Ser Ala Lys Leu Phe Cys Leu Ala Gly Arg Cys Ala Ala
415                 420                 425                 430

acg cgg gca aag tta aga cca tca atg gat gaa gtt tta aat act ctt     1344
Thr Arg Ala Lys Leu Arg Pro Ser Met Asp Glu Val Leu Asn Thr Leu
431                 436                 441                 446

gaa agt act caa gcc agc ttg tat ttt gct gaa gat cct ccc aca tca     1392
Glu Ser Thr Gln Ala Ser Leu Tyr Phe Ala Glu Asp Pro Pro Thr Ser
447                 452                 457                 462

cta aag tcc ttc agg tgt cct tct cct cta ttc ctg gag aat gta cca     1440
Leu Lys Ser Phe Arg Cys Pro Ser Pro Leu Phe Leu Glu Asn Val Pro
463                 468                 473                 478

agt att cca gtg gaa gat gat gaa agc cag aat aac aat tta cta cct     1488
Ser Ile Pro Val Glu Asp Asp Glu Ser Gln Asn Asn Asn Leu Leu Pro
479                 484                 489                 494

tct gat gaa ggc ctg agg ata gac aga atg act cag aaa act cct ttt     1536
Ser Asp Glu Gly Leu Arg Ile Asp Arg Met Thr Gln Lys Thr Pro Phe
495                 500                 505                 510

gaa tgc agc cag tct gag gtt atg ttt ctg agc ttg gac aaa aag cca     1584
Glu Cys Ser Gln Ser Glu Val Met Phe Leu Ser Leu Asp Lys Lys Pro
511                 516                 521                 526
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gag agc aag aga aat gag gaa gct tgc aac atg ccc agt tct tct tgt     1632
Glu Ser Lys Arg Asn Glu Glu Ala Cys Asn Met Pro Ser Ser Ser Cys
527                 532                 537                 542

gaa gaa agt tgg ttc cca aag tat ata gtt cca tcc cag gac tta agg     1680
Glu Glu Ser Trp Phe Pro Lys Tyr Ile Val Pro Ser Gln Asp Leu Arg
543                 548                 553                 558

ccc tat aag gta aat ata gat cct tct tca gaa gct cca ggg cat tct     1728
Pro Tyr Lys Val Asn Ile Asp Pro Ser Ser Glu Ala Pro Gly His Ser
559                 564                 569                 574

tgc agg agc agg cca gtg gag agc agc tgt tcc tcc aaa ttt tcc tgg     1776
Cys Arg Ser Arg Pro Val Glu Ser Ser Cys Ser Ser Lys Phe Ser Trp
575                 580                 585                 590

gat gaa tat gaa cag tac aaa aaa gaa taa a ttctaccaga agataaagaa     1827
Asp Glu Tyr Glu Gln Tyr Lys Lys Glu  *
591                 596

aaaagcaagt attgcatagg cacctgagca taggtatgac cttgggaaga cattggctcc   1887

ataagcaatg ccaagagaat gatcaatagt gagtttgggt gatgcagata aacaatctgg   1947

ataattccat ttctttttc ccaaaccctc aaacagagtg ccttaaaaaa ttgttttatc   2007

aggataattg tctcatgacc aaatccacgc tcaattagag ccattcaaaa ttccttaaga   2067

tcatgggttc tgacttcagc caaacaaaac aatcaaaacc taccaaaaag ggactggatt   2127

gtaatgtcct ctccatcatc ctcagtgtga gtcctcagag cctccatctg ccaagaacat   2187

tcagttggat tccatcgttt ggtttagctt gcttgcacgg gttgtaggaa atgtctaatt   2247

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tgctgcattt aaa   atg cag cgc aaa agt aaa aaa ggt cag aaa gct aac     169
                 Met Gln Arg Lys Ser Lys Lys Gly Gln Lys Ala Asn
                   1               5                  10
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aac tta aat aca cca aat aat gga aag ttt gtt tat ttt ttg cca tca      217
Asn Leu Asn Thr Pro Asn Asn Gly Lys Phe Val Tyr Phe Leu Pro Ser
 13                  18                  23                  28

ccg gtg aac agc tca aat cca ttt ttt aca tca cag acc aaa gcc aat      265
Pro Val Asn Ser Ser Asn Pro Phe Phe Thr Ser Gln Thr Lys Ala Asn
 29                  34                  39                  44

ggg aat cct gct tgt tcg gcc cag ttg cag cat gtc tcg cca ccc att      313
Gly Asn Pro Ala Cys Ser Ala Gln Leu Gln His Val Ser Pro Pro Ile
 45                  50                  55                  60

ttt cca gct cat tta gca agt gtg tca act cca ttg ttg tcc tca atg      361
Phe Pro Ala His Leu Ala Ser Val Ser Thr Pro Leu Leu Ser Ser Met
 61                  66                  71                  76

gaa agt gtc ata aat cca aat ata act tct cag gat aaa aat gaa caa      409
Glu Ser Val Ile Asn Pro Asn Ile Thr Ser Gln Asp Lys Asn Glu Gln
 77                  82                  87                  92

ggt ggt atg tta tgt tcc caa atg gaa aat tta cct agt act gcc ttg      457
Gly Gly Met Leu Cys Ser Gln Met Glu Asn Leu Pro Ser Thr Ala Leu
 93                  98                 103                 108

cca gca caa atg gaa gat cta acc aaa aca gtt ctg cct ttg aat att      505
Pro Ala Gln Met Glu Asp Leu Thr Lys Thr Val Leu Pro Leu Asn Ile
109                 114                 119                 124

gac agt ggc tca gat cct ttc ctt cct tta cct gca gaa agt agt tca      553
Asp Ser Gly Ser Asp Pro Phe Leu Pro Leu Pro Ala Glu Ser Ser Ser
125                 130                 135                 140

atg tct ctc ttc cct tca cca gca gat agt ggg act aat tct gtt ttt      601
Met Ser Leu Phe Pro Ser Pro Ala Asp Ser Gly Thr Asn Ser Val Phe
141                 146                 151                 156

tcc caa ctg gaa aat aat aca aat cat tat tcc tca cag att gaa gga      649
Ser Gln Leu Glu Asn Asn Thr Asn His Tyr Ser Ser Gln Ile Glu Gly
157                 162                 167                 172

aac act aat tcc tcc ttt cta aag ggg ggt aat ggt gaa aat gca gtt      697
Asn Thr Asn Ser Ser Phe Leu Lys Gly Gly Asn Gly Glu Asn Ala Val
173                 178                 183                 188

ttt cct tca caa gtg aat gtt gca aat aac ttc agt agc acc aat gcc      745
Phe Pro Ser Gln Val Asn Val Ala Asn Asn Phe Ser Ser Thr Asn Ala
189                 194                 199                 204

caa cag tct gca cct gaa aaa gtt aaa aaa gac cgt ggg cgg ggc cca      793
Gln Gln Ser Ala Pro Glu Lys Val Lys Lys Asp Arg Gly Arg Gly Pro
205                 210                 215                 220

aat ggg aag gaa aga aaa cct aag cac aac aaa agg gct aaa tgg cct      841
Asn Gly Lys Glu Arg Lys Pro Lys His Asn Lys Arg Ala Lys Trp Pro
221                 226                 231                 236

gca att atc aga gat ggg aaa ttt atc tgt agc agg tgt tac agg gct      889
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Application/Control Number: 10/564,000

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Ala Ile Ile Arg Asp Gly Lys Phe Ile Cys Ser Arg Cys Tyr Arg Ala
237                 242                 247                 252

ttt act aat ccc aga tca ctg ggt ggg cac tta tcc aag cga tct tac      937
Phe Thr Asn Pro Arg Ser Leu Gly Gly His Leu Ser Lys Arg Ser Tyr
253                 258                 263                 268

tgt aaa cca ctg gat gga gcc gaa att gct caa gaa ctt cta cag agt      985
Cys Lys Pro Leu Asp Gly Ala Glu Ile Ala Gln Glu Leu Leu Gln Ser
269                 274                 279                 284

aat gga cag cct tct ctt ctt gcc agc atg att ctc tcc aca aat gca     1033
Asn Gly Gln Pro Ser Leu Leu Ala Ser Met Ile Leu Ser Thr Asn Ala
285                 290                 295                 300

gta aat ttg cag cag cca caa caa tct acc ttc aat cca gaa gca tgt     1081
Val Asn Leu Gln Gln Pro Gln Gln Ser Thr Phe Asn Pro Glu Ala Cys
301                 306                 311                 316

ttt aaa gat cca tca ttt cta cag ctt ctt gct gaa aat cgc tcg cca     1129
Phe Lys Asp Pro Ser Phe Leu Gln Leu Leu Ala Glu Asn Arg Ser Pro
317                 322                 327                 332

gca ttt tta cca aat aca ttt cct cga tct ggt gtg act aac ttt aat     1177
Ala Phe Leu Pro Asn Thr Phe Pro Arg Ser Gly Val Thr Asn Phe Asn
333                 338                 343                 348

acc agt gtc agt caa gaa ggt agt gaa att att aaa cag gct ttg gaa     1225
Thr Ser Val Ser Gln Glu Gly Ser Glu Ile Ile Lys Gln Ala Leu Glu
349                 354                 359                 364

act gct ggc att ccc agt aca ttt gag ggt gcc gaa atg ctt tct cat     1273
Thr Ala Gly Ile Pro Ser Thr Phe Glu Gly Ala Glu Met Leu Ser His
365                 370                 375                 380

gtt tca aca ggt tgt gtc tct gat gca tca caa gta aat gca acg gtg     1321
Val Ser Thr Gly Cys Val Ser Asp Ala Ser Gln Val Asn Ala Thr Val
381                 386                 391                 396

atg cca aat cca act gta cca ccc ctg ttg cac act gta tgc cat cca     1369
Met Pro Asn Pro Thr Val Pro Pro Leu Leu His Thr Val Cys His Pro
397                 402                 407                 412

aac acc ttg ctg acc aac cag aat agg acg tca aac tcc aaa act tcc     1417
Asn Thr Leu Leu Thr Asn Gln Asn Arg Thr Ser Asn Ser Lys Thr Ser
413                 418                 423                 428

tcc att gag gaa tgt agc agc ttg cct gtt ttt cca acg aat gac tta     1465
Ser Ile Glu Glu Cys Ser Ser Leu Pro Val Phe Pro Thr Asn Asp Leu
429                 434                 439                 444

cta ctg aag act gtt gaa aat ggt ttg tgc tct agt tca ttt cct aat     1513
Leu Leu Lys Thr Val Glu Asn Gly Leu Cys Ser Ser Ser Phe Pro Asn
445                 450                 455                 460

tct ggt ggg cca tca caa aat ttt acc agt aac agt tct cgt gtt tct     1561
Ser Gly Gly Pro Ser Gln Asn Phe Thr Ser Asn Ser Ser Arg Val Ser
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461                 466                 471                 476

gtt ata agt ggt cct cag aac aca aga tcc agt cat tta aat aaa aag     1609
Val Ile Ser Gly Pro Gln Asn Thr Arg Ser Ser His Leu Asn Lys Lys
477                 482                 487                 492

gga aac agt gct tct aag aga aga aag aaa gtt gct cct cca cta att     1657
Gly Asn Ser Ala Ser Lys Arg Arg Lys Lys Val Ala Pro Pro Leu Ile
493                 498                 503                 508

gca cct aac gct tcc caa aac ttg gta aca agt gac tta aca aca atg     1705
Ala Pro Asn Ala Ser Gln Asn Leu Val Thr Ser Asp Leu Thr Thr Met
509                 514                 519                 524

gga ctc ata gca aag agt gtt gaa atc cca act act aac ctt cat tca     1753
Gly Leu Ile Ala Lys Ser Val Glu Ile Pro Thr Thr Asn Leu His Ser
525                 530                 535                 540

aat gta att cca act tgt gaa cct cag agt ttg gtg gaa aat cta aca     1801
Asn Val Ile Pro Thr Cys Glu Pro Gln Ser Leu Val Glu Asn Leu Thr
541                 546                 551                 556

cag aaa tta aat aat gtt aac aat cag tta ttt atg act gat gta aaa     1849
Gln Lys Leu Asn Asn Val Asn Asn Gln Leu Phe Met Thr Asp Val Lys
557                 562                 567                 572

gag aat ttc aaa acc agt ctt gag tcc cat aca gtg tta gcc cct tta     1897
Glu Asn Phe Lys Thr Ser Leu Glu Ser His Thr Val Leu Ala Pro Leu
573                 578                 583                 588

aca tta aaa act gaa aat ggt gat tcc caa atg atg gct ttg aat tca     1945
Thr Leu Lys Thr Glu Asn Gly Asp Ser Gln Met Met Ala Leu Asn Ser
589                 594                 599                 604

tgc aca act tca gta aat tct gat ttg cag att tct gaa gac aat gtt     1993
Cys Thr Thr Ser Val Asn Ser Asp Leu Gln Ile Ser Glu Asp Asn Val
605                 610                 615                 620

ata caa aac ttt gaa aag act ctt gaa att att aaa act gct atg aat     2041
Ile Gln Asn Phe Glu Lys Thr Leu Glu Ile Ile Lys Thr Ala Met Asn
621                 626                 631                 636

tct caa ata ctt gag gta aaa agt gga tct cag ggt gct ggt gaa act     2089
Ser Gln Ile Leu Glu Val Lys Ser Gly Ser Gln Gly Ala Gly Glu Thr
637                 642                 647                 652

tca caa aat gct caa ata aat tat aac att cag ctt cct tca gta aac     2137
Ser Gln Asn Ala Gln Ile Asn Tyr Asn Ile Gln Leu Pro Ser Val Asn
653                 658                 663                 668

act gtg caa aat aac aaa tta ccc gat tct tct ccg ttt tcc tcc ttt     2185
Thr Val Gln Asn Asn Lys Leu Pro Asp Ser Ser Pro Phe Ser Ser Phe
669                 674                 679                 684

ata agt gtc atg cca aca aaa agt aac att cct cag tct gaa gta tca     2233
Ile Ser Val Met Pro Thr Lys Ser Asn Ile Pro Gln Ser Glu Val Ser
685                 690                 695                 700
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cat aag gag gat caa ata cag gaa att tta gaa ggc tta cag aaa tta     2281
His Lys Glu Asp Gln Ile Gln Glu Ile Leu Glu Gly Leu Gln Lys Leu
701                 706                 711                 716

aaa tta gaa aat gac cta tcc act cca gca tcc caa tgt gta ctg ata     2329
Lys Leu Glu Asn Asp Leu Ser Thr Pro Ala Ser Gln Cys Val Leu Ile
717                 722                 727                 732

aat aca tca gtg aca ctg act ccc acg cct gtt aaa tca act gca gat     2377
Asn Thr Ser Val Thr Leu Thr Pro Thr Pro Val Lys Ser Thr Ala Asp
733                 738                 743                 748

atc aca gtt att cag cca gtt tct gaa atg ata aac att caa ttt aat     2425
Ile Thr Val Ile Gln Pro Val Ser Glu Met Ile Asn Ile Gln Phe Asn
749                 754                 759                 764

gac aaa gtt aat aaa ccc ttt gtg tgt caa aac caa ggc tgt aac tac     2473
Asp Lys Val Asn Lys Pro Phe Val Cys Gln Asn Gln Gly Cys Asn Tyr
765                 770                 775                 780

agt gct atg aca aag gat gca cta ttt aag cac tat ggt aaa att cat     2521
Ser Ala Met Thr Lys Asp Ala Leu Phe Lys His Tyr Gly Lys Ile His
781                 786                 791                 796

caa tac act cca gaa atg att ctt gaa att aag aag aat caa ttg aaa     2569
Gln Tyr Thr Pro Glu Met Ile Leu Glu Ile Lys Lys Asn Gln Leu Lys
797                 802                 807                 812

ttt gct ccc ttt aaa tgt gta gta cct aca tgt aca aaa aca ttt aca     2617
Phe Ala Pro Phe Lys Cys Val Val Pro Thr Cys Thr Lys Thr Phe Thr
813                 818                 823                 828

aga aat tct aac ctc cgg gca cac tgt cag ttg gtg cat cat ttt aca     2665
Arg Asn Ser Asn Leu Arg Ala His Cys Gln Leu Val His His Phe Thr
829                 834                 839                 844

act gaa gaa atg gta aag tta aaa att aaa agg cct tat gga aga aaa     2713
Thr Glu Glu Met Val Lys Leu Lys Ile Lys Arg Pro Tyr Gly Arg Lys
845                 850                 855                 860

tct cag agt gaa aat gtg ccg gcc tca cga agt aca caa gtg aaa aaa     2761
Ser Gln Ser Glu Asn Val Pro Ala Ser Arg Ser Thr Gln Val Lys Lys
861                 866                 871                 876

cag cta gct atg aca gag gaa aat aaa aag gaa tct cag cct gct tta     2809
Gln Leu Ala Met Thr Glu Glu Asn Lys Lys Glu Ser Gln Pro Ala Leu
877                 882                 887                 892

gaa ttg aga gca gag acc caa aat acc cac agt aat gta gca gtg atc     2857
Glu Leu Arg Ala Glu Thr Gln Asn Thr His Ser Asn Val Ala Val Ile
893                 898                 903                 908

cca gaa aaa caa ctt gta gaa aaa aaa agt cct gac aaa aca gaa agt     2905
Pro Glu Lys Gln Leu Val Glu Lys Lys Ser Pro Asp Lys Thr Glu Ser
909                 914                 919                 924
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tct tta caa gtg att aca gtt act tca gaa caa tgt aat aca aat gca     2953
Ser Leu Gln Val Ile Thr Val Thr Ser Glu Gln Cys Asn Thr Asn Ala
925                 930                 935                 940

ctc aca aac aca caa acc aaa gga cgg aag att agg agg cat aaa aaa     3001
Leu Thr Asn Thr Gln Thr Lys Gly Arg Lys Ile Arg Arg His Lys Lys
941                 946                 951                 956

gaa aag gag gag aaa aaa cga aag aag cca gtt tcc caa tcc ctt gag     3049
Glu Lys Glu Glu Lys Lys Arg Lys Lys Pro Val Ser Gln Ser Leu Glu
957                 962                 967                 972

ttt cca aca aga tac agt cct tac aga cct tat cga tgt gtt cac cag     3097
Phe Pro Thr Arg Tyr Ser Pro Tyr Arg Pro Tyr Arg Cys Val His Gln
973                 978                 983                 988

gga tgc ttt gct gcc ttt acg ata cag caa aat ttg att ctc cat tac     3145
Gly Cys Phe Ala Ala Phe Thr Ile Gln Gln Asn Leu Ile Leu His Tyr
989                 994                 999                1004

cag gct gta cac aaa tca gat cta cct gca ttt tca gca gag gtc gaa     3193
Gln Ala Val His Lys Ser Asp Leu Pro Ala Phe Ser Ala Glu Val Glu
1005                1010                1015                1020

gag gaa agt gaa gct ggt aaa gaa agt gaa gaa act gaa act aaa caa     3241
Glu Glu Ser Glu Ala Gly Lys Glu Ser Glu Glu Thr Glu Thr Lys Gln
1021                1026                1031                1036

act ttg aaa gaa ttt cga tgt cag gta agt gac tgt tct cga att ttc     3289
Thr Leu Lys Glu Phe Arg Cys Gln Val Ser Asp Cys Ser Arg Ile Phe
1037                1042                1047                1052

caa gca att act ggc cta ata caa cac tac atg aaa ctt cat gaa atg     3337
Gln Ala Ile Thr Gly Leu Ile Gln His Tyr Met Lys Leu His Glu Met
1053                1058                1063                1068

act cct gaa gaa att gaa agt atg act gct tca gtg gat gtt ggg aag     3385
Thr Pro Glu Glu Ile Glu Ser Met Thr Ala Ser Val Asp Val Gly Lys
1069                1074                1079                1084

ttt cca tgt gac cag tta gag tgt aaa tct tca ttt act aca tat ttg     3433
Phe Pro Cys Asp Gln Leu Glu Cys Lys Ser Ser Phe Thr Thr Tyr Leu
1085                1090                1095                1100

aac tat gtt gtt cat cta gag gca gac cac ggg att gga cta agg gca     3481
Asn Tyr Val Val His Leu Glu Ala Asp His Gly Ile Gly Leu Arg Ala
1101                1106                1111                1116

agt aaa aca gaa gaa gat ggt gta tac aaa tgt gat tgt gaa ggc tgt     3529
Ser Lys Thr Glu Glu Asp Gly Val Tyr Lys Cys Asp Cys Glu Gly Cys
1117                1122                1127                1132

gac cgt ata tat gca acc cgg tcg aat ctc ctc cga cac att ttt aat     3577
Asp Arg Ile Tyr Ala Thr Arg Ser Asn Leu Leu Arg His Ile Phe Asn
1133                1138                1143                1148

aag cat aat gac aaa cat aag gct cat ttg att cgt cca aga aga tta     3625
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 Lys His Asn Asp Lys His Lys Ala His Leu Ile Arg Pro Arg Arg Leu
1149                1154                1159                1164

 aca cca ggc cag gaa aat atg tca agc aag gca aac caa gaa aaa tca     3673
 Thr Pro Gly Gln Glu Asn Met Ser Ser Lys Ala Asn Gln Glu Lys Ser
1165                1170                1175                1180

 aag tct aaa cat cgg ggg acg aag cac agc aga tgt gga aag gaa gga     3721
 Lys Ser Lys His Arg Gly Thr Lys His Ser Arg Cys Gly Lys Glu Gly
1181                1186                1191                1196

 ata aaa atg ccc aag acc aaa cga aag aaa aaa aat aat tta gaa aac     3769
 Ile Lys Met Pro Lys Thr Lys Arg Lys Lys Lys Asn Asn Leu Glu Asn
1197                1202                1207                1212

 aag aat gca aag att gtg cag att gaa gaa aat aag cct tat tct ctg     3817
 Lys Asn Ala Lys Ile Val Gln Ile Glu Glu Asn Lys Pro Tyr Ser Leu
1213                1218                1223                1228

 aaa cgt ggg aag cat gta tat tct ata aag gct aga aat gat gcc ctg     3865
 Lys Arg Gly Lys His Val Tyr Ser Ile Lys Ala Arg Asn Asp Ala Leu
1229                1234                1239                1244

 tct gag tgt aca agc aga ttt gta acc cag tat cca tgt atg ata aag     3913
 Ser Glu Cys Thr Ser Arg Phe Val Thr Gln Tyr Pro Cys Met Ile Lys
1245                1250                1255                1260

 gga tgt act tca gtt gtt aca agt gaa agc aat ata att aga cat tat     3961
 Gly Cys Thr Ser Val Val Thr Ser Glu Ser Asn Ile Ile Arg His Tyr
1261                1266                1271                1276

 aag tgc cat aaa tta tct aag gca ttt aca tca caa cac cga aat ctt     4009
 Lys Cys His Lys Leu Ser Lys Ala Phe Thr Ser Gln His Arg Asn Leu
1277                1282                1287                1292

 ctt att gta ttc aaa cgg tgt tgc aac tca caa gta aag gaa acg tct     4057
 Leu Ile Val Phe Lys Arg Cys Cys Asn Ser Gln Val Lys Glu Thr Ser
1293                1298                1303                1308

 gag caa gaa ggt gct aag aat gat gtg aaa gat tct gac acg tgt gta     4105
 Glu Gln Glu Gly Ala Lys Asn Asp Val Lys Asp Ser Asp Thr Cys Val
1309                1314                1319                1324

 tca gag agc aat gat aat tca aga aca aca gct aca gtt tca caa aag     4153
 Ser Glu Ser Asn Asp Asn Ser Arg Thr Thr Ala Thr Val Ser Gln Lys
1325                1330                1335                1340

 gaa gtt gaa aaa aat gaa aaa gat gaa atg gat gaa cta aca gaa ttg     4201
 Glu Val Glu Lys Asn Glu Lys Asp Glu Met Asp Glu Leu Thr Glu Leu
1341                1346                1351                1356

 ttt att aca aaa tta ata aat gaa gat agc aca agt gta gag acc caa     4249
 Phe Ile Thr Lys Leu Ile Asn Glu Asp Ser Thr Ser Val Glu Thr Gln
1357                1362                1367                1372

 gct aat act tct tca aat gta agt aat gat ttt cag gaa gat aac ctc     4297
 Ala Asn Thr Ser Ser Asn Val Ser Asn Asp Phe Gln Glu Asp Asn Leu
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 tgc cag tca gaa aga caa aaa gca agt aat ttg aag aga gtt aat aag     4345
 Cys Gln Ser Glu Arg Gln Lys Ala Ser Asn Leu Lys Arg Val Asn Lys
1389                1394                1399                1404

 gaa aaa aat gtc tca caa aat aaa aaa agg aaa gtt gaa aaa gct gaa     4393
 Glu Lys Asn Val Ser Gln Asn Lys Lys Arg Lys Val Glu Lys Ala Glu
1405                1410                1415                1420

 cca gca tca gca gct gag tta agt agc gtg cgt aaa gaa gaa gaa act     4441
 Pro Ala Ser Ala Ala Glu Leu Ser Ser Val Arg Lys Glu Glu Glu Thr
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 gct gtt gcc att caa acc att gag gag cat cct gca tct ttt gac tgg     4489
 Ala Val Ala Ile Gln Thr Ile Glu Glu His Pro Ala Ser Phe Asp Trp
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 agc tct ttt aag cca atg gga ttt gaa gta tca ttt ctg aag ttt ctt     4537
 Ser Ser Phe Lys Pro Met Gly Phe Glu Val Ser Phe Leu Lys Phe Leu
1453                1458                1463                1468

 gag gag tct gca gtg aag cag aag aaa aat act gac aaa gac cat ccg     4585
 Glu Glu Ser Ala Val Lys Gln Lys Lys Asn Thr Asp Lys Asp His Pro
1469                1474                1479                1484

 aat act gga aac aaa aaa gga tcc cat tca aat tca aga aaa aat att     4633
 Asn Thr Gly Asn Lys Lys Gly Ser His Ser Asn Ser Arg Lys Asn Ile
1485                1490                1495                1500

 gat aag act gct gtg act agt gga aat cat gta tgt cct tgt aaa gaa     4681
 Asp Lys Thr Ala Val Thr Ser Gly Asn His Val Cys Pro Cys Lys Glu
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 agc gaa acg ttt gta cag ttt gcc aat cca tca cag ctt cag tgc agt     4729
 Ser Glu Thr Phe Val Gln Phe Ala Asn Pro Ser Gln Leu Gln Cys Ser
1517                1522                1527                1532

 gat aat gta aaa att gtt tta gac aag aat ctt aaa gat tgc act gag     4777
 Asp Asn Val Lys Ile Val Leu Asp Lys Asn Leu Lys Asp Cys Thr Glu
1533                1538                1543                1548

 ctt gtc tta aag caa ctt cag gaa atg aaa cct acc gtc agt ctg aaa     4825
 Leu Val Leu Lys Gln Leu Gln Glu Met Lys Pro Thr Val Ser Leu Lys
1549                1554                1559                1564

 aaa ctt gaa gta cat tca aat gat cca gat atg tct gtt atg aaa gat     4873
 Lys Leu Glu Val His Ser Asn Asp Pro Asp Met Ser Val Met Lys Asp
1565                1570                1575                1580

 atc agt ata ggt aaa gcc aca ggc aga ggt cag tac tga taattaatgt      4922
 Ile Ser Ile Gly Lys Ala Thr Gly Arg Gly Gln Tyr  *
1581                1586                1591

 agtataaata catcatttac cattttattt taaataggaa gccatcaagc atgctagaat   4982

 tgtgaaactt tcattatatt tttttgttgt tgacatgaat taacctggcc aaaaacaaaa   5042
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ggggaggaga gggaacccca ggcgcgagcg ggaagagggg acctgcagcc acaacttctc    180

tggtcctctg catcccttct gtccctccac ccgtcccctt ccccaccctc tggcccccac    240

cttcttggag gcgacaaccc ccgggaggca ttagaaggga tttttcccgc aggttgcgaa    300

gggaagcaaa cttggtggca acttgcctcc cggtgcgggc gtctctcccc caccgtctca    360

ac   atg ctt agg ggt ccg ggg ccc ggg ctg ctg ctg ctg gcc gtc ctg     407
     Met Leu Arg Gly Pro Gly Pro Gly Leu Leu Leu Leu Ala Val Leu
       1               5                  10

tgc ctg ggg aca gcg gtg ccc tcc acg gga gcc tcg aag agc aag agg      455
Cys Leu Gly Thr Ala Val Pro Ser Thr Gly Ala Ser Lys Ser Lys Arg
 16                  21                  26                  31

cag gct cag caa atg gtt cag ccc cag tcc ccg gtg gct gtc agt caa      503
Gln Ala Gln Gln Met Val Gln Pro Gln Ser Pro Val Ala Val Ser Gln
 32                  37                  42                  47

agc aag ccc ggt tgt tat gac aat gga aaa cac tat cag ata aat caa      551
Ser Lys Pro Gly Cys Tyr Asp Asn Gly Lys His Tyr Gln Ile Asn Gln
 48                  53                  58                  63

cag tgg gag cgg acc tac cta ggc aat gcg ttg gtt tgt act tgt tat      599
Gln Trp Glu Arg Thr Tyr Leu Gly Asn Ala Leu Val Cys Thr Cys Tyr
 64                  69                  74                  79

gga gga agc cga ggt ttt aac tgc gag agt aaa cct gaa gct gaa gag      647
Gly Gly Ser Arg Gly Phe Asn Cys Glu Ser Lys Pro Glu Ala Glu Glu
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act tgc ttt gac aag tac act ggg aac act tac cga gtg ggt gac act      695
Thr Cys Phe Asp Lys Tyr Thr Gly Asn Thr Tyr Arg Val Gly Asp Thr
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Tyr Glu Arg Pro Lys Asp Ser Met Ile Trp Asp Cys Thr Cys Ile Gly
112                 117                 122                 127

gct ggg cga ggg aga ata agc tgt acc atc gca aac cgc tgc cat gaa      791
Ala Gly Arg Gly Arg Ile Ser Cys Thr Ile Ala Asn Arg Cys His Glu
128                 133                 138                 143

ggg ggt cag tcc tac aag att ggt gac acc tgg agg aga cca cat gag      839
Gly Gly Gln Ser Tyr Lys Ile Gly Asp Thr Trp Arg Arg Pro His Glu
144                 149                 154                 159

act ggt ggt tac atg tta gag tgt gtg tgt ctt ggt aat gga aaa gga      887
Thr Gly Gly Tyr Met Leu Glu Cys Val Cys Leu Gly Asn Gly Lys Gly
160                 165                 170                 175

gaa tgg acc tgc aag ccc ata gct gag aag tgt ttt gat cat gct gct      935
Glu Trp Thr Cys Lys Pro Ile Ala Glu Lys Cys Phe Asp His Ala Ala
176                 181                 186                 191

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Gly Thr Ser Tyr Val Val Gly Glu Thr Trp Glu Lys Pro Tyr Gln Gly
192                 197                 202                 207

tgg atg atg gta gat tgt act tgc ctg gga gaa ggc agc gga cgc atc     1031
Trp Met Met Val Asp Cys Thr Cys Leu Gly Glu Gly Ser Gly Arg Ile
208                 213                 218                 223

act tgc act tct aga aat aga tgc aac gat cag gac aca agg aca tcc     1079
Thr Cys Thr Ser Arg Asn Arg Cys Asn Asp Gln Asp Thr Arg Thr Ser
224                 229                 234                 239

tat aga att gga gac acc tgg agc aag aag gat aat cga gga aac ctg     1127
Tyr Arg Ile Gly Asp Thr Trp Ser Lys Lys Asp Asn Arg Gly Asn Leu
240                 245                 250                 255

ctc cag tgc atc tgc aca ggc aac ggc cga gga gag tgg aag tgt gag     1175
Leu Gln Cys Ile Cys Thr Gly Asn Gly Arg Gly Glu Trp Lys Cys Glu
256                 261                 266                 271

agg cac acc tct gtg cag acc aca tcg agc gga tct ggc ccc ttc acc     1223
Arg His Thr Ser Val Gln Thr Thr Ser Ser Gly Ser Gly Pro Phe Thr
272                 277                 282                 287

gat gtt cgt gca gct gtt tac caa ccg cag cct cac ccc cag cct cct     1271
Asp Val Arg Ala Ala Val Tyr Gln Pro Gln Pro His Pro Gln Pro Pro
288                 293                 298                 303

ccc tat ggc cac tgt gtc aca gac agt ggt gtg gtc tac tct gtg ggg     1319
Pro Tyr Gly His Cys Val Thr Asp Ser Gly Val Val Tyr Ser Val Gly
304                 309                 314                 319

atg cag tgg ctg aag aca caa gga aat aag caa atg ctt tgc acg tgc     1367
Met Gln Trp Leu Lys Thr Gln Gly Asn Lys Gln Met Leu Cys Thr Cys
320                 325                 330                 335

ctg ggc aac gga gtc agc tgc caa gag aca gct gta acc cag act tac     1415
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Leu Gly Asn Gly Val Ser Cys Gln Glu Thr Ala Val Thr Gln Thr Tyr
336                 341                 346                 351

ggt ggc aac tca aat gga gag cca tgt gtc tta cca ttc acc tac aat     1463
Gly Gly Asn Ser Asn Gly Glu Pro Cys Val Leu Pro Phe Thr Tyr Asn
352                 357                 362                 367

ggc agg acg ttc tac tcc tgc acc aca gaa ggg cga cag gac gga cat     1511
Gly Arg Thr Phe Tyr Ser Cys Thr Thr Glu Gly Arg Gln Asp Gly His
368                 373                 378                 383

ctt tgg tgc agc aca act tcg aat tat gag cag gac cag aaa tac tct     1559
Leu Trp Cys Ser Thr Thr Ser Asn Tyr Glu Gln Asp Gln Lys Tyr Ser
384                 389                 394                 399

ttc tgc aca gac cac act gtt ttg gtt cag act cga gga gga aat tcc     1607
Phe Cys Thr Asp His Thr Val Leu Val Gln Thr Arg Gly Gly Asn Ser
400                 405                 410                 415

aat ggt gcc ttg tgc cac ttc ccc ttc cta tac aac aac cac aat tac     1655
Asn Gly Ala Leu Cys His Phe Pro Phe Leu Tyr Asn Asn His Asn Tyr
416                 421                 426                 431

act gat tgc act tct gag ggc aga aga gac aac atg aag tgg tgt ggg     1703
Thr Asp Cys Thr Ser Glu Gly Arg Arg Asp Asn Met Lys Trp Cys Gly
432                 437                 442                 447

acc aca cag aac tat gat gcc gac cag aag ttt ggg ttc tgc ccc atg     1751
Thr Thr Gln Asn Tyr Asp Ala Asp Gln Lys Phe Gly Phe Cys Pro Met
448                 453                 458                 463

gct gcc cac gag gaa atc tgc aca acc aat gaa ggg gtc atg tac cgc     1799
Ala Ala His Glu Glu Ile Cys Thr Thr Asn Glu Gly Val Met Tyr Arg
464                 469                 474                 479

att gga gat cag tgg gat aag cag cat gac atg ggt cac atg atg agg     1847
Ile Gly Asp Gln Trp Asp Lys Gln His Asp Met Gly His Met Met Arg
480                 485                 490                 495

tgc acg tgt gtt ggg aat ggt cgt ggg gaa tgg aca tgc att gcc tac     1895
Cys Thr Cys Val Gly Asn Gly Arg Gly Glu Trp Thr Cys Ile Ala Tyr
496                 501                 506                 511

tcg caa ctt cga gat cag tgc att gtt gat gac atc act tac aat gtg     1943
Ser Gln Leu Arg Asp Gln Cys Ile Val Asp Asp Ile Thr Tyr Asn Val
512                 517                 522                 527

aac gac aca ttc cac aag cgt cat gaa gag ggg cac atg ctg aac tgt     1991
Asn Asp Thr Phe His Lys Arg His Glu Glu Gly His Met Leu Asn Cys
528                 533                 538                 543

aca tgc ttc ggt cag ggt cgg ggc agg tgg aag tgt gat ccc gtc gac     2039
Thr Cys Phe Gly Gln Gly Arg Gly Arg Trp Lys Cys Asp Pro Val Asp
544                 549                 554                 559

caa tgc cag gat tca gag act ggg acg ttt tat caa att gga gat tca     2087
Gln Cys Gln Asp Ser Glu Thr Gly Thr Phe Tyr Gln Ile Gly Asp Ser
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560                 565                 570                 575

tgg gag aag tat gtg cat ggt gtc aga tac cag tgc tac tgc tat ggc     2135
Trp Glu Lys Tyr Val His Gly Val Arg Tyr Gln Cys Tyr Cys Tyr Gly
576                 581                 586                 591

cgt ggc att ggg gag tgg cat tgc caa cct tta cag acc tat cca agc     2183
Arg Gly Ile Gly Glu Trp His Cys Gln Pro Leu Gln Thr Tyr Pro Ser
592                 597                 602                 607

tca agt ggt cct gtc gaa gta ttt atc act gag act ccg agt cag ccc     2231
Ser Ser Gly Pro Val Glu Val Phe Ile Thr Glu Thr Pro Ser Gln Pro
608                 613                 618                 623

aac tcc cac ccc atc cag tgg aat gca cca cag cca tct cac att tcc     2279
Asn Ser His Pro Ile Gln Trp Asn Ala Pro Gln Pro Ser His Ile Ser
624                 629                 634                 639

aag tac att ctc agg tgg aga cct aaa aat tct gta ggc cgt tgg aag     2327
Lys Tyr Ile Leu Arg Trp Arg Pro Lys Asn Ser Val Gly Arg Trp Lys
640                 645                 650                 655

gaa gct acc ata cca ggc cac tta aac tcc tac acc atc aaa ggc ctg     2375
Glu Ala Thr Ile Pro Gly His Leu Asn Ser Tyr Thr Ile Lys Gly Leu
656                 661                 666                 671

aag cct ggt gtg gta tac gag ggc cag ctc atc agc atc cag cag tac     2423
Lys Pro Gly Val Val Tyr Glu Gly Gln Leu Ile Ser Ile Gln Gln Tyr
672                 677                 682                 687

ggc cac caa gaa gtg act cgc ttt gac ttc acc acc acc agc acc agc     2471
Gly His Gln Glu Val Thr Arg Phe Asp Phe Thr Thr Thr Ser Thr Ser
688                 693                 698                 703

aca cct gtg acc agc aac acc gtg aca gga gag acg act ccc ttt tct     2519
Thr Pro Val Thr Ser Asn Thr Val Thr Gly Glu Thr Thr Pro Phe Ser
704                 709                 714                 719

cct ctt gtg gcc act tct gaa tct gtg acc gaa atc aca gcc agt agc     2567
Pro Leu Val Ala Thr Ser Glu Ser Val Thr Glu Ile Thr Ala Ser Ser
720                 725                 730                 735

ttt gtg gtc tcc tgg gtc tca gct tcc gac acc gtg tcg gga ttc cgg     2615
Phe Val Val Ser Trp Val Ser Ala Ser Asp Thr Val Ser Gly Phe Arg
736                 741                 746                 751

gtg gaa tat gag ctg agt gag gag gga gat gag cca cag tac ctg gat     2663
Val Glu Tyr Glu Leu Ser Glu Glu Gly Asp Glu Pro Gln Tyr Leu Asp
752                 757                 762                 767

ctt cca agc aca gcc act tct gtg aac atc cct gac ctg ctt cct ggc     2711
Leu Pro Ser Thr Ala Thr Ser Val Asn Ile Pro Asp Leu Leu Pro Gly
768                 773                 778                 783

cga aaa tac att gta aat gtc tat cag ata tct gag gat ggg gag cag     2759
Arg Lys Tyr Ile Val Asn Val Tyr Gln Ile Ser Glu Asp Gly Glu Gln
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Ser Leu Ile Leu Ser Thr Ser Gln Thr Thr Ala Pro Asp Ala Pro Pro
800                 805                 810                 815

gac ccg act gtg gac caa gtt gat gac acc tca att gtt gtt cgc tgg     2855
Asp Pro Thr Val Asp Gln Val Asp Asp Thr Ser Ile Val Val Arg Trp
816                 821                 826                 831

agc aga ccc cag gct ccc atc aca ggg tac aga ata gtc tat tcg cca     2903
Ser Arg Pro Gln Ala Pro Ile Thr Gly Tyr Arg Ile Val Tyr Ser Pro
832                 837                 842                 847

tca gta gaa ggt agc agc aca gaa ctc aac ctt cct gaa act gca aac     2951
Ser Val Glu Gly Ser Ser Thr Glu Leu Asn Leu Pro Glu Thr Ala Asn
848                 853                 858                 863

tcc gtc acc ctc agt gac ttg caa cct ggt gtt cag tat aac atc act     2999
Ser Val Thr Leu Ser Asp Leu Gln Pro Gly Val Gln Tyr Asn Ile Thr
864                 869                 874                 879

atc tat gct gtg gaa gaa aat caa gaa agt aca cct gtt gtc att caa     3047
Ile Tyr Ala Val Glu Glu Asn Gln Glu Ser Thr Pro Val Val Ile Gln
880                 885                 890                 895

caa gaa acc act ggc acc cca cgc tca gat aca gtg ccc tct ccc agg     3095
Gln Glu Thr Thr Gly Thr Pro Arg Ser Asp Thr Val Pro Ser Pro Arg
896                 901                 906                 911

gac ctg cag ttt gtg gaa gtg aca gac gtg aag gtc acc atc atg tgg     3143
Asp Leu Gln Phe Val Glu Val Thr Asp Val Lys Val Thr Ile Met Trp
912                 917                 922                 927

aca ccg cct gag agt gca gtg acc ggc tac cgt gtg gat gtg atc ccc     3191
Thr Pro Pro Glu Ser Ala Val Thr Gly Tyr Arg Val Asp Val Ile Pro
928                 933                 938                 943

gtc aac ctg cct ggc gag cac ggg cag agg ctg ccc atc agc agg aac     3239
Val Asn Leu Pro Gly Glu His Gly Gln Arg Leu Pro Ile Ser Arg Asn
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acc ttt gca gaa gtc acc ggg ctg tcc cct ggg gtc acc tat tac ttc     3287
Thr Phe Ala Glu Val Thr Gly Leu Ser Pro Gly Val Thr Tyr Tyr Phe
960                 965                 970                 975

aaa gtc ttt gca gtg agc cat ggg agg gag agc aag cct ctg act gct     3335
Lys Val Phe Ala Val Ser His Gly Arg Glu Ser Lys Pro Leu Thr Ala
976                 981                 986                 991

caa cag aca acc aaa ctg gat gct ccc act aac ctc cag ttt gtc aat     3383
Gln Gln Thr Thr Lys Leu Asp Ala Pro Thr Asn Leu Gln Phe Val Asn
992                 997                1002                1007

gaa act gat tct act gtc ctg gtg aga tgg act cca cct cgg gcc cag     3431
Glu Thr Asp Ser Thr Val Leu Val Arg Trp Thr Pro Pro Arg Ala Gln
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 agg cag tac aat gtg ggt ccc tct gtc tcc aag tac cca ctg agg aat     3527
 Arg Gln Tyr Asn Val Gly Pro Ser Val Ser Lys Tyr Pro Leu Arg Asn
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 ctg cag cct gca tct gag tac acc gta tcc ctc gtg gcc ata aag ggc     3575
 Leu Gln Pro Ala Ser Glu Tyr Thr Val Ser Leu Val Ala Ile Lys Gly
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 aac caa gag agc ccc aaa gcc act gga gtc ttt acc aca ctg cag cct     3623
 Asn Gln Glu Ser Pro Lys Ala Thr Gly Val Phe Thr Thr Leu Gln Pro
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 Gly Ser Ser Ile Pro Pro Tyr Asn Thr Glu Val Thr Glu Thr Thr Ile
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 Val Ile Thr Trp Thr Pro Ala Pro Arg Ile Gly Phe Lys Leu Gly Val
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 cga cca agc cag gga gga gag gca cca cga gaa gtg act tca gac tca     3767
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 gga agc atc gtt gtg tcc ggc ttg act cca gga gta gaa tac gtc tac     3815
 Gly Ser Ile Val Val Ser Gly Leu Thr Pro Gly Val Glu Tyr Val Tyr
1136                1141                1146                1151

 acc atc caa gtc ctg aga gat gga cag gaa aga gat gcg cca att gta     3863
 Thr Ile Gln Val Leu Arg Asp Gly Gln Glu Arg Asp Ala Pro Ile Val
1152                1157                1162                1167

 aac aaa gtg gtg aca cca ttg tct cca cca aca aac ttg cat ctg gag     3911
 Asn Lys Val Val Thr Pro Leu Ser Pro Pro Thr Asn Leu His Leu Glu
1168                1173                1178                1183

 gca aac cct gac act gga gtg ctc aca gtc tcc tgg gag agg agc acc     3959
 Ala Asn Pro Asp Thr Gly Val Leu Thr Val Ser Trp Glu Arg Ser Thr
1184                1189                1194                1199

 acc cca gac att act ggt tat aga att acc aca acc cct aca aac ggc     4007
 Thr Pro Asp Ile Thr Gly Tyr Arg Ile Thr Thr Thr Pro Thr Asn Gly
1200                1205                1210                1215

 cag cag gga aat tct ttg gaa gaa gtg gtc cat gct gat cag agc tcc     4055
 Gln Gln Gly Asn Ser Leu Glu Glu Val Val His Ala Asp Gln Ser Ser
1216                1221                1226                1231

 tgc act ttt gat aac ctg agt ccc ggc ctg gag tac aat gtc agt gtt     4103
 Cys Thr Phe Asp Asn Leu Ser Pro Gly Leu Glu Tyr Asn Val Ser Val
1232                1237                1242                1247

 tac act gtc aag gat gac aag gaa agt gtc cct atc tct gat acc atc     4151
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 Tyr Thr Val Lys Asp Asp Lys Glu Ser Val Pro Ile Ser Asp Thr Ile
1248                1253                1258                1263

 atc cca gct gtt cct cct ccc act gac ctg cga ttc acc aac att ggt     4199
 Ile Pro Ala Val Pro Pro Pro Thr Asp Leu Arg Phe Thr Asn Ile Gly
1264                1269                1274                1279

 cca gac acc atg cgt gtc acc tgg gct cca ccc cca tcc att gat tta     4247
 Pro Asp Thr Met Arg Val Thr Trp Ala Pro Pro Pro Ser Ile Asp Leu
1280                1285                1290                1295

 acc aac ttc ctg gtg cgt tac tca cct gtg aaa aat gag gaa gat gtt     4295
 Thr Asn Phe Leu Val Arg Tyr Ser Pro Val Lys Asn Glu Glu Asp Val
1296                1301                1306                1311

 gca gag ttg tca att tct cct tca gac aat gca gtg gtc tta aca aat     4343
 Ala Glu Leu Ser Ile Ser Pro Ser Asp Asn Ala Val Val Leu Thr Asn
1312                1317                1322                1327

 ctc ctg cct ggt aca gaa tat gta gtg agt gtc tcc agt gtc tac gaa     4391
 Leu Leu Pro Gly Thr Glu Tyr Val Val Ser Val Ser Ser Val Tyr Glu
1328                1333                1338                1343

 caa cat gag agc aca cct ctt aga gga aga cag aaa aca ggt ctt gat     4439
 Gln His Glu Ser Thr Pro Leu Arg Gly Arg Gln Lys Thr Gly Leu Asp
1344                1349                1354                1359

 tcc cca act ggc att gac ttt tct gat att act gcc aac tct ttt act     4487
 Ser Pro Thr Gly Ile Asp Phe Ser Asp Ile Thr Ala Asn Ser Phe Thr
1360                1365                1370                1375

 gtg cac tgg att gct cct cga gcc acc atc act ggc tac agg atc cgc     4535
 Val His Trp Ile Ala Pro Arg Ala Thr Ile Thr Gly Tyr Arg Ile Arg
1376                1381                1386                1391

 cat cat ccc gag cac ttc agt ggg aga cct cga gaa gat cgg gtg ccc     4583
 His His Pro Glu His Phe Ser Gly Arg Pro Arg Glu Asp Arg Val Pro
1392                1397                1402                1407

 cac tct cgg aat tcc atc acc ctc acc aac ctc act cca ggc aca gag     4631
 His Ser Arg Asn Ser Ile Thr Leu Thr Asn Leu Thr Pro Gly Thr Glu
1408                1413                1418                1423

 tat gtg gtc agc atc gtt gct ctt aat ggc aga gag gaa agt ccc tta     4679
 Tyr Val Val Ser Ile Val Ala Leu Asn Gly Arg Glu Glu Ser Pro Leu
1424                1429                1434                1439

 ttg att ggc caa caa tca aca gtt tct gat gtt ccg agg gac ctg gaa     4727
 Leu Ile Gly Gln Gln Ser Thr Val Ser Asp Val Pro Arg Asp Leu Glu
1440                1445                1450                1455

 gtt gtt gct gcg acc ccc acc agc cta ctg atc agc tgg gat gct cct     4775
 Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro
1456                1461                1466                1471

 gct gtc aca gtg aga tat tac agg atc act tac gga gaa aca gga gga     4823
 Ala Val Thr Val Arg Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly
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1472                1477                1482                1487

 aat agc cct gtc cag gag ttc act gtg cct ggg agc aag tct aca gct     4871
 Asn Ser Pro Val Gln Glu Phe Thr Val Pro Gly Ser Lys Ser Thr Ala
1488                1493                1498                1503

 acc atc agc ggc ctt aaa cct gga gtt gat tat acc atc act gtg tat     4919
 Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr
1504                1509                1514                1519

 gct gtc act ggc cgt gga gac agc ccc gca agc agc aag cca att tcc     4967
 Ala Val Thr Gly Arg Gly Asp Ser Pro Ala Ser Ser Lys Pro Ile Ser
1520                1525                1530                1535

 att aat tac cga aca gaa att gac aaa cca tcc cag atg caa gtg acc     5015
 Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln Met Gln Val Thr
1536                1541                1546                1551

 gat gtt cag gac aac agc att agt gtc aag tgg ctg cct tca agt tcc     5063
 Asp Val Gln Asp Asn Ser Ile Ser Val Lys Trp Leu Pro Ser Ser Ser
1552                1557                1562                1567

 cct gtt act ggt tac aga gta acc acc act ccc aaa aat gga cca gga     5111
 Pro Val Thr Gly Tyr Arg Val Thr Thr Thr Pro Lys Asn Gly Pro Gly
1568                1573                1578                1583

 cca aca aaa act aaa act gca ggt cca gat caa aca gaa atg act att     5159
 Pro Thr Lys Thr Lys Thr Ala Gly Pro Asp Gln Thr Glu Met Thr Ile
1584                1589                1594                1599

 gaa ggc ttg cag ccc aca gtg gag tat gtg gtt agt gtc tat gct cag     5207
 Glu Gly Leu Gln Pro Thr Val Glu Tyr Val Val Ser Val Tyr Ala Gln
1600                1605                1610                1615

 aat cca agc gga gag agt cag cct ctg gtt cag act gca gta acc aac     5255
 Asn Pro Ser Gly Glu Ser Gln Pro Leu Val Gln Thr Ala Val Thr Asn
1616                1621                1626                1631

 att gat cgc cct aaa gga ctg gca ttc act gat gtg gat gtc gat tcc     5303
 Ile Asp Arg Pro Lys Gly Leu Ala Phe Thr Asp Val Asp Val Asp Ser
1632                1637                1642                1647

 atc aaa att gct tgg gaa agc cca cag ggg caa gtt tcc agg tac agg     5351
 Ile Lys Ile Ala Trp Glu Ser Pro Gln Gly Gln Val Ser Arg Tyr Arg
1648                1653                1658                1663

 gtg acc tac tcg agc cct gag gat gga atc cat gag cta ttc cct gca     5399
 Val Thr Tyr Ser Ser Pro Glu Asp Gly Ile His Glu Leu Phe Pro Ala
1664                1669                1674                1679

 cct gat ggt gaa gaa gac act gca gag ctg caa ggc ctc aga ccg ggt     5447
 Pro Asp Gly Glu Glu Asp Thr Ala Glu Leu Gln Gly Leu Arg Pro Gly
1680                1685                1690                1695

 tct gag tac aca gtc agt gtg gtt gcc ttg cac gat gat atg gag agc     5495
 Ser Glu Tyr Thr Val Ser Val Val Ala Leu His Asp Asp Met Glu Ser
1696                1701                1706                1711
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 cag ccc ctg att gga acc cag tcc aca gct att cct gca cca act gac     5543
 Gln Pro Leu Ile Gly Thr Gln Ser Thr Ala Ile Pro Ala Pro Thr Asp
1712                1717                1722                1727

 ctg aag ttc act cag gtc aca ccc aca agc ctg agc gcc cag tgg aca     5591
 Leu Lys Phe Thr Gln Val Thr Pro Thr Ser Leu Ser Ala Gln Trp Thr
1728                1733                1738                1743

 cca ccc aat gtt cag ctc act gga tat cga gtg cgg gtg acc ccc aag     5639
 Pro Pro Asn Val Gln Leu Thr Gly Tyr Arg Val Arg Val Thr Pro Lys
1744                1749                1754                1759

 gag aag acc gga cca atg aaa gaa atc aac ctt gct cct gac agc tca     5687
 Glu Lys Thr Gly Pro Met Lys Glu Ile Asn Leu Ala Pro Asp Ser Ser
1760                1765                1770                1775

 tcc gtg gtt gta tca gga ctt atg gtg gcc acc aaa tat gaa gtg agt     5735
 Ser Val Val Val Ser Gly Leu Met Val Ala Thr Lys Tyr Glu Val Ser
1776                1781                1786                1791

 gtc tat gct ctt aag gac act ttg aca agc aga cca gct cag gga gtt     5783
 Val Tyr Ala Leu Lys Asp Thr Leu Thr Ser Arg Pro Ala Gln Gly Val
1792                1797                1802                1807

 gtc acc act ctg gag aat gtc agc cca cca aga agg gct cgt gtg aca     5831
 Val Thr Thr Leu Glu Asn Val Ser Pro Pro Arg Arg Ala Arg Val Thr
1808                1813                1818                1823

 gat gct act gag acc acc atc acc att agc tgg aga acc aag act gag     5879
 Asp Ala Thr Glu Thr Thr Ile Thr Ile Ser Trp Arg Thr Lys Thr Glu
1824                1829                1834                1839

 acg atc act ggc ttc caa gtt gat gcc gtt cca gcc aat ggc cag act     5927
 Thr Ile Thr Gly Phe Gln Val Asp Ala Val Pro Ala Asn Gly Gln Thr
1840                1845                1850                1855

 cca atc cag aga acc atc aag cca gat gtc aga agc tac acc atc aca     5975
 Pro Ile Gln Arg Thr Ile Lys Pro Asp Val Arg Ser Tyr Thr Ile Thr
1856                1861                1866                1871

 ggt tta caa cca ggc act gac tac aag atc tac ctg tac acc ttg aat     6023
 Gly Leu Gln Pro Gly Thr Asp Tyr Lys Ile Tyr Leu Tyr Thr Leu Asn
1872                1877                1882                1887

 gac aat gct cgg agc tcc cct gtg gtc atc gac gcc tcc act gcc att     6071
 Asp Asn Ala Arg Ser Ser Pro Val Val Ile Asp Ala Ser Thr Ala Ile
1888                1893                1898                1903

 gat gca cca tcc aac ctg cgt ttc ctg gcc acc aca ccc aat tcc ttg     6119
 Asp Ala Pro Ser Asn Leu Arg Phe Leu Ala Thr Thr Pro Asn Ser Leu
1904                1909                1914                1919

 ctg gta tca tgg cag ccg cca cgt gcc agg att acc ggc tac atc atc     6167
 Leu Val Ser Trp Gln Pro Pro Arg Ala Arg Ile Thr Gly Tyr Ile Ile
1920                1925                1930                1935
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 aag tat gag aag cct ggg tct cct ccc aga gaa gtg gtc cct cgg ccc     6215
 Lys Tyr Glu Lys Pro Gly Ser Pro Pro Arg Glu Val Val Pro Arg Pro
1936                1941                1946                1951

 cgc cct ggt gtc aca gag gct act att cct ggc ctg gaa ccg gga acc     6263
 Arg Pro Gly Val Thr Glu Ala Thr Ile Pro Gly Leu Glu Pro Gly Thr
1952                1957                1962                1967

 gaa tat aca att tat gtc att gcc ctg aag aat aat cag aag agc gag     6311
 Glu Tyr Thr Ile Tyr Val Ile Ala Leu Lys Asn Asn Gln Lys Ser Glu
1968                1973                1978                1983

 ccc ctg att gga agg aaa aag aca gtt caa aag acc cct ttc gtc acc     6359
 Pro Leu Ile Gly Arg Lys Lys Thr Val Gln Lys Thr Pro Phe Val Thr
1984                1989                1994                1999

 cac cct ggg tat gac act gga aat ggt att cag ctt cct ggc act tct     6407
 His Pro Gly Tyr Asp Thr Gly Asn Gly Ile Gln Leu Pro Gly Thr Ser
2000                2005                2010                2015

 ggt cag caa ccc agt gtt ggg caa caa atg atc ttt gag gaa cat ggt     6455
 Gly Gln Gln Pro Ser Val Gly Gln Gln Met Ile Phe Glu Glu His Gly
2016                2021                2026                2031

 ttt agg cgg acc aca ccg ccc aca acg gcc acc ccc ata agg cat agg     6503
 Phe Arg Arg Thr Thr Pro Pro Thr Thr Ala Thr Pro Ile Arg His Arg
2032                2037                2042                2047

 cca aga cca tac ccg ccg aat gta gga caa gaa gct ctc tct cag aca     6551
 Pro Arg Pro Tyr Pro Pro Asn Val Gly Gln Glu Ala Leu Ser Gln Thr
2048                2053                2058                2063

 acc atc tca tgg gcc cca ttc cag gac act tct gag tac atc att tca     6599
 Thr Ile Ser Trp Ala Pro Phe Gln Asp Thr Ser Glu Tyr Ile Ile Ser
2064                2069                2074                2079

 tgt cat cct gtt ggc act gat gaa gaa ccc tta cag ttc agg gtt cct     6647
 Cys His Pro Val Gly Thr Asp Glu Glu Pro Leu Gln Phe Arg Val Pro
2080                2085                2090                2095

 gga act tct acc agt gcc act ctg aca ggc ctc acc aga ggt gcc acc     6695
 Gly Thr Ser Thr Ser Ala Thr Leu Thr Gly Leu Thr Arg Gly Ala Thr
2096                2101                2106                2111

 tac aac atc ata gtg gag gca ctg aaa gac cag cag agg cat aag gtt     6743
 Tyr Asn Ile Ile Val Glu Ala Leu Lys Asp Gln Gln Arg His Lys Val
2112                2117                2122                2127

 cgg gaa gag gtt gtt acc gtg ggc aac tct gtc aac gaa ggc ttg aac     6791
 Arg Glu Glu Val Val Thr Val Gly Asn Ser Val Asn Glu Gly Leu Asn
2128                2133                2138                2143

 caa cct acg gat gac tcg tgc ttt gac ccc tac aca gtt tcc cat tat     6839
 Gln Pro Thr Asp Asp Ser Cys Phe Asp Pro Tyr Thr Val Ser His Tyr
2144                2149                2154                2159

 gcc gtt gga gat gag tgg gaa cga atg tct gaa tca ggc ttt aaa ctg     6887
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 Ala Val Gly Asp Glu Trp Glu Arg Met Ser Glu Ser Gly Phe Lys Leu
2160                2165                2170                2175

 ttg tgc cag tgc tta ggc ttt gga agt ggt cat ttc aga tgt gat tca     6935
 Leu Cys Gln Cys Leu Gly Phe Gly Ser Gly His Phe Arg Cys Asp Ser
2176                2181                2186                2191

 tct aga tgg tgc cat gac aat ggt gtg aac tac aag att gga gag aag     6983
 Ser Arg Trp Cys His Asp Asn Gly Val Asn Tyr Lys Ile Gly Glu Lys
2192                2197                2202                2207

 tgg gac cgt cag gga gaa aat ggc cag atg atg agc tgc aca tgt ctt     7031
 Trp Asp Arg Gln Gly Glu Asn Gly Gln Met Met Ser Cys Thr Cys Leu
2208                2213                2218                2223

 ggg aac gga aaa gga gaa ttc aag tgt gac cct cat gag gca acg tgt     7079
 Gly Asn Gly Lys Gly Glu Phe Lys Cys Asp Pro His Glu Ala Thr Cys
2224                2229                2234                2239

 tac gat gat ggg aag aca tac cac gta gga gaa cag tgg cag aag gaa     7127
 Tyr Asp Asp Gly Lys Thr Tyr His Val Gly Glu Gln Trp Gln Lys Glu
2240                2245                2250                2255

 tat ctc ggt gcc att tgc tcc tgc aca tgc ttt gga ggc cag cgg ggc     7175
 Tyr Leu Gly Ala Ile Cys Ser Cys Thr Cys Phe Gly Gly Gln Arg Gly
2256                2261                2266                2271

 tgg cgc tgt gac aac tgc cgc aga cct ggg ggt gaa ccc agt ccc gaa     7223
 Trp Arg Cys Asp Asn Cys Arg Arg Pro Gly Gly Glu Pro Ser Pro Glu
2272                2277                2282                2287

 ggc act act ggc cag tcc tac aac cag tat tct cag aga tac cat cag     7271
 Gly Thr Thr Gly Gln Ser Tyr Asn Gln Tyr Ser Gln Arg Tyr His Gln
2288                2293                2298                2303

 aga aca aac act aat gtt aat tgc cca att gag tgc ttc atg cct tta     7319
 Arg Thr Asn Thr Asn Val Asn Cys Pro Ile Glu Cys Phe Met Pro Leu
2304                2309                2314                2319

 gat gta cag gct gac aga gaa gat tcc cga gag taa atca tctttccaat     7369
 Asp Val Gln Ala Asp Arg Glu Asp Ser Arg Glu  *
2320                2325                2330

 ccagaggaac aagcatgtct ctctgccaag atccatctaa actggagtga tgttagcaga   7429

 cccagcttag agttcttctt tctttcttaa gccctttgct ctggaggaag ttctccagct   7489

 tcagctcaac tcacagcttc tccaagcatc accctgggag tttcctgagg gttttctcat   7549

 aaatgagggc tgcacattgc ctgttctgct tcgaagtatt caataccgct cagtatttta   7609

 aatgaagtga ttctaagatt tggtttggga tcaataggaa agcatatgca gccaaccaag   7669

 atgcaaatgt tttgaaatga tatgaccaaa attttaagta ggaaagtcac ccaaacactt   7729

 ctgctttcac ttaagtgtct ggcccgcaat actgtaggaa caagcatgat cttgttactg   7789
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tgatatttta aatatccaca gtactcactt tttccaaatg atcctagtaa ttgcctagaa   7849

atatctttct cttacctgtt atttatcaat ttttcccagt atttttatac ggaaaaaatt   7909

gtattgaaaa cacttagtat gcagttgata agaggaattt ggtataatta tggtgggtga   7969

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aaagatttac attccaaaaa aaaaaaaaaa aaa                                8062
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<211> 7867
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<400> 6

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aaaaaagaga tctctcgagg atccgaattc gcggccgcgt cgaccggctg tgctgcacag    120

ggggaggaga gggaacccca ggcgcgagcg ggaagagggg acctgcagcc acaacttctc    180

tggtcctctg catcccttct gtccctccac ccgtcccctt ccccaccctc tggcccccac    240

cttcttggag gcgacaaccc ccgggaggca ttagaaggga tttttcccgc aggttgcgaa    300

gggaagcaaa cttggtggca acttgcctcc cggtgcgggc gtctctcccc caccgtctca    360

ac   atg ctt agg ggt ccg ggg ccc ggg ctg ctg ctg ctg gcc gtc ctg     407
     Met Leu Arg Gly Pro Gly Pro Gly Leu Leu Leu Leu Ala Val Leu
       1               5                  10

tgc ctg ggg aca gcg gtg ccc tcc acg gga gcc tcg aag agc aag agg      455
Cys Leu Gly Thr Ala Val Pro Ser Thr Gly Ala Ser Lys Ser Lys Arg
 16                  21                  26                  31

cag gct cag caa atg gtt cag ccc cag tcc ccg gtg gct gtc agt caa      503
Gln Ala Gln Gln Met Val Gln Pro Gln Ser Pro Val Ala Val Ser Gln
 32                  37                  42                  47

agc aag ccc ggt tgt tat gac aat gga aaa cac tat cag ata aat caa      551
Ser Lys Pro Gly Cys Tyr Asp Asn Gly Lys His Tyr Gln Ile Asn Gln
 48                  53                  58                  63

cag tgg gag cgg acc tac cta ggc aat gcg ttg gtt tgt act tgt tat      599
Gln Trp Glu Arg Thr Tyr Leu Gly Asn Ala Leu Val Cys Thr Cys Tyr
 64                  69                  74                  79

gga gga agc cga ggt ttt aac tgc gag agt aaa cct gaa gct gaa gag      647
Gly Gly Ser Arg Gly Phe Asn Cys Glu Ser Lys Pro Glu Ala Glu Glu
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 80                  85                  90                  95

act tgc ttt gac aag tac act ggg aac act tac cga gtg ggt gac act      695
Thr Cys Phe Asp Lys Tyr Thr Gly Asn Thr Tyr Arg Val Gly Asp Thr
 96                 101                 106                 111

tat gag cgt cct aaa gac tcc atg atc tgg gac tgt acc tgc atc ggg      743
Tyr Glu Arg Pro Lys Asp Ser Met Ile Trp Asp Cys Thr Cys Ile Gly
112                 117                 122                 127

gct ggg cga ggg aga ata agc tgt acc atc gca aac cgc tgc cat gaa      791
Ala Gly Arg Gly Arg Ile Ser Cys Thr Ile Ala Asn Arg Cys His Glu
128                 133                 138                 143

ggg ggt cag tcc tac aag att ggt gac acc tgg agg aga cca cat gag      839
Gly Gly Gln Ser Tyr Lys Ile Gly Asp Thr Trp Arg Arg Pro His Glu
144                 149                 154                 159

act ggt ggt tac atg tta gag tgt gtg tgt ctt ggt aat gga aaa gga      887
Thr Gly Gly Tyr Met Leu Glu Cys Val Cys Leu Gly Asn Gly Lys Gly
160                 165                 170                 175

gaa tgg acc tgc aag ccc ata gct gag aag tgt ttt gat cat gct gct      935
Glu Trp Thr Cys Lys Pro Ile Ala Glu Lys Cys Phe Asp His Ala Ala
176                 181                 186                 191

ggg act tcc tat gtg gtc gga gaa acg tgg gag aag ccc tac caa ggc      983
Gly Thr Ser Tyr Val Val Gly Glu Thr Trp Glu Lys Pro Tyr Gln Gly
192                 197                 202                 207

tgg atg atg gta gat tgt act tgc ctg gga gaa ggc agc gga cgc atc     1031
Trp Met Met Val Asp Cys Thr Cys Leu Gly Glu Gly Ser Gly Arg Ile
208                 213                 218                 223

act tgc act tct aga aat aga tgc aac gat cag gac aca agg aca tcc     1079
Thr Cys Thr Ser Arg Asn Arg Cys Asn Asp Gln Asp Thr Arg Thr Ser
224                 229                 234                 239

tat aga att gga gac acc tgg agc aag aag gat aat cga gga aac ctg     1127
Tyr Arg Ile Gly Asp Thr Trp Ser Lys Lys Asp Asn Arg Gly Asn Leu
240                 245                 250                 255

ctc cag tgc atc tgc aca ggc aac ggc cga gga gag tgg aag tgt gag     1175
Leu Gln Cys Ile Cys Thr Gly Asn Gly Arg Gly Glu Trp Lys Cys Glu
256                 261                 266                 271

agg cac acc tct gtg cag acc aca tcg agc gga tct ggc ccc ttc acc     1223
Arg His Thr Ser Val Gln Thr Thr Ser Ser Gly Ser Gly Pro Phe Thr
272                 277                 282                 287

gat gtt cgt gca gct gtt tac caa ccg cag cct cac ccc cag cct cct     1271
Asp Val Arg Ala Ala Val Tyr Gln Pro Gln Pro His Pro Gln Pro Pro
288                 293                 298                 303

ccc tat ggc cac tgt gtc aca gac agt ggt gtg gtc tac tct gtg ggg     1319
Pro Tyr Gly His Cys Val Thr Asp Ser Gly Val Val Tyr Ser Val Gly
304                 309                 314                 319
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atg cag tgg ctg aag aca caa gga aat aag caa atg ctt tgc acg tgc     1367
Met Gln Trp Leu Lys Thr Gln Gly Asn Lys Gln Met Leu Cys Thr Cys
320                 325                 330                 335

ctg ggc aac gga gtc agc tgc caa gag aca gct gta acc cag act tac     1415
Leu Gly Asn Gly Val Ser Cys Gln Glu Thr Ala Val Thr Gln Thr Tyr
336                 341                 346                 351

ggt ggc aac tca aat gga gag cca tgt gtc tta cca ttc acc tac aat     1463
Gly Gly Asn Ser Asn Gly Glu Pro Cys Val Leu Pro Phe Thr Tyr Asn
352                 357                 362                 367

ggc agg acg ttc tac tcc tgc acc aca gaa ggg cga cag gac gga cat     1511
Gly Arg Thr Phe Tyr Ser Cys Thr Thr Glu Gly Arg Gln Asp Gly His
368                 373                 378                 383

ctt tgg tgc agc aca act tcg aat tat gag cag gac cag aaa tac tct     1559
Leu Trp Cys Ser Thr Thr Ser Asn Tyr Glu Gln Asp Gln Lys Tyr Ser
384                 389                 394                 399

ttc tgc aca gac cac act gtt ttg gtt cag act cga gga gga aat tcc     1607
Phe Cys Thr Asp His Thr Val Leu Val Gln Thr Arg Gly Gly Asn Ser
400                 405                 410                 415

aat ggt gcc ttg tgc cac ttc ccc ttc cta tac aac aac cac aat tac     1655
Asn Gly Ala Leu Cys His Phe Pro Phe Leu Tyr Asn Asn His Asn Tyr
416                 421                 426                 431

act gat tgc act tct gag ggc aga aga gac aac atg aag tgg tgt ggg     1703
Thr Asp Cys Thr Ser Glu Gly Arg Arg Asp Asn Met Lys Trp Cys Gly
432                 437                 442                 447

acc aca cag aac tat gat gcc gac cag aag ttt ggg ttc tgc ccc atg     1751
Thr Thr Gln Asn Tyr Asp Ala Asp Gln Lys Phe Gly Phe Cys Pro Met
448                 453                 458                 463

gct gcc cac gag gaa atc tgc aca acc aat gaa ggg gtc atg tac cgc     1799
Ala Ala His Glu Glu Ile Cys Thr Thr Asn Glu Gly Val Met Tyr Arg
464                 469                 474                 479

att gga gat cag tgg gat aag cag cat gac atg ggt cac atg atg agg     1847
Ile Gly Asp Gln Trp Asp Lys Gln His Asp Met Gly His Met Met Arg
480                 485                 490                 495

tgc acg tgt gtt ggg aat ggt cgt ggg gaa tgg aca tgc att gcc tac     1895
Cys Thr Cys Val Gly Asn Gly Arg Gly Glu Trp Thr Cys Ile Ala Tyr
496                 501                 506                 511

tcg caa ctt cga gat cag tgc att gtt gat gac atc act tac aat gtg     1943
Ser Gln Leu Arg Asp Gln Cys Ile Val Asp Asp Ile Thr Tyr Asn Val
512                 517                 522                 527

aac gac aca ttc cac aag cgt cat gaa gag ggg cac atg ctg aac tgt     1991
Asn Asp Thr Phe His Lys Arg His Glu Glu Gly His Met Leu Asn Cys
528                 533                 538                 543
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aca tgc ttc ggt cag ggt cgg ggc agg tgg aag tgt gat ccc gtc gac     2039
Thr Cys Phe Gly Gln Gly Arg Gly Arg Trp Lys Cys Asp Pro Val Asp
544                 549                 554                 559

caa tgc cag gat tca gag act ggg acg ttt tat caa att gga gat tca     2087
Gln Cys Gln Asp Ser Glu Thr Gly Thr Phe Tyr Gln Ile Gly Asp Ser
560                 565                 570                 575

tgg gag aag tat gtg cat ggt gtc aga tac cag tgc tac tgc tat ggc     2135
Trp Glu Lys Tyr Val His Gly Val Arg Tyr Gln Cys Tyr Cys Tyr Gly
576                 581                 586                 591

cgt ggc att ggg gag tgg cat tgc caa cct tta cag acc tat cca agc     2183
Arg Gly Ile Gly Glu Trp His Cys Gln Pro Leu Gln Thr Tyr Pro Ser
592                 597                 602                 607

tca agt ggt cct gtc gaa gta ttt atc act gag act ccg agt cag ccc     2231
Ser Ser Gly Pro Val Glu Val Phe Ile Thr Glu Thr Pro Ser Gln Pro
608                 613                 618                 623

aac tcc cac ccc atc cag tgg aat gca cca cag cca tct cac att tcc     2279
Asn Ser His Pro Ile Gln Trp Asn Ala Pro Gln Pro Ser His Ile Ser
624                 629                 634                 639

aag tac att ctc agg tgg aga cct aaa aat tct gta ggc cgt tgg aag     2327
Lys Tyr Ile Leu Arg Trp Arg Pro Lys Asn Ser Val Gly Arg Trp Lys
640                 645                 650                 655

gaa gct acc ata cca ggc cac tta aac tcc tac acc atc aaa ggc ctg     2375
Glu Ala Thr Ile Pro Gly His Leu Asn Ser Tyr Thr Ile Lys Gly Leu
656                 661                 666                 671

aag cct ggt gtg gta tac gag ggc cag ctc atc agc atc cag cag tac     2423
Lys Pro Gly Val Val Tyr Glu Gly Gln Leu Ile Ser Ile Gln Gln Tyr
672                 677                 682                 687

ggc cac caa gaa gtg act cgc ttt gac ttc acc acc acc agc acc agc     2471
Gly His Gln Glu Val Thr Arg Phe Asp Phe Thr Thr Thr Ser Thr Ser
688                 693                 698                 703

aca cct gtg acc agc aac acc gtg aca gga gag acg act ccc ttt tct     2519
Thr Pro Val Thr Ser Asn Thr Val Thr Gly Glu Thr Thr Pro Phe Ser
704                 709                 714                 719

cct ctt gtg gcc act tct gaa tct gtg acc gaa atc aca gcc agt agc     2567
Pro Leu Val Ala Thr Ser Glu Ser Val Thr Glu Ile Thr Ala Ser Ser
720                 725                 730                 735

ttt gtg gtc tcc tgg gtc tca gct tcc gac acc gtg tcg gga ttc cgg     2615
Phe Val Val Ser Trp Val Ser Ala Ser Asp Thr Val Ser Gly Phe Arg
736                 741                 746                 751

gtg gaa tat gag ctg agt gag gag gga gat gag cca cag tac ctg gat     2663
Val Glu Tyr Glu Leu Ser Glu Glu Gly Asp Glu Pro Gln Tyr Leu Asp
752                 757                 762                 767

ctt cca agc aca gcc act tct gtg aac atc cct gac ctg ctt cct ggc     2711
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Leu Pro Ser Thr Ala Thr Ser Val Asn Ile Pro Asp Leu Leu Pro Gly
768                 773                 778                 783

cga aaa tac att gta aat gtc tat cag ata tct gag gat ggg gag cag     2759
Arg Lys Tyr Ile Val Asn Val Tyr Gln Ile Ser Glu Asp Gly Glu Gln
784                 789                 794                 799

agt ttg atc ctg tct act tca caa aca aca gcg cct gat gcc cct cct     2807
Ser Leu Ile Leu Ser Thr Ser Gln Thr Thr Ala Pro Asp Ala Pro Pro
800                 805                 810                 815

gac ccg act gtg gac caa gtt gat gac acc tca att gtt gtt cgc tgg     2855
Asp Pro Thr Val Asp Gln Val Asp Asp Thr Ser Ile Val Val Arg Trp
816                 821                 826                 831

agc aga ccc cag gct ccc atc aca ggg tac aga ata gtc tat tcg cca     2903
Ser Arg Pro Gln Ala Pro Ile Thr Gly Tyr Arg Ile Val Tyr Ser Pro
832                 837                 842                 847

tca gta gaa ggt agc agc aca gaa ctc aac ctt cct gaa act gca aac     2951
Ser Val Glu Gly Ser Ser Thr Glu Leu Asn Leu Pro Glu Thr Ala Asn
848                 853                 858                 863

tcc gtc acc ctc agt gac ttg caa cct ggt gtt cag tat aac atc act     2999
Ser Val Thr Leu Ser Asp Leu Gln Pro Gly Val Gln Tyr Asn Ile Thr
864                 869                 874                 879

atc tat gct gtg gaa gaa aat caa gaa agt aca cct gtt gtc att caa     3047
Ile Tyr Ala Val Glu Glu Asn Gln Glu Ser Thr Pro Val Val Ile Gln
880                 885                 890                 895

caa gaa acc act ggc acc cca cgc tca gat aca gtg ccc tct ccc agg     3095
Gln Glu Thr Thr Gly Thr Pro Arg Ser Asp Thr Val Pro Ser Pro Arg
896                 901                 906                 911

gac ctg cag ttt gtg gaa gtg aca gac gtg aag gtc acc atc atg tgg     3143
Asp Leu Gln Phe Val Glu Val Thr Asp Val Lys Val Thr Ile Met Trp
912                 917                 922                 927

aca ccg cct gag agt gca gtg acc ggc tac cgt gtg gat gtg atc ccc     3191
Thr Pro Pro Glu Ser Ala Val Thr Gly Tyr Arg Val Asp Val Ile Pro
928                 933                 938                 943

gtc aac ctg cct ggc gag cac ggg cag agg ctg ccc atc agc agg aac     3239
Val Asn Leu Pro Gly Glu His Gly Gln Arg Leu Pro Ile Ser Arg Asn
944                 949                 954                 959

acc ttt gca gaa gtc acc ggg ctg tcc cct ggg gtc acc tat tac ttc     3287
Thr Phe Ala Glu Val Thr Gly Leu Ser Pro Gly Val Thr Tyr Tyr Phe
960                 965                 970                 975

aaa gtc ttt gca gtg agc cat ggg agg gag agc aag cct ctg act gct     3335
Lys Val Phe Ala Val Ser His Gly Arg Glu Ser Lys Pro Leu Thr Ala
976                 981                 986                 991

caa cag aca acc aaa ctg gat gct ccc act aac ctc cag ttt gtc aat     3383
Gln Gln Thr Thr Lys Leu Asp Ala Pro Thr Asn Leu Gln Phe Val Asn
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992                 997                1002                1007

gaa act gat tct act gtc ctg gtg aga tgg act cca cct cgg gcc cag     3431
Glu Thr Asp Ser Thr Val Leu Val Arg Trp Thr Pro Pro Arg Ala Gln
1008                1013                1018                1023

ata aca gga tac cga ctg acc gtg ggc ctt acc cga aga gga cag ccc     3479
Ile Thr Gly Tyr Arg Leu Thr Val Gly Leu Thr Arg Arg Gly Gln Pro
1024                1029                1034                1039

agg cag tac aat gtg ggt ccc tct gtc tcc aag tac cca ctg agg aat     3527
Arg Gln Tyr Asn Val Gly Pro Ser Val Ser Lys Tyr Pro Leu Arg Asn
1040                1045                1050                1055

ctg cag cct gca tct gag tac acc gta tcc ctc gtg gcc ata aag ggc     3575
Leu Gln Pro Ala Ser Glu Tyr Thr Val Ser Leu Val Ala Ile Lys Gly
1056                1061                1066                1071

aac caa gag agc ccc aaa gcc act gga gtc ttt acc aca ctg cag cct     3623
Asn Gln Glu Ser Pro Lys Ala Thr Gly Val Phe Thr Thr Leu Gln Pro
1072                1077                1082                1087

ggg agc tct att cca cct tac aac acc gag gtg act gag acc acc att     3671
Gly Ser Ser Ile Pro Pro Tyr Asn Thr Glu Val Thr Glu Thr Thr Ile
1088                1093                1098                1103

gtg atc aca tgg acg cct gct cca aga att ggt ttt aag ctg ggt gta     3719
Val Ile Thr Trp Thr Pro Ala Pro Arg Ile Gly Phe Lys Leu Gly Val
1104                1109                1114                1119

cga cca agc cag gga gga gag gca cca cga gaa gtg act tca gac tca     3767
Arg Pro Ser Gln Gly Gly Glu Ala Pro Arg Glu Val Thr Ser Asp Ser
1120                1125                1130                1135

gga agc atc gtt gtg tcc ggc ttg act cca gga gta gaa tac gtc tac     3815
Gly Ser Ile Val Val Ser Gly Leu Thr Pro Gly Val Glu Tyr Val Tyr
1136                1141                1146                1151

acc atc caa gtc ctg aga gat gga cag gaa aga gat gcg cca att gta     3863
Thr Ile Gln Val Leu Arg Asp Gly Gln Glu Arg Asp Ala Pro Ile Val
1152                1157                1162                1167

aac aaa gtg gtg aca cca ttg tct cca cca aca aac ttg cat ctg gag     3911
Asn Lys Val Val Thr Pro Leu Ser Pro Pro Thr Asn Leu His Leu Glu
1168                1173                1178                1183

gca aac cct gac act gga gtg ctc aca gtc tcc tgg gag agg agc acc     3959
Ala Asn Pro Asp Thr Gly Val Leu Thr Val Ser Trp Glu Arg Ser Thr
1184                1189                1194                1199

acc cca gac att act ggt tat aga att acc aca acc cct aca aac ggc     4007
Thr Pro Asp Ile Thr Gly Tyr Arg Ile Thr Thr Thr Pro Thr Asn Gly
1200                1205                1210                1215

cag cag gga aat tct ttg gaa gaa gtg gtc cat gct gat cag agc tcc     4055
Gln Gln Gly Asn Ser Leu Glu Glu Val Val His Ala Asp Gln Ser Ser
1216                1221                1226                1231
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 tgc act ttt gat aac ctg agt ccc ggc ctg gag tac aat gtc agt gtt     4103
 Cys Thr Phe Asp Asn Leu Ser Pro Gly Leu Glu Tyr Asn Val Ser Val
1232                 1237                 1242                 1247

 tac act gtc aag gat gac aag gaa agt gtc cct atc tct gat acc atc     4151
 Tyr Thr Val Lys Asp Asp Lys Glu Ser Val Pro Ile Ser Asp Thr Ile
1248                 1253                 1258                 1263

 atc cca gct gtt cct cct ccc act gac ctg cga ttc acc aac att ggt     4199
 Ile Pro Ala Val Pro Pro Pro Thr Asp Leu Arg Phe Thr Asn Ile Gly
1264                 1269                 1274                 1279

 cca gac acc atg cgt gtc acc tgg gct cca ccc cca tcc att gat tta     4247
 Pro Asp Thr Met Arg Val Thr Trp Ala Pro Pro Pro Ser Ile Asp Leu
1280                 1285                 1290                 1295

 acc aac ttc ctg gtg cgt tac tca cct gtg aaa aat gag gaa gat gtt     4295
 Thr Asn Phe Leu Val Arg Tyr Ser Pro Val Lys Asn Glu Glu Asp Val
1296                 1301                 1306                 1311

 gca gag ttg tca att tct cct tca gac aat gca gtg gtc tta aca aat     4343
 Ala Glu Leu Ser Ile Ser Pro Ser Asp Asn Ala Val Val Leu Thr Asn
1312                 1317                 1322                 1327

 ctc ctg cct ggt aca gaa tat gta gtg agt gtc tcc agt gtc tac gaa     4391
 Leu Leu Pro Gly Thr Glu Tyr Val Val Ser Val Ser Ser Val Tyr Glu
1328                 1333                 1338                 1343

 caa cat gag agc aca cct ctt aga gga aga cag aaa aca ggt ctt gat     4439
 Gln His Glu Ser Thr Pro Leu Arg Gly Arg Gln Lys Thr Gly Leu Asp
1344                 1349                 1354                 1359

 tcc cca act ggc att gac ttt tct gat att act gcc aac tct ttt act     4487
 Ser Pro Thr Gly Ile Asp Phe Ser Asp Ile Thr Ala Asn Ser Phe Thr
1360                 1365                 1370                 1375

 gtg cac tgg att gct cct cga gcc acc atc act ggc tac agg atc cgc     4535
 Val His Trp Ile Ala Pro Arg Ala Thr Ile Thr Gly Tyr Arg Ile Arg
1376                 1381                 1386                 1391

 cat cat ccc gag cac ttc agt ggg aga cct cga gaa gat cgg gtg ccc     4583
 His His Pro Glu His Phe Ser Gly Arg Pro Arg Glu Asp Arg Val Pro
1392                 1397                 1402                 1407

 cac tct cgg aat tcc atc acc ctc acc aac ctc act cca ggc aca gag     4631
 His Ser Arg Asn Ser Ile Thr Leu Thr Asn Leu Thr Pro Gly Thr Glu
1408                 1413                 1418                 1423

 tat gtg gtc agc atc gtt gct ctt aat ggc aga gag gaa agt ccc tta     4679
 Tyr Val Val Ser Ile Val Ala Leu Asn Gly Arg Glu Glu Ser Pro Leu
1424                 1429                 1434                 1439

 ttg att ggc caa caa tca aca gtt tct gat gtt ccg agg gac ctg gaa     4727
 Leu Ile Gly Gln Gln Ser Thr Val Ser Asp Val Pro Arg Asp Leu Glu
1440                 1445                 1450                 1455
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 gtt gtt gct gcg acc ccc acc agc cta ctg atc agc tgg gat gct cct     4775
 Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro
1456                1461                1466                1471

 gct gtc aca gtg aga tat tac agg atc act tac gga gaa aca gga gga     4823
 Ala Val Thr Val Arg Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly
1472                1477                1482                1487

 aat agc cct gtc cag gag ttc act gtg cct ggg agc aag tct aca gct     4871
 Asn Ser Pro Val Gln Glu Phe Thr Val Pro Gly Ser Lys Ser Thr Ala
1488                1493                1498                1503

 acc atc agc ggc ctt aaa cct gga gtt gat tat acc atc act gtg tat     4919
 Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr
1504                1509                1514                1519

 gct gtc act ggc cgt gga gac agc ccc gca agc agc aag cca att tcc     4967
 Ala Val Thr Gly Arg Gly Asp Ser Pro Ala Ser Ser Lys Pro Ile Ser
1520                1525                1530                1535

 att aat tac cga aca gaa att gac aaa cca tcc cag atg caa gtg acc     5015
 Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln Met Gln Val Thr
1536                1541                1546                1551

 gat gtt cag gac aac agc att agt gtc aag tgg ctg cct tca agt tcc     5063
 Asp Val Gln Asp Asn Ser Ile Ser Val Lys Trp Leu Pro Ser Ser Ser
1552                1557                1562                1567

 cct gtt act ggt tac aga gta acc acc act ccc aaa aat gga cca gga     5111
 Pro Val Thr Gly Tyr Arg Val Thr Thr Thr Pro Lys Asn Gly Pro Gly
1568                1573                1578                1583

 cca aca aaa act aaa act gca ggt cca gat caa aca gaa atg act att     5159
 Pro Thr Lys Thr Lys Thr Ala Gly Pro Asp Gln Thr Glu Met Thr Ile
1584                1589                1594                1599

 gaa ggc ttg cag ccc aca gtg gag tat gtg gtt agt gtc tat gct cag     5207
 Glu Gly Leu Gln Pro Thr Val Glu Tyr Val Val Ser Val Tyr Ala Gln
1600                1605                1610                1615

 aat cca agc gga gag agt cag cct ctg gtt cag act gca gta acc act     5255
 Asn Pro Ser Gly Glu Ser Gln Pro Leu Val Gln Thr Ala Val Thr Thr
1616                1621                1626                1631

 att cct gca cca act gac ctg aag ttc act cag gtc aca ccc aca agc     5303
 Ile Pro Ala Pro Thr Asp Leu Lys Phe Thr Gln Val Thr Pro Thr Ser
1632                1637                1642                1647

 ctg agc gcc cag tgg aca cca ccc aat gtt cag ctc act gga tat cga     5351
 Leu Ser Ala Gln Trp Thr Pro Pro Asn Val Gln Leu Thr Gly Tyr Arg
1648                1653                1658                1663

 gtg cgg gtg acc ccc aag gag aag acc gga cca atg aaa gaa atc aac     5399
 Val Arg Val Thr Pro Lys Glu Lys Thr Gly Pro Met Lys Glu Ile Asn
1664                1669                1674                1679

 ctt gct cct gac agc tca tcc gtg gtt gta tca gga ctt atg gtg gcc     5447
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 Leu Ala Pro Asp Ser Ser Ser Val Val Val Ser Gly Leu Met Val Ala
1680                1685                1690                1695

 acc aaa tat gaa gtg agt gtc tat gct ctt aag gac act ttg aca agc     5495
 Thr Lys Tyr Glu Val Ser Val Tyr Ala Leu Lys Asp Thr Leu Thr Ser
1696                1701                1706                1711

 aga cca gct cag gga gtt gtc acc act ctg gag aat gtc agc cca cca     5543
 Arg Pro Ala Gln Gly Val Val Thr Thr Leu Glu Asn Val Ser Pro Pro
1712                1717                1722                1727

 aga agg gct cgt gtg aca gat gct act gag acc acc atc acc att agc     5591
 Arg Arg Ala Arg Val Thr Asp Ala Thr Glu Thr Thr Ile Thr Ile Ser
1728                1733                1738                1743

 tgg aga acc aag act gag acg atc act ggc ttc caa gtt gat gcc gtt     5639
 Trp Arg Thr Lys Thr Glu Thr Ile Thr Gly Phe Gln Val Asp Ala Val
1744                1749                1754                1759

 cca gcc aat ggc cag act cca atc cag aga acc atc aag cca gat gtc     5687
 Pro Ala Asn Gly Gln Thr Pro Ile Gln Arg Thr Ile Lys Pro Asp Val
1760                1765                1770                1775

 aga agc tac acc atc aca ggt tta caa cca ggc act gac tac aag atc     5735
 Arg Ser Tyr Thr Ile Thr Gly Leu Gln Pro Gly Thr Asp Tyr Lys Ile
1776                1781                1786                1791

 tac ctg tac acc ttg aat gac aat gct cgg agc tcc cct gtg gtc atc     5783
 Tyr Leu Tyr Thr Leu Asn Asp Asn Ala Arg Ser Ser Pro Val Val Ile
1792                1797                1802                1807

 gac gcc tcc act gcc att gat gca cca tcc aac ctg cgt ttc ctg gcc     5831
 Asp Ala Ser Thr Ala Ile Asp Ala Pro Ser Asn Leu Arg Phe Leu Ala
1808                1813                1818                1823

 acc aca ccc aat tcc ttg ctg gta tca tgg cag ccg cca cgt gcc agg     5879
 Thr Thr Pro Asn Ser Leu Leu Val Ser Trp Gln Pro Pro Arg Ala Arg
1824                1829                1834                1839

 att acc ggc tac atc atc aag tat gag aag cct ggg tct cct ccc aga     5927
 Ile Thr Gly Tyr Ile Ile Lys Tyr Glu Lys Pro Gly Ser Pro Pro Arg
1840                1845                1850                1855

 gaa gtg gtc cct cgg ccc cgc cct ggt gtc aca gag gct act att cct     5975
 Glu Val Val Pro Arg Pro Arg Pro Gly Val Thr Glu Ala Thr Ile Pro
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 ggc ctg gaa ccg gga acc gaa tat aca att tat gtc att gcc ctg aag     6023
 Gly Leu Glu Pro Gly Thr Glu Tyr Thr Ile Tyr Val Ile Ala Leu Lys
1872                1877                1882                1887

 aat aat cag aag agc gag ccc ctg att gga agg aaa aag aca gac gag     6071
 Asn Asn Gln Lys Ser Glu Pro Leu Ile Gly Arg Lys Lys Thr Asp Glu
1888                1893                1898                1903

 ctt ccc caa ctg gta acc ctt cca cac ccc aat ctt cat gga cca gag     6119
 Leu Pro Gln Leu Val Thr Leu Pro His Pro Asn Leu His Gly Pro Glu
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 atc ttg gat gtt cct tcc aca gtt caa aag acc cct ttc gtc acc cac     6167
 Ile Leu Asp Val Pro Ser Thr Val Gln Lys Thr Pro Phe Val Thr His
1920                1925                1930                1935

 cct ggg tat gac act gga aat ggt att cag ctt cct ggc act tct ggt     6215
 Pro Gly Tyr Asp Thr Gly Asn Gly Ile Gln Leu Pro Gly Thr Ser Gly
1936                1941                1946                1951

 cag caa ccc agt gtt ggg caa caa atg atc ttt gag gaa cat ggt ttt     6263
 Gln Gln Pro Ser Val Gly Gln Gln Met Ile Phe Glu Glu His Gly Phe
1952                1957                1962                1967

 agg cgg acc aca ccg ccc aca acg gcc acc ccc ata agg cat agg cca     6311
 Arg Arg Thr Thr Pro Pro Thr Thr Ala Thr Pro Ile Arg His Arg Pro
1968                1973                1978                1983

 aga cca tac ccg ccg aat gta gga caa gaa gct ctc tct cag aca acc     6359
 Arg Pro Tyr Pro Pro Asn Val Gly Gln Glu Ala Leu Ser Gln Thr Thr
1984                1989                1994                1999

 atc tca tgg gcc cca ttc cag gac act tct gag tac atc att tca tgt     6407
 Ile Ser Trp Ala Pro Phe Gln Asp Thr Ser Glu Tyr Ile Ile Ser Cys
2000                2005                2010                2015

 cat cct gtt ggc act gat gaa gaa ccc tta cag ttc agg gtt cct gga     6455
 His Pro Val Gly Thr Asp Glu Glu Pro Leu Gln Phe Arg Val Pro Gly
2016                2021                2026                2031

 act tct acc agt gcc act ctg aca ggc ctc acc aga ggt gcc acc tac     6503
 Thr Ser Thr Ser Ala Thr Leu Thr Gly Leu Thr Arg Gly Ala Thr Tyr
2032                2037                2042                2047

 aac atc ata gtg gag gca ctg aaa gac cag cag agg cat aag gtt cgg     6551
 Asn Ile Ile Val Glu Ala Leu Lys Asp Gln Gln Arg His Lys Val Arg
2048                2053                2058                2063

 gaa gag gtt gtt acc gtg ggc aac tct gtc aac gaa ggc ttg aac caa     6599
 Glu Glu Val Val Thr Val Gly Asn Ser Val Asn Glu Gly Leu Asn Gln
2064                2069                2074                2079

 cct acg gat gac tcg tgc ttt gac ccc tac aca gtt tcc cat tat gcc     6647
 Pro Thr Asp Asp Ser Cys Phe Asp Pro Tyr Thr Val Ser His Tyr Ala
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 gtt gga gat gag tgg gaa cga atg tct gaa tca ggc ttt aaa ctg ttg     6695
 Val Gly Asp Glu Trp Glu Arg Met Ser Glu Ser Gly Phe Lys Leu Leu
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 tgc cag tgc tta ggc ttt gga agt ggt cat ttc aga tgt gat tca tct     6743
 Cys Gln Cys Leu Gly Phe Gly Ser Gly His Phe Arg Cys Asp Ser Ser
2112                2117                2122                2127

 aga tgg tgc cat gac aat ggt gtg aac tac aag att gga gag aag tgg     6791
 Arg Trp Cys His Asp Asn Gly Val Asn Tyr Lys Ile Gly Glu Lys Trp
2128                2133                2138                2143
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 aac gga aaa gga gaa ttc aag tgt gac cct cat gag gca acg tgt tac     6887
 Asn Gly Lys Gly Glu Phe Lys Cys Asp Pro His Glu Ala Thr Cys Tyr
2160                 2165                 2170                 2175

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 Asp Asp Gly Lys Thr Tyr His Val Gly Glu Gln Trp Gln Lys Glu Tyr
2176                 2181                 2186                 2191

 ctc ggt gcc att tgc tcc tgc aca tgc ttt gga ggc cag cgg ggc tgg     6983
 Leu Gly Ala Ile Cys Ser Cys Thr Cys Phe Gly Gly Gln Arg Gly Trp
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 Arg Cys Asp Asn Cys Arg Arg Pro Gly Gly Glu Pro Ser Pro Glu Gly
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 Thr Thr Gly Gln Ser Tyr Asn Gln Tyr Ser Gln Arg Tyr His Gln Arg
2224                 2229                 2234                 2239

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 Thr Asn Thr Asn Val Asn Cys Pro Ile Glu Cys Phe Met Pro Leu Asp
2240                 2245                 2250                 2255

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 Val Gln Ala Asp Arg Glu Asp Ser Arg Glu  *
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gct ggg cga ggg aga ata agc tgt acc atc gca aac cgc tgc cat gaa      791
Ala Gly Arg Gly Arg Ile Ser Cys Thr Ile Ala Asn Arg Cys His Glu
128                 133                 138                 143

ggg ggt cag tcc tac aag att ggt gac acc tgg agg aga cca cat gag      839
Gly Gly Gln Ser Tyr Lys Ile Gly Asp Thr Trp Arg Arg Pro His Glu
144                 149                 154                 159

act ggt ggt tac atg tta gag tgt gtg tgt ctt ggt aat gga aaa gga      887
Thr Gly Gly Tyr Met Leu Glu Cys Val Cys Leu Gly Asn Gly Lys Gly
160                 165                 170                 175

gaa tgg acc tgc aag ccc ata gct gag aag tgt ttt gat cat gct gct      935
Glu Trp Thr Cys Lys Pro Ile Ala Glu Lys Cys Phe Asp His Ala Ala
176                 181                 186                 191

ggg act tcc tat gtg gtc gga gaa acg tgg gag aag ccc tac caa ggc      983
Gly Thr Ser Tyr Val Val Gly Glu Thr Trp Glu Lys Pro Tyr Gln Gly
192                 197                 202                 207

tgg atg atg gta gat tgt act tgc ctg gga gaa ggc agc gga cgc atc     1031
Trp Met Met Val Asp Cys Thr Cys Leu Gly Glu Gly Ser Gly Arg Ile
208                 213                 218                 223

act tgc act tct aga aat aga tgc aac gat cag gac aca agg aca tcc     1079
Thr Cys Thr Ser Arg Asn Arg Cys Asn Asp Gln Asp Thr Arg Thr Ser
224                 229                 234                 239

tat aga att gga gac acc tgg agc aag aag gat aat cga gga aac ctg     1127
Tyr Arg Ile Gly Asp Thr Trp Ser Lys Lys Asp Asn Arg Gly Asn Leu
240                 245                 250                 255

ctc cag tgc atc tgc aca ggc aac ggc cga gga gag tgg aag tgt gag     1175
Leu Gln Cys Ile Cys Thr Gly Asn Gly Arg Gly Glu Trp Lys Cys Glu
256                 261                 266                 271

agg cac acc tct gtg cag acc aca tcg agc gga tct ggc ccc ttc acc     1223
Arg His Thr Ser Val Gln Thr Thr Ser Ser Gly Ser Gly Pro Phe Thr
272                 277                 282                 287

gat gtt cgt gca gct gtt tac caa ccg cag cct cac ccc cag cct cct     1271
Asp Val Arg Ala Ala Val Tyr Gln Pro Gln Pro His Pro Gln Pro Pro
288                 293                 298                 303

ccc tat ggc cac tgt gtc aca gac agt ggt gtg gtc tac tct gtg ggg     1319
Pro Tyr Gly His Cys Val Thr Asp Ser Gly Val Val Tyr Ser Val Gly
304                 309                 314                 319

atg cag tgg ctg aag aca caa gga aat aag caa atg ctt tgc acg tgc     1367
Met Gln Trp Leu Lys Thr Gln Gly Asn Lys Gln Met Leu Cys Thr Cys
320                 325                 330                 335

ctg ggc aac gga gtc agc tgc caa gag aca gct gta acc cag act tac     1415
Leu Gly Asn Gly Val Ser Cys Gln Glu Thr Ala Val Thr Gln Thr Tyr
336                 341                 346                 351

ggt ggc aac tca aat gga gag cca tgt gtc tta cca ttc acc tac aat     1463
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Gly Gly Asn Ser Asn Gly Glu Pro Cys Val Leu Pro Phe Thr Tyr Asn
352                 357                 362                 367

ggc agg acg ttc tac tcc tgc acc aca gaa ggg cga cag gac gga cat     1511
Gly Arg Thr Phe Tyr Ser Cys Thr Thr Glu Gly Arg Gln Asp Gly His
368                 373                 378                 383

ctt tgg tgc agc aca act tcg aat tat gag cag gac cag aaa tac tct     1559
Leu Trp Cys Ser Thr Thr Ser Asn Tyr Glu Gln Asp Gln Lys Tyr Ser
384                 389                 394                 399

ttc tgc aca gac cac act gtt ttg gtt cag act cga gga gga aat tcc     1607
Phe Cys Thr Asp His Thr Val Leu Val Gln Thr Arg Gly Gly Asn Ser
400                 405                 410                 415

aat ggt gcc ttg tgc cac ttc ccc ttc cta tac aac aac cac aat tac     1655
Asn Gly Ala Leu Cys His Phe Pro Phe Leu Tyr Asn Asn His Asn Tyr
416                 421                 426                 431

act gat tgc act tct gag ggc aga aga gac aac atg aag tgg tgt ggg     1703
Thr Asp Cys Thr Ser Glu Gly Arg Arg Asp Asn Met Lys Trp Cys Gly
432                 437                 442                 447

acc aca cag aac tat gat gcc gac cag aag ttt ggg ttc tgc ccc atg     1751
Thr Thr Gln Asn Tyr Asp Ala Asp Gln Lys Phe Gly Phe Cys Pro Met
448                 453                 458                 463

gct gcc cac gag gaa atc tgc aca acc aat gaa ggg gtc atg tac cgc     1799
Ala Ala His Glu Glu Ile Cys Thr Thr Asn Glu Gly Val Met Tyr Arg
464                 469                 474                 479

att gga gat cag tgg gat aag cag cat gac atg ggt cac atg atg agg     1847
Ile Gly Asp Gln Trp Asp Lys Gln His Asp Met Gly His Met Met Arg
480                 485                 490                 495

tgc acg tgt gtt ggg aat ggt cgt ggg gaa tgg aca tgc att gcc tac     1895
Cys Thr Cys Val Gly Asn Gly Arg Gly Glu Trp Thr Cys Ile Ala Tyr
496                 501                 506                 511

tcg caa ctt cga gat cag tgc att gtt gat gac atc act tac aat gtg     1943
Ser Gln Leu Arg Asp Gln Cys Ile Val Asp Asp Ile Thr Tyr Asn Val
512                 517                 522                 527

aac gac aca ttc cac aag cgt cat gaa gag ggg cac atg ctg aac tgt     1991
Asn Asp Thr Phe His Lys Arg His Glu Glu Gly His Met Leu Asn Cys
528                 533                 538                 543

aca tgc ttc ggt cag ggt cgg ggc agg tgg aag tgt gat ccc gtc gac     2039
Thr Cys Phe Gly Gln Gly Arg Gly Arg Trp Lys Cys Asp Pro Val Asp
544                 549                 554                 559

caa tgc cag gat tca gag act ggg acg ttt tat caa att gga gat tca     2087
Gln Cys Gln Asp Ser Glu Thr Gly Thr Phe Tyr Gln Ile Gly Asp Ser
560                 565                 570                 575

tgg gag aag tat gtg cat ggt gtc aga tac cag tgc tac tgc tat ggc     2135
Trp Glu Lys Tyr Val His Gly Val Arg Tyr Gln Cys Tyr Cys Tyr Gly
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US 6,500,930 B2

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576                 581                 586                 591

cgt ggc att ggg gag tgg cat tgc caa cct tta cag acc tat cca agc     2183
Arg Gly Ile Gly Glu Trp His Cys Gln Pro Leu Gln Thr Tyr Pro Ser
592                 597                 602                 607

tca agt ggt cct gtc gaa gta ttt atc act gag act ccg agt cag ccc     2231
Ser Ser Gly Pro Val Glu Val Phe Ile Thr Glu Thr Pro Ser Gln Pro
608                 613                 618                 623

aac tcc cac ccc atc cag tgg aat gca cca cag cca tct cac att tcc     2279
Asn Ser His Pro Ile Gln Trp Asn Ala Pro Gln Pro Ser His Ile Ser
624                 629                 634                 639

aag tac att ctc agg tgg aga cct aaa aat tct gta ggc cgt tgg aag     2327
Lys Tyr Ile Leu Arg Trp Arg Pro Lys Asn Ser Val Gly Arg Trp Lys
640                 645                 650                 655

gaa gct acc ata cca ggc cac tta aac tcc tac acc atc aaa ggc ctg     2375
Glu Ala Thr Ile Pro Gly His Leu Asn Ser Tyr Thr Ile Lys Gly Leu
656                 661                 666                 671

aag cct ggt gtg gta tac gag ggc cag ctc atc agc atc cag cag tac     2423
Lys Pro Gly Val Val Tyr Glu Gly Gln Leu Ile Ser Ile Gln Gln Tyr
672                 677                 682                 687

ggc cac caa gaa gtg act cgc ttt gac ttc acc acc acc agc acc agc     2471
Gly His Gln Glu Val Thr Arg Phe Asp Phe Thr Thr Thr Ser Thr Ser
688                 693                 698                 703

aca cct gtg acc agc aac acc gtg aca gga gag acg act ccc ttt tct     2519
Thr Pro Val Thr Ser Asn Thr Val Thr Gly Glu Thr Thr Pro Phe Ser
704                 709                 714                 719

cct ctt gtg gcc act tct gaa tct gtg acc gaa atc aca gcc agt agc     2567
Pro Leu Val Ala Thr Ser Glu Ser Val Thr Glu Ile Thr Ala Ser Ser
720                 725                 730                 735

ttt gtg gtc tcc tgg gtc tca gct tcc gac acc gtg tcg gga ttc cgg     2615
Phe Val Val Ser Trp Val Ser Ala Ser Asp Thr Val Ser Gly Phe Arg
736                 741                 746                 751

gtg gaa tat gag ctg agt gag gag gga gat gag cca cag tac ctg gat     2663
Val Glu Tyr Glu Leu Ser Glu Glu Gly Asp Glu Pro Gln Tyr Leu Asp
752                 757                 762                 767

ctt cca agc aca gcc act tct gtg aac atc cct gac ctg ctt cct ggc     2711
Leu Pro Ser Thr Ala Thr Ser Val Asn Ile Pro Asp Leu Leu Pro Gly
768                 773                 778                 783

cga aaa tac att gta aat gtc tat cag ata tct gag gat ggg gag cag     2759
Arg Lys Tyr Ile Val Asn Val Tyr Gln Ile Ser Glu Asp Gly Glu Gln
784                 789                 794                 799

agt ttg atc ctg tct act tca caa aca aca gcg cct gat gcc cct cct     2807
Ser Leu Ile Leu Ser Thr Ser Gln Thr Thr Ala Pro Asp Ala Pro Pro
800                 805                 810                 815
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gac ccg act gtg gac caa gtt gat gac acc tca att gtt gtt cgc tgg     2855
Asp Pro Thr Val Asp Gln Val Asp Asp Thr Ser Ile Val Val Arg Trp
816                 821                 826                 831

agc aga ccc cag gct ccc atc aca ggg tac aga ata gtc tat tcg cca     2903
Ser Arg Pro Gln Ala Pro Ile Thr Gly Tyr Arg Ile Val Tyr Ser Pro
832                 837                 842                 847

tca gta gaa ggt agc agc aca gaa ctc aac ctt cct gaa act gca aac     2951
Ser Val Glu Gly Ser Ser Thr Glu Leu Asn Leu Pro Glu Thr Ala Asn
848                 853                 858                 863

tcc gtc acc ctc agt gac ttg caa cct ggt gtt cag tat aac atc act     2999
Ser Val Thr Leu Ser Asp Leu Gln Pro Gly Val Gln Tyr Asn Ile Thr
864                 869                 874                 879

atc tat gct gtg gaa gaa aat caa gaa agt aca cct gtt gtc att caa     3047
Ile Tyr Ala Val Glu Glu Asn Gln Glu Ser Thr Pro Val Val Ile Gln
880                 885                 890                 895

caa gaa acc act ggc acc cca cgc tca gat aca gtg ccc tct ccc agg     3095
Gln Glu Thr Thr Gly Thr Pro Arg Ser Asp Thr Val Pro Ser Pro Arg
896                 901                 906                 911

gac ctg cag ttt gtg gaa gtg aca gac gtg aag gtc acc atc atg tgg     3143
Asp Leu Gln Phe Val Glu Val Thr Asp Val Lys Val Thr Ile Met Trp
912                 917                 922                 927

aca ccg cct gag agt gca gtg acc ggc tac cgt gtg gat gtg atc ccc     3191
Thr Pro Pro Glu Ser Ala Val Thr Gly Tyr Arg Val Asp Val Ile Pro
928                 933                 938                 943

gtc aac ctg cct ggc gag cac ggg cag agg ctg ccc atc agc agg aac     3239
Val Asn Leu Pro Gly Glu His Gly Gln Arg Leu Pro Ile Ser Arg Asn
944                 949                 954                 959

acc ttt gca gaa gtc acc ggg ctg tcc cct ggg gtc acc tat tac ttc     3287
Thr Phe Ala Glu Val Thr Gly Leu Ser Pro Gly Val Thr Tyr Tyr Phe
960                 965                 970                 975

aaa gtc ttt gca gtg agc cat ggg agg gag agc aag cct ctg act gct     3335
Lys Val Phe Ala Val Ser His Gly Arg Glu Ser Lys Pro Leu Thr Ala
976                 981                 986                 991

caa cag aca acc aaa ctg gat gct ccc act aac ctc cag ttt gtc aat     3383
Gln Gln Thr Thr Lys Leu Asp Ala Pro Thr Asn Leu Gln Phe Val Asn
992                 997                1002                1007

gaa act gat tct act gtc ctg gtg aga tgg act cca cct cgg gcc cag     3431
Glu Thr Asp Ser Thr Val Leu Val Arg Trp Thr Pro Pro Arg Ala Gln
1008                1013                1018                1023

ata aca gga tac cga ctg acc gtg ggc ctt acc cga aga gga cag ccc     3479
Ile Thr Gly Tyr Arg Leu Thr Val Gly Leu Thr Arg Arg Gly Gln Pro
1024                1029                1034                1039
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agg cag tac aat gtg ggt ccc tct gtc tcc aag tac cca ctg agg aat     3527
Arg Gln Tyr Asn Val Gly Pro Ser Val Ser Lys Tyr Pro Leu Arg Asn
1040                1045                1050                1055

ctg cag cct gca tct gag tac acc gta tcc ctc gtg gcc ata aag ggc     3575
Leu Gln Pro Ala Ser Glu Tyr Thr Val Ser Leu Val Ala Ile Lys Gly
1056                1061                1066                1071

aac caa gag agc ccc aaa gcc act gga gtc ttt acc aca ctg cag cct     3623
Asn Gln Glu Ser Pro Lys Ala Thr Gly Val Phe Thr Thr Leu Gln Pro
1072                1077                1082                1087

ggg agc tct att cca cct tac aac acc gag gtg act gag acc acc att     3671
Gly Ser Ser Ile Pro Pro Tyr Asn Thr Glu Val Thr Glu Thr Thr Ile
1088                1093                1098                1103

gtg atc aca tgg acg cct gct cca aga att ggt ttt aag ctg ggt gta     3719
Val Ile Thr Trp Thr Pro Ala Pro Arg Ile Gly Phe Lys Leu Gly Val
1104                1109                1114                1119

cga cca agc cag gga gga gag gca cca cga gaa gtg act tca gac tca     3767
Arg Pro Ser Gln Gly Gly Glu Ala Pro Arg Glu Val Thr Ser Asp Ser
1120                1125                1130                1135

gga agc atc gtt gtg tcc ggc ttg act cca gga gta gaa tac gtc tac     3815
Gly Ser Ile Val Val Ser Gly Leu Thr Pro Gly Val Glu Tyr Val Tyr
1136                1141                1146                1151

acc atc caa gtc ctg aga gat gga cag gaa aga gat gcg cca att gta     3863
Thr Ile Gln Val Leu Arg Asp Gly Gln Glu Arg Asp Ala Pro Ile Val
1152                1157                1162                1167

aac aaa gtg gtg aca cca ttg tct cca cca aca aac ttg cat ctg gag     3911
Asn Lys Val Val Thr Pro Leu Ser Pro Pro Thr Asn Leu His Leu Glu
1168                1173                1178                1183

gca aac cct gac act gga gtg ctc aca gtc tcc tgg gag agg agc acc     3959
Ala Asn Pro Asp Thr Gly Val Leu Thr Val Ser Trp Glu Arg Ser Thr
1184                1189                1194                1199

acc cca gac att act ggt tat aga att acc aca acc cct aca aac ggc     4007
Thr Pro Asp Ile Thr Gly Tyr Arg Ile Thr Thr Thr Pro Thr Asn Gly
1200                1205                1210                1215

cag cag gga aat tct ttg gaa gaa gtg gtc cat gct gat cag agc tcc     4055
Gln Gln Gly Asn Ser Leu Glu Glu Val Val His Ala Asp Gln Ser Ser
1216                1221                1226                1231

tgc act ttt gat aac ctg agt ccc ggc ctg gag tac aat gtc agt gtt     4103
Cys Thr Phe Asp Asn Leu Ser Pro Gly Leu Glu Tyr Asn Val Ser Val
1232                1237                1242                1247

tac act gtc aag gat gac aag gaa agt gtc cct atc tct gat acc atc     4151
Tyr Thr Val Lys Asp Asp Lys Glu Ser Val Pro Ile Ser Asp Thr Ile
1248                1253                1258                1263

atc cca gct gtt cct cct ccc act gac ctg cga ttc acc aac att ggt     4199
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 Ile Pro Ala Val Pro Pro Pro Thr Asp Leu Arg Phe Thr Asn Ile Gly
1264                1269                1274                1279

 cca gac acc atg cgt gtc acc tgg gct cca ccc cca tcc att gat tta     4247
 Pro Asp Thr Met Arg Val Thr Trp Ala Pro Pro Pro Ser Ile Asp Leu
1280                1285                1290                1295

 acc aac ttc ctg gtg cgt tac tca cct gtg aaa aat gag gaa gat gtt     4295
 Thr Asn Phe Leu Val Arg Tyr Ser Pro Val Lys Asn Glu Glu Asp Val
1296                1301                1306                1311

 gca gag ttg tca att tct cct tca gac aat gca gtg gtc tta aca aat     4343
 Ala Glu Leu Ser Ile Ser Pro Ser Asp Asn Ala Val Val Leu Thr Asn
1312                1317                1322                1327

 ctc ctg cct ggt aca gaa tat gta gtg agt gtc tcc agt gtc tac gaa     4391
 Leu Leu Pro Gly Thr Glu Tyr Val Val Ser Val Ser Ser Val Tyr Glu
1328                1333                1338                1343

 caa cat gag agc aca cct ctt aga gga aga cag aaa aca ggt ctt gat     4439
 Gln His Glu Ser Thr Pro Leu Arg Gly Arg Gln Lys Thr Gly Leu Asp
1344                1349                1354                1359

 tcc cca act ggc att gac ttt tct gat att act gcc aac tct ttt act     4487
 Ser Pro Thr Gly Ile Asp Phe Ser Asp Ile Thr Ala Asn Ser Phe Thr
1360                1365                1370                1375

 gtg cac tgg att gct cct cga gcc acc atc act ggc tac agg atc cgc     4535
 Val His Trp Ile Ala Pro Arg Ala Thr Ile Thr Gly Tyr Arg Ile Arg
1376                1381                1386                1391

 cat cat ccc gag cac ttc agt ggg aga cct cga gaa gat cgg gtg ccc     4583
 His His Pro Glu His Phe Ser Gly Arg Pro Arg Glu Asp Arg Val Pro
1392                1397                1402                1407

 cac tct cgg aat tcc atc acc ctc acc aac ctc act cca ggc aca gag     4631
 His Ser Arg Asn Ser Ile Thr Leu Thr Asn Leu Thr Pro Gly Thr Glu
1408                1413                1418                1423

 tat gtg gtc agc atc gtt gct ctt aat ggc aga gag gaa agt ccc tta     4679
 Tyr Val Val Ser Ile Val Ala Leu Asn Gly Arg Glu Glu Ser Pro Leu
1424                1429                1434                1439

 ttg att ggc caa caa tca aca gtt tct gat gtt ccg agg gac ctg gaa     4727
 Leu Ile Gly Gln Gln Ser Thr Val Ser Asp Val Pro Arg Asp Leu Glu
1440                1445                1450                1455

 gtt gtt gct gcg acc ccc acc agc cta ctg atc agc tgg gat gct cct     4775
 Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro
1456                1461                1466                1471

 gct gtc aca gtg aga tat tac agg atc act tac gga gaa aca gga gga     4823
 Ala Val Thr Val Arg Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly
1472                1477                1482                1487

 aat agc cct gtc cag gag ttc act gtg cct ggg agc aag tct aca gct     4871
 Asn Ser Pro Val Gln Glu Phe Thr Val Pro Gly Ser Lys Ser Thr Ala
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1488                1493                1498                1503

 acc atc agc ggc ctt aaa cct gga gtt gat tat acc atc act gtg tat     4919
 Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr
1504                1509                1514                1519

 gct gtc act ggc cgt gga gac agc ccc gca agc agc aag cca att tcc     4967
 Ala Val Thr Gly Arg Gly Asp Ser Pro Ala Ser Ser Lys Pro Ile Ser
1520                1525                1530                1535

 att aat tac cga aca gaa att gac aaa cca tcc cag atg caa gtg acc     5015
 Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln Met Gln Val Thr
1536                1541                1546                1551

 gat gtt cag gac aac agc att agt gtc aag tgg ctg cct tca agt tcc     5063
 Asp Val Gln Asp Asn Ser Ile Ser Val Lys Trp Leu Pro Ser Ser Ser
1552                1557                1562                1567

 cct gtt act ggt tac aga gta acc acc act ccc aaa aat gga cca gga     5111
 Pro Val Thr Gly Tyr Arg Val Thr Thr Thr Pro Lys Asn Gly Pro Gly
1568                1573                1578                1583

 cca aca aaa act aaa act gca ggt cca gat caa aca gaa atg act att     5159
 Pro Thr Lys Thr Lys Thr Ala Gly Pro Asp Gln Thr Glu Met Thr Ile
1584                1589                1594                1599

 gaa ggc ttg cag ccc aca gtg gag tat gtg gtt agt gtc tat gct cag     5207
 Glu Gly Leu Gln Pro Thr Val Glu Tyr Val Val Ser Val Tyr Ala Gln
1600                1605                1610                1615

 aat cca agc gga gag agt cag cct ctg gtt cag act gca gta acc aac     5255
 Asn Pro Ser Gly Glu Ser Gln Pro Leu Val Gln Thr Ala Val Thr Asn
1616                1621                1626                1631

 att gat cgc cct aaa gga ctg gca ttc act gat gtg gat gtc gat tcc     5303
 Ile Asp Arg Pro Lys Gly Leu Ala Phe Thr Asp Val Asp Val Asp Ser
1632                1637                1642                1647

 atc aaa att gct tgg gaa agc cca cag ggg caa gtt tcc agg tac agg     5351
 Ile Lys Ile Ala Trp Glu Ser Pro Gln Gly Gln Val Ser Arg Tyr Arg
1648                1653                1658                1663

 gtg acc tac tcg agc cct gag gat gga atc cat gag cta ttc cct gca     5399
 Val Thr Tyr Ser Ser Pro Glu Asp Gly Ile His Glu Leu Phe Pro Ala
1664                1669                1674                1679

 cct gat ggt gaa gaa gac act gca gag ctg caa ggc ctc aga ccg ggt     5447
 Pro Asp Gly Glu Glu Asp Thr Ala Glu Leu Gln Gly Leu Arg Pro Gly
1680                1685                1690                1695

 tct gag tac aca gtc agt gtg gtt gcc ttg cac gat gat atg gag agc     5495
 Ser Glu Tyr Thr Val Ser Val Val Ala Leu His Asp Asp Met Glu Ser
1696                1701                1706                1711

 cag ccc ctg att gga acc cag tcc aca gct att cct gca cca act gac     5543
 Gln Pro Leu Ile Gly Thr Gln Ser Thr Ala Ile Pro Ala Pro Thr Asp
1712                1717                1722                1727
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 ctg aag ttc act cag gtc aca ccc aca agc ctg agc gcc cag tgg aca     5591
 Leu Lys Phe Thr Gln Val Thr Pro Thr Ser Leu Ser Ala Gln Trp Thr
1728                1733                1738                1743

 cca ccc aat gtt cag ctc act gga tat cga gtg cgg gtg acc ccc aag     5639
 Pro Pro Asn Val Gln Leu Thr Gly Tyr Arg Val Arg Val Thr Pro Lys
1744                1749                1754                1759

 gag aag acc gga cca atg aaa gaa atc aac ctt gct cct gac agc tca     5687
 Glu Lys Thr Gly Pro Met Lys Glu Ile Asn Leu Ala Pro Asp Ser Ser
1760                1765                1770                1775

 tcc gtg gtt gta tca gga ctt atg gtg gcc acc aaa tat gaa gtg agt     5735
 Ser Val Val Val Ser Gly Leu Met Val Ala Thr Lys Tyr Glu Val Ser
1776                1781                1786                1791

 gtc tat gct ctt aag gac act ttg aca agc aga cca gct cag gga gtt     5783
 Val Tyr Ala Leu Lys Asp Thr Leu Thr Ser Arg Pro Ala Gln Gly Val
1792                1797                1802                1807

 gtc acc act ctg gag aat gtc agc cca cca aga agg gct cgt gtg aca     5831
 Val Thr Thr Leu Glu Asn Val Ser Pro Pro Arg Arg Ala Arg Val Thr
1808                1813                1818                1823

 gat gct act gag acc acc atc acc att agc tgg aga acc aag act gag     5879
 Asp Ala Thr Glu Thr Thr Ile Thr Ile Ser Trp Arg Thr Lys Thr Glu
1824                1829                1834                1839

 acg atc act ggc ttc caa gtt gat gcc gtt cca gcc aat ggc cag act     5927
 Thr Ile Thr Gly Phe Gln Val Asp Ala Val Pro Ala Asn Gly Gln Thr
1840                1845                1850                1855

 cca atc cag aga acc atc aag cca gat gtc aga agc tac acc atc aca     5975
 Pro Ile Gln Arg Thr Ile Lys Pro Asp Val Arg Ser Tyr Thr Ile Thr
1856                1861                1866                1871

 ggt tta caa cca ggc act gac tac aag atc tac ctg tac acc ttg aat     6023
 Gly Leu Gln Pro Gly Thr Asp Tyr Lys Ile Tyr Leu Tyr Thr Leu Asn
1872                1877                1882                1887

 gac aat gct cgg agc tcc cct gtg gtc atc gac gcc tcc act gcc att     6071
 Asp Asn Ala Arg Ser Ser Pro Val Val Ile Asp Ala Ser Thr Ala Ile
1888                1893                1898                1903

 gat gca cca tcc aac ctg cgt ttc ctg gcc acc aca ccc aat tcc ttg     6119
 Asp Ala Pro Ser Asn Leu Arg Phe Leu Ala Thr Thr Pro Asn Ser Leu
1904                1909                1914                1919

 ctg gta tca tgg cag ccg cca cgt gcc agg att acc ggc tac atc atc     6167
 Leu Val Ser Trp Gln Pro Pro Arg Ala Arg Ile Thr Gly Tyr Ile Ile
1920                1925                1930                1935

 aag tat gag aag cct ggg tct cct ccc aga gaa gtg gtc cct cgg ccc     6215
 Lys Tyr Glu Lys Pro Gly Ser Pro Pro Arg Glu Val Val Pro Arg Pro
1936                1941                1946                1951
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US 2005/0260750 A1

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 cgc cct ggt gtc aca gag gct act att cct ggc ctg gaa ccg gga acc     6263
 Arg Pro Gly Val Thr Glu Ala Thr Ile Pro Gly Leu Glu Pro Gly Thr
1952                1957                1962                1967

 gaa tat aca att tat gtc att gcc ctg aag aat aat cag aag agc gag     6311
 Glu Tyr Thr Ile Tyr Val Ile Ala Leu Lys Asn Asn Gln Lys Ser Glu
1968                1973                1978                1983

 ccc ctg att gga agg aaa aag aca gac gag ctt ccc caa ctg gta acc     6359
 Pro Leu Ile Gly Arg Lys Lys Thr Asp Glu Leu Pro Gln Leu Val Thr
1984                1989                1994                1999

 ctt cca cac ccc aat ctt cat gga cca gag atc ttg gat gtt cct tcc     6407
 Leu Pro His Pro Asn Leu His Gly Pro Glu Ile Leu Asp Val Pro Ser
2000                2005                2010                2015

 aca gtt caa aag acc cct ttc gtc acc cac cct ggg tat gac act gga     6455
 Thr Val Gln Lys Thr Pro Phe Val Thr His Pro Gly Tyr Asp Thr Gly
2016                2021                2026                2031

 aat ggt att cag ctt cct ggc act tct ggt cag caa ccc agt gtt ggg     6503
 Asn Gly Ile Gln Leu Pro Gly Thr Ser Gly Gln Gln Pro Ser Val Gly
2032                2037                2042                2047

 caa caa atg atc ttt gag gaa cat ggt ttt agg cgg acc aca ccg ccc     6551
 Gln Gln Met Ile Phe Glu Glu His Gly Phe Arg Arg Thr Thr Pro Pro
2048                2053                2058                2063

 aca acg gcc acc ccc ata agg cat agg cca aga cca tac ccg ccg aat     6599
 Thr Thr Ala Thr Pro Ile Arg His Arg Pro Arg Pro Tyr Pro Pro Asn
2064                2069                2074                2079

 gta ggt gag gaa atc caa att ggt cac atc ccc agg gaa gat gta gac     6647
 Val Gly Glu Glu Ile Gln Ile Gly His Ile Pro Arg Glu Asp Val Asp
2080                2085                2090                2095

 tat cac ctg tac cca cac ggt ccg ggg ctc aat cca aat gcc tct aca     6695
 Tyr His Leu Tyr Pro His Gly Pro Gly Leu Asn Pro Asn Ala Ser Thr
2096                2101                2106                2111

 gga caa gaa gct ctc tct cag aca acc atc tca tgg gcc cca ttc cag     6743
 Gly Gln Glu Ala Leu Ser Gln Thr Thr Ile Ser Trp Ala Pro Phe Gln
2112                2117                2122                2127

 gac act tct gag tac atc att tca tgt cat cct gtt ggc act gat gaa     6791
 Asp Thr Ser Glu Tyr Ile Ile Ser Cys His Pro Val Gly Thr Asp Glu
2128                2133                2138                2143

 gaa ccc tta cag ttc agg gtt cct gga act tct acc agt gcc act ctg     6839
 Glu Pro Leu Gln Phe Arg Val Pro Gly Thr Ser Thr Ser Ala Thr Leu
2144                2149                2154                2159

 aca ggc ctc acc aga ggt gcc acc tac aac atc ata gtg gag gca ctg     6887
 Thr Gly Leu Thr Arg Gly Ala Thr Tyr Asn Ile Ile Val Glu Ala Leu
2160                2165                2170                2175

 aaa gac cag cag agg cat aag gtt cgg gaa gag gtt gtt acc gtg ggc     6935
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 Lys Asp Gln Gln Arg His Lys Val Arg Glu Glu Val Val Thr Val Gly
2176                2181                2186                2191

 aac tct gtc aac gaa ggc ttg aac caa cct acg gat gac tcg tgc ttt     6983
 Asn Ser Val Asn Glu Gly Leu Asn Gln Pro Thr Asp Asp Ser Cys Phe
2192                2197                2202                2207

 gac ccc tac aca gtt tcc cat tat gcc gtt gga gat gag tgg gaa cga     7031
 Asp Pro Tyr Thr Val Ser His Tyr Ala Val Gly Asp Glu Trp Glu Arg
2208                2213                2218                2223

 atg tct gaa tca ggc ttt aaa ctg ttg tgc cag tgc tta ggc ttt gga     7079
 Met Ser Glu Ser Gly Phe Lys Leu Leu Cys Gln Cys Leu Gly Phe Gly
2224                2229                2234                2239

 agt ggt cat ttc aga tgt gat tca tct aga tgg tgc cat gac aat ggt     7127
 Ser Gly His Phe Arg Cys Asp Ser Ser Arg Trp Cys His Asp Asn Gly
2240                2245                2250                2255

 gtg aac tac aag att gga gag aag tgg gac cgt cag gga gaa aat ggc     7175
 Val Asn Tyr Lys Ile Gly Glu Lys Trp Asp Arg Gln Gly Glu Asn Gly
2256                2261                2266                2271

 cag atg atg agc tgc aca tgt ctt ggg aac gga aaa gga gaa ttc aag     7223
 Gln Met Met Ser Cys Thr Cys Leu Gly Asn Gly Lys Gly Glu Phe Lys
2272                2277                2282                2287

 tgt gac cct cat gag gca acg tgt tac gat gat ggg aag aca tac cac     7271
 Cys Asp Pro His Glu Ala Thr Cys Tyr Asp Asp Gly Lys Thr Tyr His
2288                2293                2298                2303

 gta gga gaa cag tgg cag aag gaa tat ctc ggt gcc att tgc tcc tgc     7319
 Val Gly Glu Gln Trp Gln Lys Glu Tyr Leu Gly Ala Ile Cys Ser Cys
2304                2309                2314                2319

 aca tgc ttt gga ggc cag cgg ggc tgg cgc tgt gac aac tgc cgc aga     7367
 Thr Cys Phe Gly Gly Gln Arg Gly Trp Arg Cys Asp Asn Cys Arg Arg
2320                2325                2330                2335

 cct ggg ggt gaa ccc agt ccc gaa ggc act act ggc cag tcc tac aac     7415
 Pro Gly Gly Glu Pro Ser Pro Glu Gly Thr Thr Gly Gln Ser Tyr Asn
2336                2341                2346                2351

 cag tat tct cag aga tac cat cag aga aca aac act aat gtt aat tgc     7463
 Gln Tyr Ser Gln Arg Tyr His Gln Arg Thr Asn Thr Asn Val Asn Cys
2352                2357                2362                2367

 cca att gag tgc ttc atg cct tta gat gta cag gct gac aga gaa gat     7511
 Pro Ile Glu Cys Phe Met Pro Leu Asp Val Gln Ala Asp Arg Glu Asp
2368                2373                2378                2383

 tcc cga gag taa atc atctttccaa tccagaggaa caagcatgtc tctctgccaa     7566
 Ser Arg Glu  *
2384

 gatccatcta aactggagtg atgttagcag acccagctta gagttcttct ttctttctta   7626
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agcccttgc tctggaggaa gttctccagc ttcagctcaa ctcacagctt ctccaagcat   7686

caccctggga gtttcctgag ggttttctca taaatgaggg ctgcacattg cctgttctgc   7746

ttcgaagtat tcaataccgc tcagtatttt aaatgaagtg attctaagat ttggtttggg   7806

atcaatagga aagcatatgc agccaaccaa gatgcaaatg ttttgaaatg atatgaccaa   7866

aattttaagt aggaaagtca cccaaacact tctgctttca cttaagtgtc tggcccgcaa   7926

tactgtagga acaagcatga tcttgttact gtgatatttt aaatatccac agtactcact   7986

ttttccaaat gatcctagta attgcctaga aatatctttc tcttacctgt tatttatcaa   8046

tttttcccag tatttttata cggaaaaaat tgtattgaaa acacttagta tgcagttgat   8106

aagaggaatt tggtataatt atggtgggtg attatttttt atactgtatg tgccaaagct   8166

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aaaa                                                               8230
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ggggaggaga gggaacccca ggcgcgagcg ggaagagggg acctgcagcc acaacttctc    180

tggtcctctg catcccttct gtccctccac ccgtcccctt ccccaccctc tggcccccac    240

cttcttggag gcgacaaccc ccgggaggca ttagaaggga tttttcccgc aggttgcgaa    300

gggaagcaaa cttggtggca acttgcctcc cggtgcgggc gtctctcccc caccgtctca    360

ac   atg ctt agg ggt ccg ggg ccc ggg ctg ctg ctg ctg gcc gtc ctg      407
     Met Leu Arg Gly Pro Gly Pro Gly Leu Leu Leu Leu Ala Val Leu
       1               5                  10

tgc ctg ggg aca gcg gtg ccc tcc acg gga gcc tcg aag agc aag agg      455
Cys Leu Gly Thr Ala Val Pro Ser Thr Gly Ala Ser Lys Ser Lys Arg
 16                  21                  26                  31

cag gct cag caa atg gtt cag ccc cag tcc ccg gtg gct gtc agt caa      503
Gln Ala Gln Gln Met Val Gln Pro Gln Ser Pro Val Ala Val Ser Gln
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 32                  37                  42                  47

agc aag ccc ggt tgt tat gac aat gga aaa cac tat cag ata aat caa      551
Ser Lys Pro Gly Cys Tyr Asp Asn Gly Lys His Tyr Gln Ile Asn Gln
 48                  53                  58                  63

cag tgg gag cgg acc tac cta ggc aat gcg ttg gtt tgt act tgt tat      599
Gln Trp Glu Arg Thr Tyr Leu Gly Asn Ala Leu Val Cys Thr Cys Tyr
 64                  69                  74                  79

gga gga agc cga ggt ttt aac tgc gag agt aaa cct gaa gct gaa gag      647
Gly Gly Ser Arg Gly Phe Asn Cys Glu Ser Lys Pro Glu Ala Glu Glu
 80                  85                  90                  95

act tgc ttt gac aag tac act ggg aac act tac cga gtg ggt gac act      695
Thr Cys Phe Asp Lys Tyr Thr Gly Asn Thr Tyr Arg Val Gly Asp Thr
 96                 101                 106                 111

tat gag cgt cct aaa gac tcc atg atc tgg gac tgt acc tgc atc ggg      743
Tyr Glu Arg Pro Lys Asp Ser Met Ile Trp Asp Cys Thr Cys Ile Gly
112                 117                 122                 127

gct ggg cga ggg aga ata agc tgt acc atc gca aac cgc tgc cat gaa      791
Ala Gly Arg Gly Arg Ile Ser Cys Thr Ile Ala Asn Arg Cys His Glu
128                 133                 138                 143

ggg ggt cag tcc tac aag att ggt gac acc tgg agg aga cca cat gag      839
Gly Gly Gln Ser Tyr Lys Ile Gly Asp Thr Trp Arg Arg Pro His Glu
144                 149                 154                 159

act ggt ggt tac atg tta gag tgt gtg tgt ctt ggt aat gga aaa gga      887
Thr Gly Gly Tyr Met Leu Glu Cys Val Cys Leu Gly Asn Gly Lys Gly
160                 165                 170                 175

gaa tgg acc tgc aag ccc ata gct gag aag tgt ttt gat cat gct gct      935
Glu Trp Thr Cys Lys Pro Ile Ala Glu Lys Cys Phe Asp His Ala Ala
176                 181                 186                 191

ggg act tcc tat gtg gtc gga gaa acg tgg gag aag ccc tac caa ggc      983
Gly Thr Ser Tyr Val Val Gly Glu Thr Trp Glu Lys Pro Tyr Gln Gly
192                 197                 202                 207

tgg atg atg gta gat tgt act tgc ctg gga gaa ggc agc gga cgc atc     1031
Trp Met Met Val Asp Cys Thr Cys Leu Gly Glu Gly Ser Gly Arg Ile
208                 213                 218                 223

act tgc act tct aga aat aga tgc aac gat cag gac aca agg aca tcc     1079
Thr Cys Thr Ser Arg Asn Arg Cys Asn Asp Gln Asp Thr Arg Thr Ser
224                 229                 234                 239

tat aga att gga gac acc tgg agc aag aag gat aat cga gga aac ctg     1127
Tyr Arg Ile Gly Asp Thr Trp Ser Lys Lys Asp Asn Arg Gly Asn Leu
240                 245                 250                 255

ctc cag tgc atc tgc aca ggc aac ggc cga gga gag tgg aag tgt gag     1175
Leu Gln Cys Ile Cys Thr Gly Asn Gly Arg Gly Glu Trp Lys Cys Glu
256                 261                 266                 271
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agg cac acc tct gtg cag acc aca tcg agc gga tct ggc ccc ttc acc     1223
Arg His Thr Ser Val Gln Thr Thr Ser Ser Gly Ser Gly Pro Phe Thr
272                 277                 282                 287

gat gtt cgt gca gct gtt tac caa ccg cag cct cac ccc cag cct cct     1271
Asp Val Arg Ala Ala Val Tyr Gln Pro Gln Pro His Pro Gln Pro Pro
288                 293                 298                 303

ccc tat ggc cac tgt gtc aca gac agt ggt gtg gtc tac tct gtg ggg     1319
Pro Tyr Gly His Cys Val Thr Asp Ser Gly Val Val Tyr Ser Val Gly
304                 309                 314                 319

atg cag tgg ctg aag aca caa gga aat aag caa atg ctt tgc acg tgc     1367
Met Gln Trp Leu Lys Thr Gln Gly Asn Lys Gln Met Leu Cys Thr Cys
320                 325                 330                 335

ctg ggc aac gga gtc agc tgc caa gag aca gct gta acc cag act tac     1415
Leu Gly Asn Gly Val Ser Cys Gln Glu Thr Ala Val Thr Gln Thr Tyr
336                 341                 346                 351

ggt ggc aac tca aat gga gag cca tgt gtc tta cca ttc acc tac aat     1463
Gly Gly Asn Ser Asn Gly Glu Pro Cys Val Leu Pro Phe Thr Tyr Asn
352                 357                 362                 367

ggc agg acg ttc tac tcc tgc acc aca gaa ggg cga cag gac gga cat     1511
Gly Arg Thr Phe Tyr Ser Cys Thr Thr Glu Gly Arg Gln Asp Gly His
368                 373                 378                 383

ctt tgg tgc agc aca act tcg aat tat gag cag gac cag aaa tac tct     1559
Leu Trp Cys Ser Thr Thr Ser Asn Tyr Glu Gln Asp Gln Lys Tyr Ser
384                 389                 394                 399

ttc tgc aca gac cac act gtt ttg gtt cag act cga gga gga aat tcc     1607
Phe Cys Thr Asp His Thr Val Leu Val Gln Thr Arg Gly Gly Asn Ser
400                 405                 410                 415

aat ggt gcc ttg tgc cac ttc ccc ttc cta tac aac aac cac aat tac     1655
Asn Gly Ala Leu Cys His Phe Pro Phe Leu Tyr Asn Asn His Asn Tyr
416                 421                 426                 431

act gat tgc act tct gag ggc aga aga gac aac atg aag tgg tgt ggg     1703
Thr Asp Cys Thr Ser Glu Gly Arg Arg Asp Asn Met Lys Trp Cys Gly
432                 437                 442                 447

acc aca cag aac tat gat gcc gac cag aag ttt ggg ttc tgc ccc atg     1751
Thr Thr Gln Asn Tyr Asp Ala Asp Gln Lys Phe Gly Phe Cys Pro Met
448                 453                 458                 463

gct gcc cac gag gaa atc tgc aca acc aat gaa ggg gtc atg tac cgc     1799
Ala Ala His Glu Glu Ile Cys Thr Thr Asn Glu Gly Val Met Tyr Arg
464                 469                 474                 479

att gga gat cag tgg gat aag cag cat gac atg ggt cac atg atg agg     1847
Ile Gly Asp Gln Trp Asp Lys Gln His Asp Met Gly His Met Met Arg
480                 485                 490                 495
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tgc acg tgt gtt ggg aat ggt cgt ggg gaa tgg aca tgc att gcc tac     1895
Cys Thr Cys Val Gly Asn Gly Arg Gly Glu Trp Thr Cys Ile Ala Tyr
496                 501                 506                 511

tcg caa ctt cga gat cag tgc att gtt gat gac atc act tac aat gtg     1943
Ser Gln Leu Arg Asp Gln Cys Ile Val Asp Asp Ile Thr Tyr Asn Val
512                 517                 522                 527

aac gac aca ttc cac aag cgt cat gaa gag ggg cac atg ctg aac tgt     1991
Asn Asp Thr Phe His Lys Arg His Glu Glu Gly His Met Leu Asn Cys
528                 533                 538                 543

aca tgc ttc ggt cag ggt cgg ggc agg tgg aag tgt gat ccc gtc gac     2039
Thr Cys Phe Gly Gln Gly Arg Gly Arg Trp Lys Cys Asp Pro Val Asp
544                 549                 554                 559

caa tgc cag gat tca gag act ggg acg ttt tat caa att gga gat tca     2087
Gln Cys Gln Asp Ser Glu Thr Gly Thr Phe Tyr Gln Ile Gly Asp Ser
560                 565                 570                 575

tgg gag aag tat gtg cat ggt gtc aga tac cag tgc tac tgc tat ggc     2135
Trp Glu Lys Tyr Val His Gly Val Arg Tyr Gln Cys Tyr Cys Tyr Gly
576                 581                 586                 591

cgt ggc att ggg gag tgg cat tgc caa cct tta cag acc tat cca agc     2183
Arg Gly Ile Gly Glu Trp His Cys Gln Pro Leu Gln Thr Tyr Pro Ser
592                 597                 602                 607

tca agt ggt cct gtc gaa gta ttt atc act gag act ccg agt cag ccc     2231
Ser Ser Gly Pro Val Glu Val Phe Ile Thr Glu Thr Pro Ser Gln Pro
608                 613                 618                 623

aac tcc cac ccc atc cag tgg aat gca cca cag cca tct cac att tcc     2279
Asn Ser His Pro Ile Gln Trp Asn Ala Pro Gln Pro Ser His Ile Ser
624                 629                 634                 639

aag tac att ctc agg tgg aga cct aaa aat tct gta ggc cgt tgg aag     2327
Lys Tyr Ile Leu Arg Trp Arg Pro Lys Asn Ser Val Gly Arg Trp Lys
640                 645                 650                 655

gaa gct acc ata cca ggc cac tta aac tcc tac acc atc aaa ggc ctg     2375
Glu Ala Thr Ile Pro Gly His Leu Asn Ser Tyr Thr Ile Lys Gly Leu
656                 661                 666                 671

aag cct ggt gtg gta tac gag ggc cag ctc atc agc atc cag cag tac     2423
Lys Pro Gly Val Val Tyr Glu Gly Gln Leu Ile Ser Ile Gln Gln Tyr
672                 677                 682                 687

ggc cac caa gaa gtg act cgc ttt gac ttc acc acc acc agc acc agc     2471
Gly His Gln Glu Val Thr Arg Phe Asp Phe Thr Thr Thr Ser Thr Ser
688                 693                 698                 703

aca cct gtg acc agc aac acc gtg aca gga gag acg act ccc ttt tct     2519
Thr Pro Val Thr Ser Asn Thr Val Thr Gly Glu Thr Thr Pro Phe Ser
704                 709                 714                 719

cct ctt gtg gcc act tct gaa tct gtg acc gaa atc aca gcc agt agc     2567
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Pro Leu Val Ala Thr Ser Glu Ser Val Thr Glu Ile Thr Ala Ser Ser
720                 725                 730                 735

ttt gtg gtc tcc tgg gtc tca gct tcc gac acc gtg tcg gga ttc cgg     2615
Phe Val Val Ser Trp Val Ser Ala Ser Asp Thr Val Ser Gly Phe Arg
736                 741                 746                 751

gtg gaa tat gag ctg agt gag gag gga gat gag cca cag tac ctg gat     2663
Val Glu Tyr Glu Leu Ser Glu Glu Gly Asp Glu Pro Gln Tyr Leu Asp
752                 757                 762                 767

ctt cca agc aca gcc act tct gtg aac atc cct gac ctg ctt cct ggc     2711
Leu Pro Ser Thr Ala Thr Ser Val Asn Ile Pro Asp Leu Leu Pro Gly
768                 773                 778                 783

cga aaa tac att gta aat gtc tat cag ata tct gag gat ggg gag cag     2759
Arg Lys Tyr Ile Val Asn Val Tyr Gln Ile Ser Glu Asp Gly Glu Gln
784                 789                 794                 799

agt ttg atc ctg tct act tca caa aca aca gcg cct gat gcc cct cct     2807
Ser Leu Ile Leu Ser Thr Ser Gln Thr Thr Ala Pro Asp Ala Pro Pro
800                 805                 810                 815

gac ccg act gtg gac caa gtt gat gac acc tca att gtt gtt cgc tgg     2855
Asp Pro Thr Val Asp Gln Val Asp Asp Thr Ser Ile Val Val Arg Trp
816                 821                 826                 831

agc aga ccc cag gct ccc atc aca ggg tac aga ata gtc tat tcg cca     2903
Ser Arg Pro Gln Ala Pro Ile Thr Gly Tyr Arg Ile Val Tyr Ser Pro
832                 837                 842                 847

tca gta gaa ggt agc agc aca gaa ctc aac ctt cct gaa act gca aac     2951
Ser Val Glu Gly Ser Ser Thr Glu Leu Asn Leu Pro Glu Thr Ala Asn
848                 853                 858                 863

tcc gtc acc ctc agt gac ttg caa cct ggt gtt cag tat aac atc act     2999
Ser Val Thr Leu Ser Asp Leu Gln Pro Gly Val Gln Tyr Asn Ile Thr
864                 869                 874                 879

atc tat gct gtg gaa gaa aat caa gaa agt aca cct gtt gtc att caa     3047
Ile Tyr Ala Val Glu Glu Asn Gln Glu Ser Thr Pro Val Val Ile Gln
880                 885                 890                 895

caa gaa acc act ggc acc cca cgc tca gat aca gtg ccc tct ccc agg     3095
Gln Glu Thr Thr Gly Thr Pro Arg Ser Asp Thr Val Pro Ser Pro Arg
896                 901                 906                 911

gac ctg cag ttt gtg gaa gtg aca gac gtg aag gtc acc atc atg tgg     3143
Asp Leu Gln Phe Val Glu Val Thr Asp Val Lys Val Thr Ile Met Trp
912                 917                 922                 927

aca ccg cct gag agt gca gtg acc ggc tac cgt gtg gat gtg atc ccc     3191
Thr Pro Pro Glu Ser Ala Val Thr Gly Tyr Arg Val Asp Val Ile Pro
928                 933                 938                 943

gtc aac ctg cct ggc gag cac ggg cag agg ctg ccc atc agc agg aac     3239
Val Asn Leu Pro Gly Glu His Gly Gln Arg Leu Pro Ile Ser Arg Asn
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944                 949                 954                 959

acc ttt gca gaa gtc acc ggg ctg tcc cct ggg gtc acc tat tac ttc     3287
Thr Phe Ala Glu Val Thr Gly Leu Ser Pro Gly Val Thr Tyr Tyr Phe
960                 965                 970                 975

aaa gtc ttt gca gtg agc cat ggg agg gag agc aag cct ctg act gct     3335
Lys Val Phe Ala Val Ser His Gly Arg Glu Ser Lys Pro Leu Thr Ala
976                 981                 986                 991

caa cag aca acc aaa ctg gat gct ccc act aac ctc cag ttt gtc aat     3383
Gln Gln Thr Thr Lys Leu Asp Ala Pro Thr Asn Leu Gln Phe Val Asn
992                 997                1002                1007

gaa act gat tct act gtc ctg gtg aga tgg act cca cct cgg gcc cag     3431
Glu Thr Asp Ser Thr Val Leu Val Arg Trp Thr Pro Pro Arg Ala Gln
1008                1013                1018                1023

ata aca gga tac cga ctg acc gtg ggc ctt acc cga aga gga cag ccc     3479
Ile Thr Gly Tyr Arg Leu Thr Val Gly Leu Thr Arg Arg Gly Gln Pro
1024                1029                1034                1039

agg cag tac aat gtg ggt ccc tct gtc tcc aag tac cca ctg agg aat     3527
Arg Gln Tyr Asn Val Gly Pro Ser Val Ser Lys Tyr Pro Leu Arg Asn
1040                1045                1050                1055

ctg cag cct gca tct gag tac acc gta tcc ctc gtg gcc ata aag ggc     3575
Leu Gln Pro Ala Ser Glu Tyr Thr Val Ser Leu Val Ala Ile Lys Gly
1056                1061                1066                1071

aac caa gag agc ccc aaa gcc act gga gtc ttt acc aca ctg cag cct     3623
Asn Gln Glu Ser Pro Lys Ala Thr Gly Val Phe Thr Thr Leu Gln Pro
1072                1077                1082                1087

ggg agc tct att cca cct tac aac acc gag gtg act gag acc acc att     3671
Gly Ser Ser Ile Pro Pro Tyr Asn Thr Glu Val Thr Glu Thr Thr Ile
1088                1093                1098                1103

gtg atc aca tgg acg cct gct cca aga att ggt ttt aag ctg ggt gta     3719
Val Ile Thr Trp Thr Pro Ala Pro Arg Ile Gly Phe Lys Leu Gly Val
1104                1109                1114                1119

cga cca agc cag gga gga gag gca cca cga gaa gtg act tca gac tca     3767
Arg Pro Ser Gln Gly Gly Glu Ala Pro Arg Glu Val Thr Ser Asp Ser
1120                1125                1130                1135

gga agc atc gtt gtg tcc ggc ttg act cca gga gta gaa tac gtc tac     3815
Gly Ser Ile Val Val Ser Gly Leu Thr Pro Gly Val Glu Tyr Val Tyr
1136                1141                1146                1151

acc atc caa gtc ctg aga gat gga cag gaa aga gat gcg cca att gta     3863
Thr Ile Gln Val Leu Arg Asp Gly Gln Glu Arg Asp Ala Pro Ile Val
1152                1157                1162                1167

aac aaa gtg gtg aca cca ttg tct cca cca aca aac ttg cat ctg gag     3911
Asn Lys Val Val Thr Pro Leu Ser Pro Pro Thr Asn Leu His Leu Glu
1168                1173                1178                1183
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 gca aac cct gac act gga gtg ctc aca gtc tcc tgg gag agg agc acc     3959
 Ala Asn Pro Asp Thr Gly Val Leu Thr Val Ser Trp Glu Arg Ser Thr
1184                1189                1194                1199

 acc cca gac att act ggt tat aga att acc aca acc cct aca aac ggc     4007
 Thr Pro Asp Ile Thr Gly Tyr Arg Ile Thr Thr Thr Pro Thr Asn Gly
1200                1205                1210                1215

 cag cag gga aat tct ttg gaa gaa gtg gtc cat gct gat cag agc tcc     4055
 Gln Gln Gly Asn Ser Leu Glu Glu Val Val His Ala Asp Gln Ser Ser
1216                1221                1226                1231

 tgc act ttt gat aac ctg agt ccc ggc ctg gag tac aat gtc agt gtt     4103
 Cys Thr Phe Asp Asn Leu Ser Pro Gly Leu Glu Tyr Asn Val Ser Val
1232                1237                1242                1247

 tac act gtc aag gat gac aag gaa agt gtc cct atc tct gat acc atc     4151
 Tyr Thr Val Lys Asp Asp Lys Glu Ser Val Pro Ile Ser Asp Thr Ile
1248                1253                1258                1263

 atc cca gct gtt cct cct ccc act gac ctg cga ttc acc aac att ggt     4199
 Ile Pro Ala Val Pro Pro Pro Thr Asp Leu Arg Phe Thr Asn Ile Gly
1264                1269                1274                1279

 cca gac acc atg cgt gtc acc tgg gct cca ccc cca tcc att gat tta     4247
 Pro Asp Thr Met Arg Val Thr Trp Ala Pro Pro Pro Ser Ile Asp Leu
1280                1285                1290                1295

 acc aac ttc ctg gtg cgt tac tca cct gtg aaa aat gag gaa gat gtt     4295
 Thr Asn Phe Leu Val Arg Tyr Ser Pro Val Lys Asn Glu Glu Asp Val
1296                1301                1306                1311

 gca gag ttg tca att tct cct tca gac aat gca gtg gtc tta aca aat     4343
 Ala Glu Leu Ser Ile Ser Pro Ser Asp Asn Ala Val Val Leu Thr Asn
1312                1317                1322                1327

 ctc ctg cct ggt aca gaa tat gta gtg agt gtc tcc agt gtc tac gaa     4391
 Leu Leu Pro Gly Thr Glu Tyr Val Val Ser Val Ser Ser Val Tyr Glu
1328                1333                1338                1343

 caa cat gag agc aca cct ctt aga gga aga cag aaa aca ggt ctt gat     4439
 Gln His Glu Ser Thr Pro Leu Arg Gly Arg Gln Lys Thr Gly Leu Asp
1344                1349                1354                1359

 tcc cca act ggc att gac ttt tct gat att act gcc aac tct ttt act     4487
 Ser Pro Thr Gly Ile Asp Phe Ser Asp Ile Thr Ala Asn Ser Phe Thr
1360                1365                1370                1375

 gtg cac tgg att gct cct cga gcc acc atc act ggc tac agg atc cgc     4535
 Val His Trp Ile Ala Pro Arg Ala Thr Ile Thr Gly Tyr Arg Ile Arg
1376                1381                1386                1391

 cat cat ccc gag cac ttc agt ggg aga cct cga gaa gat cgg gtg ccc     4583
 His His Pro Glu His Phe Ser Gly Arg Pro Arg Glu Asp Arg Val Pro
1392                1397                1402                1407
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 cac tct cgg aat tcc atc acc ctc acc aac ctc act cca ggc aca gag     4631
 His Ser Arg Asn Ser Ile Thr Leu Thr Asn Leu Thr Pro Gly Thr Glu
1408                1413                1418                1423

 tat gtg gtc agc atc gtt gct ctt aat ggc aga gag gaa agt ccc tta     4679
 Tyr Val Val Ser Ile Val Ala Leu Asn Gly Arg Glu Glu Ser Pro Leu
1424                1429                1434                1439

 ttg att ggc caa caa tca aca gtt tct gat gtt ccg agg gac ctg gaa     4727
 Leu Ile Gly Gln Gln Ser Thr Val Ser Asp Val Pro Arg Asp Leu Glu
1440                1445                1450                1455

 gtt gtt gct gcg acc ccc acc agc cta ctg atc agc tgg gat gct cct     4775
 Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro
1456                1461                1466                1471

 gct gtc aca gtg aga tat tac agg atc act tac gga gaa aca gga gga     4823
 Ala Val Thr Val Arg Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly
1472                1477                1482                1487

 aat agc cct gtc cag gag ttc act gtg cct ggg agc aag tct aca gct     4871
 Asn Ser Pro Val Gln Glu Phe Thr Val Pro Gly Ser Lys Ser Thr Ala
1488                1493                1498                1503

 acc atc agc ggc ctt aaa cct gga gtt gat tat acc atc act gtg tat     4919
 Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr
1504                1509                1514                1519

 gct gtc act ggc cgt gga gac agc ccc gca agc agc aag cca att tcc     4967
 Ala Val Thr Gly Arg Gly Asp Ser Pro Ala Ser Ser Lys Pro Ile Ser
1520                1525                1530                1535

 att aat tac cga aca gaa att gac aaa cca tcc cag atg caa gtg acc     5015
 Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln Met Gln Val Thr
1536                1541                1546                1551

 gat gtt cag gac aac agc att agt gtc aag tgg ctg cct tca agt tcc     5063
 Asp Val Gln Asp Asn Ser Ile Ser Val Lys Trp Leu Pro Ser Ser Ser
1552                1557                1562                1567

 cct gtt act ggt tac aga gta acc acc act ccc aaa aat gga cca gga     5111
 Pro Val Thr Gly Tyr Arg Val Thr Thr Thr Pro Lys Asn Gly Pro Gly
1568                1573                1578                1583

 cca aca aaa act aaa act gca ggt cca gat caa aca gaa atg act att     5159
 Pro Thr Lys Thr Lys Thr Ala Gly Pro Asp Gln Thr Glu Met Thr Ile
1584                1589                1594                1599

 gaa ggc ttg cag ccc aca gtg gag tat gtg gtt agt gtc tat gct cag     5207
 Glu Gly Leu Gln Pro Thr Val Glu Tyr Val Val Ser Val Tyr Ala Gln
1600                1605                1610                1615

 aat cca agc gga gag agt cag cct ctg gtt cag act gca gta acc aac     5255
 Asn Pro Ser Gly Glu Ser Gln Pro Leu Val Gln Thr Ala Val Thr Asn
1616                1621                1626                1631

 att gat cgc cct aaa gga ctg gca ttc act gat gtg gat gtc gat tcc     5303
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 Ile Asp Arg Pro Lys Gly Leu Ala Phe Thr Asp Val Asp Val Asp Ser
1632                1637                1642                1647

 atc aaa att gct tgg gaa agc cca cag ggg caa gtt tcc agg tac agg     5351
 Ile Lys Ile Ala Trp Glu Ser Pro Gln Gly Gln Val Ser Arg Tyr Arg
1648                1653                1658                1663

 gtg acc tac tcg agc cct gag gat gga atc cat gag cta ttc cct gca     5399
 Val Thr Tyr Ser Ser Pro Glu Asp Gly Ile His Glu Leu Phe Pro Ala
1664                1669                1674                1679

 cct gat ggt gaa gaa gac act gca gag ctg caa ggc ctc aga ccg ggt     5447
 Pro Asp Gly Glu Glu Asp Thr Ala Glu Leu Gln Gly Leu Arg Pro Gly
1680                1685                1690                1695

 tct gag tac aca gtc agt gtg gtt gcc ttg cac gat gat atg gag agc     5495
 Ser Glu Tyr Thr Val Ser Val Val Ala Leu His Asp Asp Met Glu Ser
1696                1701                1706                1711

 cag ccc ctg att gga acc cag tcc aca gct att cct gca cca act gac     5543
 Gln Pro Leu Ile Gly Thr Gln Ser Thr Ala Ile Pro Ala Pro Thr Asp
1712                1717                1722                1727

 ctg aag ttc act cag gtc aca ccc aca agc ctg agc gcc cag tgg aca     5591
 Leu Lys Phe Thr Gln Val Thr Pro Thr Ser Leu Ser Ala Gln Trp Thr
1728                1733                1738                1743

 cca ccc aat gtt cag ctc act gga tat cga gtg cgg gtg acc ccc aag     5639
 Pro Pro Asn Val Gln Leu Thr Gly Tyr Arg Val Arg Val Thr Pro Lys
1744                1749                1754                1759

 gag aag acc gga cca atg aaa gaa atc aac ctt gct cct gac agc tca     5687
 Glu Lys Thr Gly Pro Met Lys Glu Ile Asn Leu Ala Pro Asp Ser Ser
1760                1765                1770                1775

 tcc gtg gtt gta tca gga ctt atg gtg gcc acc aaa tat gaa gtg agt     5735
 Ser Val Val Val Ser Gly Leu Met Val Ala Thr Lys Tyr Glu Val Ser
1776                1781                1786                1791

 gtc tat gct ctt aag gac act ttg aca agc aga cca gct cag gga gtt     5783
 Val Tyr Ala Leu Lys Asp Thr Leu Thr Ser Arg Pro Ala Gln Gly Val
1792                1797                1802                1807

 gtc acc act ctg gag aat gtc agc cca cca aga agg gct cgt gtg aca     5831
 Val Thr Thr Leu Glu Asn Val Ser Pro Pro Arg Arg Ala Arg Val Thr
1808                1813                1818                1823

 gat gct act gag acc acc atc acc att agc tgg aga acc aag act gag     5879
 Asp Ala Thr Glu Thr Thr Ile Thr Ile Ser Trp Arg Thr Lys Thr Glu
1824                1829                1834                1839

 acg atc act ggc ttc caa gtt gat gcc gtt cca gcc aat ggc cag act     5927
 Thr Ile Thr Gly Phe Gln Val Asp Ala Val Pro Ala Asn Gly Gln Thr
1840                1845                1850                1855

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 Pro Ile Gln Arg Thr Ile Lys Pro Asp Val Arg Ser Tyr Thr Ile Thr
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1856                1861                1866                1871

 ggt tta caa cca ggc act gac tac aag atc tac ctg tac acc ttg aat     6023
 Gly Leu Gln Pro Gly Thr Asp Tyr Lys Ile Tyr Leu Tyr Thr Leu Asn
1872                1877                1882                1887

 gac aat gct cgg agc tcc cct gtg gtc atc gac gcc tcc act gcc att     6071
 Asp Asn Ala Arg Ser Ser Pro Val Val Ile Asp Ala Ser Thr Ala Ile
1888                1893                1898                1903

 gat gca cca tcc aac ctg cgt ttc ctg gcc acc aca ccc aat tcc ttg     6119
 Asp Ala Pro Ser Asn Leu Arg Phe Leu Ala Thr Thr Pro Asn Ser Leu
1904                1909                1914                1919

 ctg gta tca tgg cag ccg cca cgt gcc agg att acc ggc tac atc atc     6167
 Leu Val Ser Trp Gln Pro Pro Arg Ala Arg Ile Thr Gly Tyr Ile Ile
1920                1925                1930                1935

 aag tat gag aag cct ggg tct cct ccc aga gaa gtg gtc cct cgg ccc     6215
 Lys Tyr Glu Lys Pro Gly Ser Pro Pro Arg Glu Val Val Pro Arg Pro
1936                1941                1946                1951

 cgc cct ggt gtc aca gag gct act att cct ggc ctg gaa ccg gga acc     6263
 Arg Pro Gly Val Thr Glu Ala Thr Ile Pro Gly Leu Glu Pro Gly Thr
1952                1957                1962                1967

 gaa tat aca att tat gtc att gcc ctg aag aat aat cag aag agc gag     6311
 Glu Tyr Thr Ile Tyr Val Ile Ala Leu Lys Asn Asn Gln Lys Ser Glu
1968                1973                1978                1983

 ccc ctg att gga agg aaa aag aca gac gag ctt ccc caa ctg gta acc     6359
 Pro Leu Ile Gly Arg Lys Lys Thr Asp Glu Leu Pro Gln Leu Val Thr
1984                1989                1994                1999

 ctt cca cac ccc aat ctt cat gga cca gag atc ttg gat gtt cct tcc     6407
 Leu Pro His Pro Asn Leu His Gly Pro Glu Ile Leu Asp Val Pro Ser
2000                2005                2010                2015

 aca gtt caa aag acc cct ttc gtc acc cac cct ggg tat gac act gga     6455
 Thr Val Gln Lys Thr Pro Phe Val Thr His Pro Gly Tyr Asp Thr Gly
2016                2021                2026                2031

 aat ggt att cag ctt cct ggc act tct ggt cag caa ccc agt gtt ggg     6503
 Asn Gly Ile Gln Leu Pro Gly Thr Ser Gly Gln Gln Pro Ser Val Gly
2032                2037                2042                2047

 caa caa atg atc ttt gag gaa cat ggt ttt agg cgg acc aca ccg ccc     6551
 Gln Gln Met Ile Phe Glu Glu His Gly Phe Arg Arg Thr Thr Pro Pro
2048                2053                2058                2063

 aca acg gcc acc ccc ata agg cat agg cca aga cca tac ccg ccg aat     6599
 Thr Thr Ala Thr Pro Ile Arg His Arg Pro Arg Pro Tyr Pro Pro Asn
2064                2069                2074                2079

 gta gga caa gaa gct ctc tct cag aca acc atc tca tgg gcc cca ttc     6647
 Val Gly Gln Glu Ala Leu Ser Gln Thr Thr Ile Ser Trp Ala Pro Phe
2080                2085                2090                2095
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 cag gac act tct gag tac atc att tca tgt cat cct gtt ggc act gat     6695
 Gln Asp Thr Ser Glu Tyr Ile Ile Ser Cys His Pro Val Gly Thr Asp
2096                2101                2106                2111

 gaa gaa ccc tta cag ttc agg gtt cct gga act tct acc agt gcc act     6743
 Glu Glu Pro Leu Gln Phe Arg Val Pro Gly Thr Ser Thr Ser Ala Thr
2112                2117                2122                2127

 ctg aca ggc ctc acc aga ggt gcc acc tac aac atc ata gtg gag gca     6791
 Leu Thr Gly Leu Thr Arg Gly Ala Thr Tyr Asn Ile Ile Val Glu Ala
2128                2133                2138                2143

 ctg aaa gac cag cag agg cat aag gtt cgg gaa gag gtt gtt acc gtg     6839
 Leu Lys Asp Gln Gln Arg His Lys Val Arg Glu Glu Val Val Thr Val
2144                2149                2154                2159

 ggc aac tct gtc aac gaa ggc ttg aac caa cct acg gat gac tcg tgc     6887
 Gly Asn Ser Val Asn Glu Gly Leu Asn Gln Pro Thr Asp Asp Ser Cys
2160                2165                2170                2175

 ttt gac ccc tac aca gtt tcc cat tat gcc gtt gga gat gag tgg gaa     6935
 Phe Asp Pro Tyr Thr Val Ser His Tyr Ala Val Gly Asp Glu Trp Glu
2176                2181                2186                2191

 cga atg tct gaa tca ggc ttt aaa ctg ttg tgc cag tgc tta ggc ttt     6983
 Arg Met Ser Glu Ser Gly Phe Lys Leu Leu Cys Gln Cys Leu Gly Phe
2192                2197                2202                2207

 gga agt ggt cat ttc aga tgt gat tca tct aga tgg tgc cat gac aat     7031
 Gly Ser Gly His Phe Arg Cys Asp Ser Ser Arg Trp Cys His Asp Asn
2208                2213                2218                2223

 ggt gtg aac tac aag att gga gag aag tgg gac cgt cag gga gaa aat     7079
 Gly Val Asn Tyr Lys Ile Gly Glu Lys Trp Asp Arg Gln Gly Glu Asn
2224                2229                2234                2239

 ggc cag atg atg agc tgc aca tgt ctt ggg aac gga aaa gga gaa ttc     7127
 Gly Gln Met Met Ser Cys Thr Cys Leu Gly Asn Gly Lys Gly Glu Phe
2240                2245                2250                2255

 aag tgt gac cct cat gag gca acg tgt tac gat gat ggg aag aca tac     7175
 Lys Cys Asp Pro His Glu Ala Thr Cys Tyr Asp Asp Gly Lys Thr Tyr
2256                2261                2266                2271

 cac gta gga gaa cag tgg cag aag gaa tat ctc ggt gcc att tgc tcc     7223
 His Val Gly Glu Gln Trp Gln Lys Glu Tyr Leu Gly Ala Ile Cys Ser
2272                2277                2282                2287

 tgc aca tgc ttt gga ggc cag cgg ggc tgg cgc tgt gac aac tgc cgc     7271
 Cys Thr Cys Phe Gly Gly Gln Arg Gly Trp Arg Cys Asp Asn Cys Arg
2288                2293                2298                2303

 aga cct ggg ggt gaa ccc agt ccc gaa ggc act act ggc cag tcc tac     7319
 Arg Pro Gly Gly Glu Pro Ser Pro Glu Gly Thr Thr Gly Gln Ser Tyr
2304                2309                2314                2319
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 aac cag tat tct cag aga tac cat cag aga aca aac act aat gtt aat     7367
 Asn Gln Tyr Ser Gln Arg Tyr His Gln Arg Thr Asn Thr Asn Val Asn
2320                2325                2330                2335

 tgc cca att gag tgc ttc atg cct tta gat gta cag gct gac aga gaa     7415
 Cys Pro Ile Glu Cys Phe Met Pro Leu Asp Val Gln Ala Asp Arg Glu
2336                2341                2346                2351

 gat tcc cga gag taa atcatctttc caatccagag gaacaagcat gtctctctgc     7470
 Asp Ser Arg Glu  *
2352

 caagatccat ctaaactgga gtgatgttag cagacccagc ttagagttct tctttctttc   7530

 ttaagccctt tgctctggag gaagttctcc agcttcagct caactcacag cttctccaag   7590

 catcaccctg ggagtttcct gagggttttc tcataaatga gggctgcaca ttgcctgttc   7650

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 gggatcaata ggaaagcata tgcagccaac caagatgcaa atgttttgaa atgatatgac   7770

 caaaatttta agtaggaaag tcacccaaac acttctgctt tcacttaagt gtctggcccg   7830

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attaaaaaat atttaatcat tcatgtgttg agactcattc ttgagtt  atg gat gac     416
                                                     Met Asp Asp
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aag gct tct gtt gga aaa atc agt gtc tct tca gac tca gta tct act      464
Lys Ala Ser Val Gly Lys Ile Ser Val Ser Ser Asp Ser Val Ser Thr
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ctt aat agt gaa gat ttt gtc ttg gtt tcc agg caa gga gat gag aca      512
Leu Asn Ser Glu Asp Phe Val Leu Val Ser Arg Gln Gly Asp Glu Thr
 20                  25                  30                  35

cca tct aca aat aat gga agt gat gat gag aaa aca gga ctc aag att      560
Pro Ser Thr Asn Asn Gly Ser Asp Asp Glu Lys Thr Gly Leu Lys Ile
 36                  41                  46                  51

gta ggg aat gga agt gaa cag cag ctg caa aaa gag cta gca gat gta      608
Val Gly Asn Gly Ser Glu Gln Gln Leu Gln Lys Glu Leu Ala Asp Val
 52                  57                  62                  67

ctg atg gat cct cca atg gac gac cag cca ggg gaa aag gag ctt gtg      656
Leu Met Asp Pro Pro Met Asp Asp Gln Pro Gly Glu Lys Glu Leu Val
 68                  73                  78                  83

aaa agg tca caa ctg gat ggt gaa gga gat ggg cct ctt tct aat cag      704
Lys Arg Ser Gln Leu Asp Gly Glu Gly Asp Gly Pro Leu Ser Asn Gln
 84                  89                  94                  99

ctc tcc gct tca tcc acc att aac cct gtg cca tta gta ggg ctc caa      752
Leu Ser Ala Ser Ser Thr Ile Asn Pro Val Pro Leu Val Gly Leu Gln
100                 105                 110                 115

aaa cca gag atg agc cta cca gtg aaa cct gga caa gga gat tct gaa      800
Lys Pro Glu Met Ser Leu Pro Val Lys Pro Gly Gln Gly Asp Ser Glu
116                 121                 126                 131

gct tca agt cct ttc aca cca gtg gcc gat gag gac agc gta gtt ttc      848
Ala Ser Ser Pro Phe Thr Pro Val Ala Asp Glu Asp Ser Val Val Phe
132                 137                 142                 147

agt aaa ctg act tac tta ggc tgt gcc tcg gta aat gct ccc agg agt      896
Ser Lys Leu Thr Tyr Leu Gly Cys Ala Ser Val Asn Ala Pro Arg Ser
148                 153                 158                 163

gaa gtg gaa gcc tta agg atg atg tcc atc tta aga agc cag tgt cag      944
Glu Val Glu Ala Leu Arg Met Met Ser Ile Leu Arg Ser Gln Cys Gln
164                 169                 174                 179

att tca cta gat gtt acc ctt tca gtg ccg aat gtg tct gaa gga att      992
Ile Ser Leu Asp Val Thr Leu Ser Val Pro Asn Val Ser Glu Gly Ile
180                 185                 190                 195

gtg aga ctc tta gat cct cag aca aac act gaa ata gca aac tac cct     1040
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Val Arg Leu Leu Asp Pro Gln Thr Asn Thr Glu Ile Ala Asn Tyr Pro
196                 201                 206                 211

atc tac aaa atc ctc ttc tgt gtc aga ggg cat gat gga act cct gag     1088
Ile Tyr Lys Ile Leu Phe Cys Val Arg Gly His Asp Gly Thr Pro Glu
212                 217                 222                 227

agt gac tgt ttt gct ttc act gaa agt cat tac aat gca gag ctc ttc     1136
Ser Asp Cys Phe Ala Phe Thr Glu Ser His Tyr Asn Ala Glu Leu Phe
228                 233                 238                 243

aga ata cac gtc ttc cgg tgt gaa ata caa gaa gct gta agc cgg ata     1184
Arg Ile His Val Phe Arg Cys Glu Ile Gln Glu Ala Val Ser Arg Ile
244                 249                 254                 259

ctt tac agt ttt gcc act gcc ttc cgc cgt tct gcc aag cag acc cca     1232
Leu Tyr Ser Phe Ala Thr Ala Phe Arg Arg Ser Ala Lys Gln Thr Pro
260                 265                 270                 275

ctt tca gcc act gct gca ccc cag act cct gac agt gac atc ttt acc     1280
Leu Ser Ala Thr Ala Ala Pro Gln Thr Pro Asp Ser Asp Ile Phe Thr
276                 281                 286                 291

ttc tct gtg tct tta gaa ata aaa gaa gat gat ggt aaa ggt tat ttt     1328
Phe Ser Val Ser Leu Glu Ile Lys Glu Asp Asp Gly Lys Gly Tyr Phe
292                 297                 302                 307

agt gca gtt ccc aaa gat aag gac aga cag tgc ttt aaa cta cgc caa     1376
Ser Ala Val Pro Lys Asp Lys Asp Arg Gln Cys Phe Lys Leu Arg Gln
308                 313                 318                 323

gga att gat aag aag att gtc atc tat gtg cag caa aca act aat aaa     1424
Gly Ile Asp Lys Lys Ile Val Ile Tyr Val Gln Gln Thr Thr Asn Lys
324                 329                 334                 339

gaa ctt gcc att gaa agg tgt ttt ggt ctt ctc ctt agt cca gga aaa     1472
Glu Leu Ala Ile Glu Arg Cys Phe Gly Leu Leu Leu Ser Pro Gly Lys
340                 345                 350                 355

gat gta cga aat agt gac atg cac tta tta gat ttg gaa tct atg ggc     1520
Asp Val Arg Asn Ser Asp Met His Leu Leu Asp Leu Glu Ser Met Gly
356                 361                 366                 371

aaa agt tca gat gga aag tcg tat gtt att acg ggg agc tgg aat cca     1568
Lys Ser Ser Asp Gly Lys Ser Tyr Val Ile Thr Gly Ser Trp Asn Pro
372                 377                 382                 387

aaa tcc cca cat ttt caa gtt gta aat gaa gaa act cct aaa gat aaa     1616
Lys Ser Pro His Phe Gln Val Val Asn Glu Glu Thr Pro Lys Asp Lys
388                 393                 398                 403

gtc ctg ttt atg acc aca gct gta gat ttg gta ata aca gaa gta cag     1664
Val Leu Phe Met Thr Thr Ala Val Asp Leu Val Ile Thr Glu Val Gln
404                 409                 414                 419

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Glu Pro Val Arg Phe Leu Leu Glu Thr Lys Val Arg Val Cys Ser Pro
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aat gaa aga tta ttc tgg ccc ttc agc aaa cgt agt act act gaa aat     1760
Asn Glu Arg Leu Phe Trp Pro Phe Ser Lys Arg Ser Thr Thr Glu Asn
436                 441                 446                 451

ttc ttt ttg aaa cta aaa cag ata aag caa agg gag aga aag aat aat     1808
Phe Phe Leu Lys Leu Lys Gln Ile Lys Gln Arg Glu Arg Lys Asn Asn
452                 457                 462                 467

act gac act tta tat gaa gtt gta tgc ttg gaa agt gaa tca gaa aga     1856
Thr Asp Thr Leu Tyr Glu Val Val Cys Leu Glu Ser Glu Ser Glu Arg
468                 473                 478                 483

gag agg agg aaa act aca gcc agt cct tca gtt cgc ctg cca cag tct     1904
Glu Arg Arg Lys Thr Thr Ala Ser Pro Ser Val Arg Leu Pro Gln Ser
484                 489                 494                 499

gga tcg caa agt tca gtg ata cct tct cct cca gaa gat gat gaa gag     1952
Gly Ser Gln Ser Ser Val Ile Pro Ser Pro Pro Glu Asp Asp Glu Glu
500                 505                 510                 515

gaa gat aat gat gaa cct ctc ctg agt gga tct ggt gat gta tcc aaa     2000
Glu Asp Asn Asp Glu Pro Leu Leu Ser Gly Ser Gly Asp Val Ser Lys
516                 521                 526                 531

gaa tgt gca gaa aaa att ctt gaa aca tgg gga gaa ctg ttg tca aaa     2048
Glu Cys Ala Glu Lys Ile Leu Glu Thr Trp Gly Glu Leu Leu Ser Lys
532                 537                 542                 547

tgg cat ctc aac ttg aat gtg aga ccg aag cag ttg tca tcc tta gta     2096
Trp His Leu Asn Leu Asn Val Arg Pro Lys Gln Leu Ser Ser Leu Val
548                 553                 558                 563

aga aac ggt gtt cct gaa gct ctt cga gga gaa gtc tgg cag ctg cta     2144
Arg Asn Gly Val Pro Glu Ala Leu Arg Gly Glu Val Trp Gln Leu Leu
564                 569                 574                 579

gca ggc tgt cat aac aat gac cac ctg gta gag aaa tac cgc att ctt     2192
Ala Gly Cys His Asn Asn Asp His Leu Val Glu Lys Tyr Arg Ile Leu
580                 585                 590                 595

atc aca aag gag tct ccc cag gac agt gct atc acc cgg gat att aac     2240
Ile Thr Lys Glu Ser Pro Gln Asp Ser Ala Ile Thr Arg Asp Ile Asn
596                 601                 606                 611

cga aca ttc cca gcc cat gac tac ttt aag gac aca gga gga gat gga     2288
Arg Thr Phe Pro Ala His Asp Tyr Phe Lys Asp Thr Gly Gly Asp Gly
612                 617                 622                 627

caa gat tcc tta tat aaa ata tgc aag gct tat tct gtg tat gat gaa     2336
Gln Asp Ser Leu Tyr Lys Ile Cys Lys Ala Tyr Ser Val Tyr Asp Glu
628                 633                 638                 643

gag att ggt tat tgc cag ggc cag tca ttt ctt gct gct gtg ctc ctt     2384
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644                 649                 654                 659
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ctc cat atg cct gaa gaa cag gca ttc agt gtt ctg gtc aag atc atg     2432
Leu His Met Pro Glu Glu Gln Ala Phe Ser Val Leu Val Lys Ile Met
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ttt gac tat ggg ctc agg gaa ctt ttc aag caa aac ttc gaa gat ttg     2480
Phe Asp Tyr Gly Leu Arg Glu Leu Phe Lys Gln Asn Phe Glu Asp Leu
676                 681                 686                 691

cat tgc aaa ttt tac cag ttg gag cgc ctc atg cag gaa tac att cct     2528
His Cys Lys Phe Tyr Gln Leu Glu Arg Leu Met Gln Glu Tyr Ile Pro
692                 697                 702                 707

gac ctg tac aac cac ttc ctg gat ata agc ctt gaa gca cac atg tat     2576
Asp Leu Tyr Asn His Phe Leu Asp Ile Ser Leu Glu Ala His Met Tyr
708                 713                 718                 723

gcc tcc cag tgg ttt ctt act ctt ttc act gca aaa ttc cct ctc tac     2624
Ala Ser Gln Trp Phe Leu Thr Leu Phe Thr Ala Lys Phe Pro Leu Tyr
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atg gtc ttc cat atc atc gac ctg ctt tta tgt gag gga ata agt gtt     2672
Met Val Phe His Ile Ile Asp Leu Leu Leu Cys Glu Gly Ile Ser Val
740                 745                 750                 755

att ttt aat gtc gcc ctt gga tta tta aag act tcg aaa gat gac ctg     2720
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ctg ttg aca gac ttt gaa ggt gcc ttg aag ttc ttt agg gtt cag ctt     2768
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772                 777                 782                 787

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Pro Lys Arg Tyr Arg Ser Glu Glu Asn Ala Lys Lys Leu Met Glu Leu
788                 793                 798                 803

gcc tgc aac atg aag att agt cag aag aag ttg aaa aaa tac gag aaa     2864
Ala Cys Asn Met Lys Ile Ser Gln Lys Lys Leu Lys Lys Tyr Glu Lys
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gaa tat cac acc atg agg gaa cag cag gcc cag caa gaa gac ccc atc     2912
Glu Tyr His Thr Met Arg Glu Gln Gln Ala Gln Gln Glu Asp Pro Ile
820                 825                 830                 835

gag cga ttt gag cgg gag aat agg cgt cta caa gaa gct aac atg agg     2960
Glu Arg Phe Glu Arg Glu Asn Arg Arg Leu Gln Glu Ala Asn Met Arg
836                 841                 846                 851

ttg gaa cag gaa aac gat gac tta gcc cat gag ctg gtg acc agc aag     3008
Leu Glu Gln Glu Asn Asp Asp Leu Ala His Glu Leu Val Thr Ser Lys
852                 857                 862                 867

att gca cta cgg aag gac ctg gat aac gct gag gaa aag gca gat gct     3056
Ile Ala Leu Arg Lys Asp Leu Asp Asn Ala Glu Glu Lys Ala Asp Ala
868                 873                 878                 883
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ctg aat aag gag ctg ctg atg acc aaa cag aag ttg att gat gca gaa     3104
Leu Asn Lys Glu Leu Leu Met Thr Lys Gln Lys Leu Ile Asp Ala Glu
884                 889                 894                 899

gaa gag aaa aga cgg ctg gaa gaa gag tct gct cag tta aaa gaa atg     3152
Glu Glu Lys Arg Arg Leu Glu Glu Glu Ser Ala Gln Leu Lys Glu Met
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tgc cgt cgg gaa ctc gac aag gca gaa tct gag att aaa aaa aac agt     3200
Cys Arg Arg Glu Leu Asp Lys Ala Glu Ser Glu Ile Lys Lys Asn Ser
916                 921                 926                 931

tct atc att ggt gac tat aag cag att tgt tct cag ttg agt gaa aga     3248
Ser Ile Ile Gly Asp Tyr Lys Gln Ile Cys Ser Gln Leu Ser Glu Arg
932                 937                 942                 947

ttg gag aag cag cag aca gcc aat aag gtg gaa att gag aaa att cgg     3296
Leu Glu Lys Gln Gln Thr Ala Asn Lys Val Glu Ile Glu Lys Ile Arg
948                 953                 958                 963

caa aaa gtg gat gac tgt gag cgg tgc cgg gaa ttt ttc aac aaa gaa     3344
Gln Lys Val Asp Asp Cys Glu Arg Cys Arg Glu Phe Phe Asn Lys Glu
964                 969                 974                 979

ggg cgt gta aaa ggc ata agc tca acc aag gag gtt tta gat gag gac     3392
Gly Arg Val Lys Gly Ile Ser Ser Thr Lys Glu Val Leu Asp Glu Asp
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acg gat gaa gag aaa gag acg ctc aag aac cag ctg aga gaa atg gag     3440
Thr Asp Glu Glu Lys Glu Thr Leu Lys Asn Gln Leu Arg Glu Met Glu
996                1001                1006                1011

cta gaa ctg gca cag acc aaa ctc cag ctg gtg gag gcc gag tgt aag     3488
Leu Glu Leu Ala Gln Thr Lys Leu Gln Leu Val Glu Ala Glu Cys Lys
1012                1017                1022                1027

ata cag gac ttg gaa cac cat tta ggg ctt gcc ctc aat gag gtg cag     3536
Ile Gln Asp Leu Glu His His Leu Gly Leu Ala Leu Asn Glu Val Gln
1028                1033                1038                1043

gca gcc aag aag acg tgg ttt aac cga aca ctg agc tcc ata aag aca     3584
Ala Ala Lys Lys Thr Trp Phe Asn Arg Thr Leu Ser Ser Ile Lys Thr
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gca acc ggg gtt caa ggg aaa gag act tgc tga gagcagct gccgcctccc     3635
Ala Thr Gly Val Gln Gly Lys Glu Thr Cys  *
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gacaccttca gaaaacacga caccttttgt tgccttcttt ggccagatgt gtgattctgt   3695

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Docket No. 0609.1710-000

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atg ttg gac ttc gcg atc ttc gcc gtt acc ttc ttg ctg gcg ttg gtg 588
Met Leu Asp Phe Ala Ile Phe Ala Val Thr Phe Leu Leu Ala Leu Val
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gga gcc gtg ctc tac ctc tat ccg gct tcc aga caa gct gca gga att 636
Gly Ala Val Leu Tyr Leu Tyr Pro Ala Ser Arg Gln Ala Ala Gly Ile
 17   22   27   32

cca ggg att act cca act gaa gaa aaa gat ggt aat ctt cca gat att 684
Pro Gly Ile Thr Pro Thr Glu Glu Lys Asp Gly Asn Leu Pro Asp Ile
 33   38   43   48

gtg aat agt gga agt ttg cat gag ttc ctg gtt aat ttg cat gag aga 732
Val Asn Ser Gly Ser Leu His Glu Phe Leu Val Asn Leu His Glu Arg
 49   54   59   64

tat ggg cct gtg gtc tcc ttc tgg ttt ggc agg cgc ctc gtg gtt agt 780
Tyr Gly Pro Val Val Ser Phe Trp Phe Gly Arg Arg Leu Val Val Ser
 65   70   75   80

ttg ggc act gtt gat gta ctg aag cag cat atc aat ccc aat aag aca 828
Leu Gly Thr Val Asp Val Leu Lys Gln His Ile Asn Pro Asn Lys Thr
 81   86   91   96

ttg gac cct ttt gaa acc atg ctg aag tca tta tta agg tat caa tct 876
Leu Asp Pro Phe Glu Thr Met Leu Lys Ser Leu Leu Arg Tyr Gln Ser
 97   102   107   112

ggt ggt ggc agt gtg agt gaa aac cac atg agg aaa aaa ttg tat gaa 924
Gly Gly Gly Ser Val Ser Glu Asn His Met Arg Lys Lys Leu Tyr Glu
113   118   123   128

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aat ggt gtg act gat tct ctg aag agt aac ttt gcc ctc ctc cta aag      972
Asn Gly Val Thr Asp Ser Leu Lys Ser Asn Phe Ala Leu Leu Leu Lys
129                 134                 139                 144

ctt tca gaa gaa tta tta gat aaa tgg ctc tcc tac cca gag acc cag     1020
Leu Ser Glu Glu Leu Leu Asp Lys Trp Leu Ser Tyr Pro Glu Thr Gln
145                 150                 155                 160

cac gtg ccc ctc agc cag cat atg ctt ggt ttt gct atg aag tct gtt     1068
His Val Pro Leu Ser Gln His Met Leu Gly Phe Ala Met Lys Ser Val
161                 166                 171                 176

aca cag atg gta atg ggt agt aca ttt gaa gat gat cag gaa gtc att     1116
Thr Gln Met Val Met Gly Ser Thr Phe Glu Asp Asp Gln Glu Val Ile
177                 182                 187                 192

cgc ttc cag aag aat cat ggc aca gtt tgg tct gag att gga aaa ggc     1164
Arg Phe Gln Lys Asn His Gly Thr Val Trp Ser Glu Ile Gly Lys Gly
193                 198                 203                 208

ttt cta gat ggg tca ctt gat aaa aac atg act cgg aaa aaa caa tat     1212
Phe Leu Asp Gly Ser Leu Asp Lys Asn Met Thr Arg Lys Lys Gln Tyr
209                 214                 219                 224

gaa gat gcc ctc atg caa ctg gag tct gtt tta agg aac atc ata aaa     1260
Glu Asp Ala Leu Met Gln Leu Glu Ser Val Leu Arg Asn Ile Ile Lys
225                 230                 235                 240

gaa cga aaa gga agg aac ttc agt caa cat att ttc att gac tcc tta     1308
Glu Arg Lys Gly Arg Asn Phe Ser Gln His Ile Phe Ile Asp Ser Leu
241                 246                 251                 256

gta caa ggg aac ctt aat gac caa cag atc cta gaa gac agt atg ata     1356
Val Gln Gly Asn Leu Asn Asp Gln Gln Ile Leu Glu Asp Ser Met Ile
257                 262                 267                 272

ttt tct ctg gcc agt tgc ata ata act gca aaa ttg tgt acc tgg gca     1404
Phe Ser Leu Ala Ser Cys Ile Ile Thr Ala Lys Leu Cys Thr Trp Ala
273                 278                 283                 288

atc tgt ttt tta acc acc tct gaa gaa gtt caa aaa aaa tta tat gaa     1452
Ile Cys Phe Leu Thr Thr Ser Glu Glu Val Gln Lys Lys Leu Tyr Glu
289                 294                 299                 304

gag ata aac caa gtt ttt gga aat ggt cct gtt act cca gag aaa att     1500
Glu Ile Asn Gln Val Phe Gly Asn Gly Pro Val Thr Pro Glu Lys Ile
305                 310                 315                 320

gag cag ctc aga tat tgt cag cat gtg ctt tgt gaa act gtt cga act     1548
Glu Gln Leu Arg Tyr Cys Gln His Val Leu Cys Glu Thr Val Arg Thr
321                 326                 331                 336

gcc aaa ctg act cca gtt tct gcc cag ctt caa gat att gaa gga aaa     1596
Ala Lys Leu Thr Pro Val Ser Ala Gln Leu Gln Asp Ile Glu Gly Lys
337                 342                 347                 352
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att gac cga ttt att att cct aga gag acc ctc gtc ctt tat gcc ctt     1644
Ile Asp Arg Phe Ile Ile Pro Arg Glu Thr Leu Val Leu Tyr Ala Leu
353                 358                 363                 368

ggt gtg gta ctt cag gat cct aat act tgg cca tct cca cac aag ttt     1692
Gly Val Val Leu Gln Asp Pro Asn Thr Trp Pro Ser Pro His Lys Phe
369                 374                 379                 384

gat cca gat cgg ttt gat gat gaa tta gta atg aaa act ttt tcc tca     1740
Asp Pro Asp Arg Phe Asp Asp Glu Leu Val Met Lys Thr Phe Ser Ser
385                 390                 395                 400

ctt gga ttc tca ggc aca cag gag tgt cca gag ttg agg ttt gca tat     1788
Leu Gly Phe Ser Gly Thr Gln Glu Cys Pro Glu Leu Arg Phe Ala Tyr
401                 406                 411                 416

atg gtg acc aca gta ctt ctt agt gta ttg gtg aag aga ctg cac cta     1836
Met Val Thr Thr Val Leu Leu Ser Val Leu Val Lys Arg Leu His Leu
417                 422                 427                 432

ctt tct gtg gag gga cag gtt att gaa aca aag tat gaa ctg gta aca     1884
Leu Ser Val Glu Gly Gln Val Ile Glu Thr Lys Tyr Glu Leu Val Thr
433                 438                 443                 448

tca tca agg gaa gaa gct tgg atc act gtc tca aag aga tat taa aat     1932
Ser Ser Arg Glu Glu Ala Trp Ile Thr Val Ser Lys Arg Tyr  *
449                 454                 459

tttatacatt taaaatcatt gttaaattga ttgaggaaaa caaccattta aaaaaaatct   1992

atgttgaatc cttttataaa ccagtatcac tttgtaatat aaacacctat ttgtacttaa   2052

ttttgtaaat ttggattttt atatatcata ttttcttaat tcattgtaca catttgactt   2112

actgcacagt atattgatca ttttaatggg aaactttagc tttctacttt ttatttttgt   2172

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ggcggcggct gctgcgaggg acg    atg agt gcc tcc ttc gtg ccg aac ggg      170
                             Met Ser Ala Ser Phe Val Pro Asn Gly
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gcc agc ctg gaa gat tgt cac tgt aac ctc ttc tgc ctg gct gac ttg      218
Ala Ser Leu Glu Asp Cys His Cys Asn Leu Phe Cys Leu Ala Asp Leu
 10                  15                  20                  25

aca gga att aag tgg aaa aaa tat gta tgg caa ggc cca act tct gcc      266
Thr Gly Ile Lys Trp Lys Lys Tyr Val Trp Gln Gly Pro Thr Ser Ala
 26                  31                  36                  41

cct att ctg ttt cct gtg aca gaa gaa gac ccc att ttg agc agt ttt      314
Pro Ile Leu Phe Pro Val Thr Glu Glu Asp Pro Ile Leu Ser Ser Phe
 42                  47                  52                  57

agt cgc tgc ctt aag gca gat gta ctt ggt gtt tgg cgg cga gat caa      362
Ser Arg Cys Leu Lys Ala Asp Val Leu Gly Val Trp Arg Arg Asp Gln
 58                  63                  68                  73

aga cct gga aga aga gaa ttg tgg ata ttt tgg tgg ggt gaa gac ccc      410
Arg Pro Gly Arg Arg Glu Leu Trp Ile Phe Trp Trp Gly Glu Asp Pro
 74                  79                  84                  89

agt ttt gct gac ctt att cac cat gac tta tca gaa gaa gaa gat gga      458
Ser Phe Ala Asp Leu Ile His His Asp Leu Ser Glu Glu Glu Asp Gly
 90                  95                 100                 105

gtg tgg gag aat gga ctt tcc tat gaa tgc cgt act ctg ctt ttc aaa      506
Val Trp Glu Asn Gly Leu Ser Tyr Glu Cys Arg Thr Leu Leu Phe Lys
106                 111                 116                 121

gca gtt cac aat cta ttg gaa cgg tgt tta atg aac agg aat ttt gta      554
Ala Val His Asn Leu Leu Glu Arg Cys Leu Met Asn Arg Asn Phe Val
122                 127                 132                 137

cgt att ggc aag tgg ttt gta aag cct tat gaa aaa gat gaa aaa cct      602
Arg Ile Gly Lys Trp Phe Val Lys Pro Tyr Glu Lys Asp Glu Lys Pro
138                 143                 148                 153

ata aat aaa agt gaa cac ttg tcc tgc tcc ttc acc ttt ttc ttg cat      650
Ile Asn Lys Ser Glu His Leu Ser Cys Ser Phe Thr Phe Phe Leu His
154                 159                 164                 169

gga gac agc aat gtt tgt acc agt gtg gaa att aac caa cat caa cct      698
Gly Asp Ser Asn Val Cys Thr Ser Val Glu Ile Asn Gln His Gln Pro
170                 175                 180                 185

gta tac ctt ctc agt gaa gag cat atc acc ctt gct caa cag tct aat      746
Val Tyr Leu Leu Ser Glu Glu His Ile Thr Leu Ala Gln Gln Ser Asn
186                 191                 196                 201

agc cca ttt caa gtt atc tta tgc cca ttt gga cta aat ggc act ctc      794
Ser Pro Phe Gln Val Ile Leu Cys Pro Phe Gly Leu Asn Gly Thr Leu
202                 207                 212                 217

aca gga cag gca ttc aag atg tct gat tca gct aca aaa aaa tta att      842
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Application: 09/955,926

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218                 223                 228                 233

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Gly Glu Trp Lys Gln Phe Tyr Pro Ile Ser Cys Cys Leu Lys Glu Met
234                 239                 244                 249

tct gaa gaa aaa cag gaa gat atg gat tgg gaa gat gat tct tta gct      938
Ser Glu Glu Lys Gln Glu Asp Met Asp Trp Glu Asp Asp Ser Leu Ala
250                 255                 260                 265

gca gta gaa gtt ctt gtt gct ggt gtc cga atg atc tac cca gca tgc      986
Ala Val Glu Val Leu Val Ala Gly Val Arg Met Ile Tyr Pro Ala Cys
266                 271                 276                 281

ttt gtt cta gtc cct cag tca gac att cct act cct agc cct gtg gga     1034
Phe Val Leu Val Pro Gln Ser Asp Ile Pro Thr Pro Ser Pro Val Gly
282                 287                 292                 297

tcc act cac tgt tca tct tct tgc ttg ggt gtc cac caa gtg cct gct     1082
Ser Thr His Cys Ser Ser Ser Cys Leu Gly Val His Gln Val Pro Ala
298                 303                 308                 313

tcc aca aga gat cct gct atg tct tcg gtt acg ctt aca cca cct acg     1130
Ser Thr Arg Asp Pro Ala Met Ser Ser Val Thr Leu Thr Pro Pro Thr
314                 319                 324                 329

tct cct gag gaa gtc caa aca gtt gat cct cag tct gtc cag aag tgg     1178
Ser Pro Glu Glu Val Gln Thr Val Asp Pro Gln Ser Val Gln Lys Trp
330                 335                 340                 345

gtc aaa ttt tct tca gta tct gat ggc ttc aac tcc gat agt act agc     1226
Val Lys Phe Ser Ser Val Ser Asp Gly Phe Asn Ser Asp Ser Thr Ser
346                 351                 356                 361

cac cat ggt ggg aaa ata ccc aga aaa tta gca aat cat gtg gtg gat     1274
His His Gly Gly Lys Ile Pro Arg Lys Leu Ala Asn His Val Val Asp
362                 367                 372                 377

aga gtt tgg caa gaa tgc aat atg aac aga gca cag aac aag agg aag     1322
Arg Val Trp Gln Glu Cys Asn Met Asn Arg Ala Gln Asn Lys Arg Lys
378                 383                 388                 393

tat tct gct tca tca ggt ggt cta tgc gaa gaa gcg aca gct gct aaa     1370
Tyr Ser Ala Ser Ser Gly Gly Leu Cys Glu Glu Ala Thr Ala Ala Lys
394                 399                 404                 409

gtg gca tcc tgg gat ttt gtt gaa gcc aca caa aga aca aat tgc agt     1418
Val Ala Ser Trp Asp Phe Val Glu Ala Thr Gln Arg Thr Asn Cys Ser
410                 415                 420                 425

tgt ttg agg cac aaa aat ctc aag tca aga aat gct gga caa caa gga     1466
Cys Leu Arg His Lys Asn Leu Lys Ser Arg Asn Ala Gly Gln Gln Gly
426                 431                 436                 441

cag gca cca tct tta ggt cag caa caa caa ata ctt cct aag cac aag     1514
Gln Ala Pro Ser Leu Gly Gln Gln Gln Gln Ile Leu Pro Lys His Lys
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442                 447                 452                 457

acc aat gag aag caa gaa aag agt gaa aag cca cag aaa cgc ccc ttg     1562
Thr Asn Glu Lys Gln Glu Lys Ser Glu Lys Pro Gln Lys Arg Pro Leu
458                 463                 468                 473

act cct ttt cac cat cgt gtg tct gtt agt gat gat gtt ggc atg gac     1610
Thr Pro Phe His His Arg Val Ser Val Ser Asp Asp Val Gly Met Asp
474                 479                 484                 489

gca gat tca gcc agc caa aga ctt gtg atc tct gct cca gac agt caa     1658
Ala Asp Ser Ala Ser Gln Arg Leu Val Ile Ser Ala Pro Asp Ser Gln
490                 495                 500                 505

gtg aga ttt tca aat atc cga act aat gat gta gca aag act cct cag     1706
Val Arg Phe Ser Asn Ile Arg Thr Asn Asp Val Ala Lys Thr Pro Gln
506                 511                 516                 521

atg cat ggc acc gaa atg gca aat tca cct caa cca ccc cca ctt agt     1754
Met His Gly Thr Glu Met Ala Asn Ser Pro Gln Pro Pro Pro Leu Ser
522                 527                 532                 537

cct cac cct tgt gat gtg gtt gat gaa gga gtg act aaa aca cct tca     1802
Pro His Pro Cys Asp Val Val Asp Glu Gly Val Thr Lys Thr Pro Ser
538                 543                 548                 553

act cct cag agt caa cat ttt tat caa atg cca aca cca gat ccc ttg     1850
Thr Pro Gln Ser Gln His Phe Tyr Gln Met Pro Thr Pro Asp Pro Leu
554                 559                 564                 569

gtt cct tct aaa cca atg gaa gat agg ata gac agt ttg tcc cag tct     1898
Val Pro Ser Lys Pro Met Glu Asp Arg Ile Asp Ser Leu Ser Gln Ser
570                 575                 580                 585

ttc cca cct caa tat cag gaa gct gta gaa cct aca gta tat gtt ggt     1946
Phe Pro Pro Gln Tyr Gln Glu Ala Val Glu Pro Thr Val Tyr Val Gly
586                 591                 596                 601

aca gca gta aac ttg gaa gaa gat gaa gcc aat ata gcc tgg aag tat     1994
Thr Ala Val Asn Leu Glu Glu Asp Glu Ala Asn Ile Ala Trp Lys Tyr
602                 607                 612                 617

tac aag ttc cca aag aaa aaa gat gta gag ttt tta cca cct caa ctt     2042
Tyr Lys Phe Pro Lys Lys Lys Asp Val Glu Phe Leu Pro Pro Gln Leu
618                 623                 628                 633

cca agt gat aaa ttc aag gat gat cca gtt gga cct ttt gga cag gaa     2090
Pro Ser Asp Lys Phe Lys Asp Asp Pro Val Gly Pro Phe Gly Gln Glu
634                 639                 644                 649

agt gta aca tca gtt aca gag tta atg gtg caa tgt aag aaa cct tta     2138
Ser Val Thr Ser Val Thr Glu Leu Met Val Gln Cys Lys Lys Pro Leu
650                 655                 660                 665

aaa gtt tct gat gaa tta gtg cag caa tat caa att aaa aac cag tgt     2186
Lys Val Ser Asp Glu Leu Val Gln Gln Tyr Gln Ile Lys Asn Gln Cys
666                 671                 676                 681
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ctt tca gca ata gca tct gat gca gaa caa gaa cct aaa att gat cca     2234
Leu Ser Ala Ile Ala Ser Asp Ala Glu Gln Glu Pro Lys Ile Asp Pro
682                 687                 692                 697

tat gca ttt gtt gaa gga gat gag gaa ttc ctt ttt cct gat aaa aaa     2282
Tyr Ala Phe Val Glu Gly Asp Glu Glu Phe Leu Phe Pro Asp Lys Lys
698                 703                 708                 713

gat aga caa aat agt gag aga gaa gct gga aaa aaa cac aag gta gaa     2330
Asp Arg Gln Asn Ser Glu Arg Glu Ala Gly Lys Lys His Lys Val Glu
714                 719                 724                 729

gat ggg aca tct agt gta aca gtg tta tca cat gaa gaa gat gct atg     2378
Asp Gly Thr Ser Ser Val Thr Val Leu Ser His Glu Glu Asp Ala Met
730                 735                 740                 745

tca tta ttt agt ccc tct atc aag caa gat gct cca cgc cct act agt     2426
Ser Leu Phe Ser Pro Ser Ile Lys Gln Asp Ala Pro Arg Pro Thr Ser
746                 751                 756                 761

cat gcc cgt cct cca tca aca agt ttg att tat gac tca gac ctg gct     2474
His Ala Arg Pro Pro Ser Thr Ser Leu Ile Tyr Asp Ser Asp Leu Ala
762                 767                 772                 777

gtc tct tat act gac ctt gat aat ctc ttc aat tct gat gaa gat gaa     2522
Val Ser Tyr Thr Asp Leu Asp Asn Leu Phe Asn Ser Asp Glu Asp Glu
778                 783                 788                 793

cta aca cct gga tct aaa aga tca gca aat gga tca gat gat aaa gcc     2570
Leu Thr Pro Gly Ser Lys Arg Ser Ala Asn Gly Ser Asp Asp Lys Ala
794                 799                 804                 809

agc tgc aag gaa tca aag aca gga aat ctg gac ccg tta tct tgc ata     2618
Ser Cys Lys Glu Ser Lys Thr Gly Asn Leu Asp Pro Leu Ser Cys Ile
810                 815                 820                 825

agc act gca gat ctt cat aaa atg tat cct aca cca cca tca ttg gaa     2666
Ser Thr Ala Asp Leu His Lys Met Tyr Pro Thr Pro Pro Ser Leu Glu
826                 831                 836                 841

caa cat att atg gga ttt tcc cca atg aat atg aat aat aaa gaa tat     2714
Gln His Ile Met Gly Phe Ser Pro Met Asn Met Asn Asn Lys Glu Tyr
842                 847                 852                 857

ggt agt atg gat aca aca cct gga gga act gtt cta gaa gga aat agt     2762
Gly Ser Met Asp Thr Thr Pro Gly Gly Thr Val Leu Glu Gly Asn Ser
858                 863                 868                 873

tct agt ata gga gcg cag ttc aaa att gag gtt gat gag gga ttc tgt     2810
Ser Ser Ile Gly Ala Gln Phe Lys Ile Glu Val Asp Glu Gly Phe Cys
874                 879                 884                 889

agc ccc aaa cct tct gaa att aaa gat ttt tct tat gtc tat aag cct     2858
Ser Pro Lys Pro Ser Glu Ile Lys Asp Phe Ser Tyr Val Tyr Lys Pro
890                 895                 900                 905
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gaa aat tgt caa att cta gtg gga tgt tcc atg ttt gca cct cta aaa     2906
Glu Asn Cys Gln Ile Leu Val Gly Cys Ser Met Phe Ala Pro Leu Lys
906                 911                 916                 921

act cta cca agc caa tat ctg ccc ctt atc aaa ttg cca gaa gag tgt     2954
Thr Leu Pro Ser Gln Tyr Leu Pro Leu Ile Lys Leu Pro Glu Glu Cys
922                 927                 932                 937

att tac cgt cag agt tgg act gtt gga aaa ttg gaa ttg ctt tct tca     3002
Ile Tyr Arg Gln Ser Trp Thr Val Gly Lys Leu Glu Leu Leu Ser Ser
938                 943                 948                 953

ggg cct tca atg cca ttc atc aaa gag ggt gat gga agt aat atg gat     3050
Gly Pro Ser Met Pro Phe Ile Lys Glu Gly Asp Gly Ser Asn Met Asp
954                 959                 964                 969

caa gaa tat ggc act gct tat aca cct caa act cat act tct tgt ggg     3098
Gln Glu Tyr Gly Thr Ala Tyr Thr Pro Gln Thr His Thr Ser Cys Gly
970                 975                 980                 985

atg cct cct agc agt gca cct cct agt aac agc gga gca gga att ctt     3146
Met Pro Pro Ser Ser Ala Pro Pro Ser Asn Ser Gly Ala Gly Ile Leu
986                 991                 996                1001

cct tct cca tcc acc cct cgg ttt cca act cca agg act cca agg act     3194
Pro Ser Pro Ser Thr Pro Arg Phe Pro Thr Pro Arg Thr Pro Arg Thr
1002                1007                1012                1017

cct cgg act cct cgt gga gct ggt gga cct gct agt gct caa ggt tca     3242
Pro Arg Thr Pro Arg Gly Ala Gly Gly Pro Ala Ser Ala Gln Gly Ser
1018                1023                1028                1033

gtc aaa tat gaa aat tca gac ttg tat tca cca gct tct acc cca tct     3290
Val Lys Tyr Glu Asn Ser Asp Leu Tyr Ser Pro Ala Ser Thr Pro Ser
1034                1039                1044                1049

aca tgc aga ccc ctt aat tct gtt gaa cct gca act gtc cct tcc atc     3338
Thr Cys Arg Pro Leu Asn Ser Val Glu Pro Ala Thr Val Pro Ser Ile
1050                1055                1060                1065

cct gaa gca cac agt ctt tat gta aac ctc atc ctt tca gaa tca gtt     3386
Pro Glu Ala His Ser Leu Tyr Val Asn Leu Ile Leu Ser Glu Ser Val
1066                1071                1076                1081

atg aat ttg ttt aaa gac tgt aac tct gat agt tgt tgc atc tgt gtt     3434
Met Asn Leu Phe Lys Asp Cys Asn Ser Asp Ser Cys Cys Ile Cys Val
1082                1087                1092                1097

tgc aac atg aac atc aag ggt gcc gat gtt gga gtt tac att cca gat     3482
Cys Asn Met Asn Ile Lys Gly Ala Asp Val Gly Val Tyr Ile Pro Asp
1098                1103                1108                1113

cca acg cag gaa gca caa tat agg tgt acc tgt ggc ttc agt gct gtc     3530
Pro Thr Gln Glu Ala Gln Tyr Arg Cys Thr Cys Gly Phe Ser Ala Val
1114                1119                1124                1129

atg aac aga aaa ttt gga aac aat tca gga tta ttt ttt gaa gat gaa     3578
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 Met Asn Arg Lys Phe Gly Asn Asn Ser Gly Leu Phe Phe Glu Asp Glu
1130                1135                1140                1145

 cta gat atc ata gga cgc aat aca gac tgt ggc aaa gaa gca gaa aaa     3626
 Leu Asp Ile Ile Gly Arg Asn Thr Asp Cys Gly Lys Glu Ala Glu Lys
1146                1151                1156                1161

 cgt ttt gaa gct ctc agg gct acc tct gct gaa cat gtt aat gga gga     3674
 Arg Phe Glu Ala Leu Arg Ala Thr Ser Ala Glu His Val Asn Gly Gly
1162                1167                1172                1177

 cta aag gaa tct gaa aaa tta tct gat gat ttg ata tta ttg cta caa     3722
 Leu Lys Glu Ser Glu Lys Leu Ser Asp Asp Leu Ile Leu Leu Leu Gln
1178                1183                1188                1193

 gat cag tgc act aat tta ttt tca ccc ttt gga gca gca gac caa gat     3770
 Asp Gln Cys Thr Asn Leu Phe Ser Pro Phe Gly Ala Ala Asp Gln Asp
1194                1199                1204                1209

 cct ttt cct aaa agt ggt gta att agc aat tgg gta cgt gtt gaa gag     3818
 Pro Phe Pro Lys Ser Gly Val Ile Ser Asn Trp Val Arg Val Glu Glu
1210                1215                1220                1225

 cgt gac tgt tgc aat gac tgc tac ctt gca tta gaa cat ggg cgt cag     3866
 Arg Asp Cys Cys Asn Asp Cys Tyr Leu Ala Leu Glu His Gly Arg Gln
1226                1231                1236                1241

 ttc atg gat aac atg tca gga gga aaa gtt gat gaa gca ctt gtg aaa     3914
 Phe Met Asp Asn Met Ser Gly Gly Lys Val Asp Glu Ala Leu Val Lys
1242                1247                1252                1257

 agt tca tgc tta cac ccc tgg tcc aaa aga aac gat gtg agt atg cag     3962
 Ser Ser Cys Leu His Pro Trp Ser Lys Arg Asn Asp Val Ser Met Gln
1258                1263                1268                1273

 tgc tca cag gat ata ctt cga atg ctc ctc tct ctt cag cca gtt ctt     4010
 Cys Ser Gln Asp Ile Leu Arg Met Leu Leu Ser Leu Gln Pro Val Leu
1274                1279                1284                1289

 cag gat gcc att cag aaa aaa aga aca gta aga cct tgg ggt gtt cag     4058
 Gln Asp Ala Ile Gln Lys Lys Arg Thr Val Arg Pro Trp Gly Val Gln
1290                1295                1300                1305

 ggt cct ctc act tgg caa caa ttt cat aaa atg gct ggc cga ggc tct     4106
 Gly Pro Leu Thr Trp Gln Gln Phe His Lys Met Ala Gly Arg Gly Ser
1306                1311                1316                1321

 tat gga act gat gaa tcc cca gaa cca ctg cca atc ccc aca ttt ttg     4154
 Tyr Gly Thr Asp Glu Ser Pro Glu Pro Leu Pro Ile Pro Thr Phe Leu
1322                1327                1332                1337

 ttg ggt tat gat tat gat tat ctg gtg ctt tct cca ttt gct ctt cct     4202
 Leu Gly Tyr Asp Tyr Asp Tyr Leu Val Leu Ser Pro Phe Ala Leu Pro
1338                1343                1348                1353

 tat tgg gag aga ctt atg ctg gaa ccc tat gga tct caa aga gat ata     4250
 Tyr Trp Glu Arg Leu Met Leu Glu Pro Tyr Gly Ser Gln Arg Asp Ile
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1354                1359                1364                1369

 gcc tat gtt gta ctg tgt cca gaa aat gaa gcc ttg tta aat gga gca     4298
 Ala Tyr Val Val Leu Cys Pro Glu Asn Glu Ala Leu Leu Asn Gly Ala
1370                1375                1380                1385

 aaa agc ttt ttt aga gat ctt act gca ata tat gag tcc tgt cga tta     4346
 Lys Ser Phe Phe Arg Asp Leu Thr Ala Ile Tyr Glu Ser Cys Arg Leu
1386                1391                1396                1401

 ggt caa cat aga cct gtt tct cga ctg tta aca gat ggg atc atg aga     4394
 Gly Gln His Arg Pro Val Ser Arg Leu Leu Thr Asp Gly Ile Met Arg
1402                1407                1412                1417

 gtt gga tct act gca tca aag aaa cta tca gaa aag ttg gta gca gaa     4442
 Val Gly Ser Thr Ala Ser Lys Lys Leu Ser Glu Lys Leu Val Ala Glu
1418                1423                1428                1433

 tgg ttt tct cag gca gct gat ggt aac aat gaa gca ttt tct aaa ctc     4490
 Trp Phe Ser Gln Ala Ala Asp Gly Asn Asn Glu Ala Phe Ser Lys Leu
1434                1439                1444                1449

 aag ctt tat gca caa gtc tgc aga tat gac cta ggt cct tat ctt gct     4538
 Lys Leu Tyr Ala Gln Val Cys Arg Tyr Asp Leu Gly Pro Tyr Leu Ala
1450                1455                1460                1465

 tcc ctg cca ttg gac agc tct cta ctt tcc cag cca aat tta gtt gcc     4586
 Ser Leu Pro Leu Asp Ser Ser Leu Leu Ser Gln Pro Asn Leu Val Ala
1466                1471                1476                1481

 cct aca agt cag tct ttg att act cca cct cag atg aca aat act gga     4634
 Pro Thr Ser Gln Ser Leu Ile Thr Pro Pro Gln Met Thr Asn Thr Gly
1482                1487                1492                1497

 aat gct aat act cca tct gcc acc tta gca tct gca gcg agc agc act     4682
 Asn Ala Asn Thr Pro Ser Ala Thr Leu Ala Ser Ala Ala Ser Ser Thr
1498                1503                1508                1513

 atg aca gtg act tca ggt gtt gcc ata tct act tca gtt gcc aca gct     4730
 Met Thr Val Thr Ser Gly Val Ala Ile Ser Thr Ser Val Ala Thr Ala
1514                1519                1524                1529

 aat tca act ttg acc aca gct tca act tca tct tca tca tcc tcc aac     4778
 Asn Ser Thr Leu Thr Thr Ala Ser Thr Ser Ser Ser Ser Ser Ser Asn
1530                1535                1540                1545

 ttg aat agt gga gta tca tca aat aaa cta cct tcg ttt cca ccc ttt     4826
 Leu Asn Ser Gly Val Ser Ser Asn Lys Leu Pro Ser Phe Pro Pro Phe
1546                1551                1556                1561

 ggc agt atg aac agt aat gct gca gga tcc atg tct aca caa gca aat     4874
 Gly Ser Met Asn Ser Asn Ala Ala Gly Ser Met Ser Thr Gln Ala Asn
1562                1567                1572                1577

 aca gtt cag agt ggt cag cta gga ggg caa cag aca tca gct cta cag     4922
 Thr Val Gln Ser Gly Gln Leu Gly Gly Gln Gln Thr Ser Ala Leu Gln
1578                1583                1588                1593
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 aca gct ggg att tct gga gaa tca tct tca ctt ccc act cag ccg cat     4970
 Thr Ala Gly Ile Ser Gly Glu Ser Ser Ser Leu Pro Thr Gln Pro His
1594                1599                1604                1609

 cct gat gtg tct gaa agc acg atg gat cgg gat aaa gtg gga atc ccc     5018
 Pro Asp Val Ser Glu Ser Thr Met Asp Arg Asp Lys Val Gly Ile Pro
1610                1615                1620                1625

 aca gat ggt gat tca cat gca gtc acg tat cca cct gca att gtt gtt     5066
 Thr Asp Gly Asp Ser His Ala Val Thr Tyr Pro Pro Ala Ile Val Val
1626                1631                1636                1641

 tat ata att gat cct ttt aca tac gaa aat aca gac gag agc act aac     5114
 Tyr Ile Ile Asp Pro Phe Thr Tyr Glu Asn Thr Asp Glu Ser Thr Asn
1642                1647                1652                1657

 tct tct agt gtg tgg aca ttg ggg cta ctt cga tgc ttt cta gaa atg     5162
 Ser Ser Ser Val Trp Thr Leu Gly Leu Leu Arg Cys Phe Leu Glu Met
1658                1663                1668                1673

 gtc cag act ctt cct cct cat atc aag agt act gtt tct gta cag att     5210
 Val Gln Thr Leu Pro Pro His Ile Lys Ser Thr Val Ser Val Gln Ile
1674                1679                1684                1689

 att cct tgt cag tac ctg ttg caa cct gtg aag cat gaa gat aga gaa     5258
 Ile Pro Cys Gln Tyr Leu Leu Gln Pro Val Lys His Glu Asp Arg Glu
1690                1695                1700                1705

 atc tat ccc cag cat tta aaa tcc ctg gct ttt tcg gcc ttt acc cag     5306
 Ile Tyr Pro Gln His Leu Lys Ser Leu Ala Phe Ser Ala Phe Thr Gln
1706                1711                1716                1721

 tgt cgg agg cca ctt cca aca tca acc aat gtg aaa aca ttg act ggc     5354
 Cys Arg Arg Pro Leu Pro Thr Ser Thr Asn Val Lys Thr Leu Thr Gly
1722                1727                1732                1737

 ttt ggt cca ggt tta gcc atg gaa act gcc ctt aga agt cct gat aga     5402
 Phe Gly Pro Gly Leu Ala Met Glu Thr Ala Leu Arg Ser Pro Asp Arg
1738                1743                1748                1753

 cca gag tgt att cga ctt tat gca cct cct ttt att ctg gct cca gtg     5450
 Pro Glu Cys Ile Arg Leu Tyr Ala Pro Pro Phe Ile Leu Ala Pro Val
1754                1759                1764                1769

 aag gac aaa cag aca gag cta gga gaa aca ttt gga gaa gct gga cag     5498
 Lys Asp Lys Gln Thr Glu Leu Gly Glu Thr Phe Gly Glu Ala Gly Gln
1770                1775                1780                1785

 aaa tat aat gtt ctt ttt gtg gga tac tgt tta tca cat gat caa agg     5546
 Lys Tyr Asn Val Leu Phe Val Gly Tyr Cys Leu Ser His Asp Gln Arg
1786                1791                1796                1801

 tgg att ctt gca tct tgc aca gat cta tat gga gaa ctt tta gaa act     5594
 Trp Ile Leu Ala Ser Cys Thr Asp Leu Tyr Gly Glu Leu Leu Glu Thr
1802                1807                1812                1817
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 tgt atc att aac atc gat gtt cca aat agg gct cgt cgg aaa aaa agt     5642
 Cys Ile Ile Asn Ile Asp Val Pro Asn Arg Ala Arg Arg Lys Lys Ser
1818                1823                1828                1833

 tct gct aga aaa ttt ggt cta cag aaa ctt tgg gag tgg tgc tta gga     5690
 Ser Ala Arg Lys Phe Gly Leu Gln Lys Leu Trp Glu Trp Cys Leu Gly
1834                1839                1844                1849

 ctt gta caa atg agt tca ttg cca tgg aga gtt gta att ggt cgt cta     5738
 Leu Val Gln Met Ser Ser Leu Pro Trp Arg Val Val Ile Gly Arg Leu
1850                1855                1860                1865

 gga agg att ggt cat gga gaa ttg aaa gat tgg agc tgt ttg ctg agt     5786
 Gly Arg Ile Gly His Gly Glu Leu Lys Asp Trp Ser Cys Leu Leu Ser
1866                1871                1876                1881

 cgt cga aac ttg cag tct cta agt aaa agg ctc aaa gac atg tgt aga     5834
 Arg Arg Asn Leu Gln Ser Leu Ser Lys Arg Leu Lys Asp Met Cys Arg
1882                1887                1892                1897

 atg tgt ggt ata tct gct gca gac tcc cct agc att ctc agt gct tgc     5882
 Met Cys Gly Ile Ser Ala Ala Asp Ser Pro Ser Ile Leu Ser Ala Cys
1898                1903                1908                1913

 ttg gtg gca atg gag ccg caa ggc tct ttt gtt att atg cca gat tct     5930
 Leu Val Ala Met Glu Pro Gln Gly Ser Phe Val Ile Met Pro Asp Ser
1914                1919                1924                1929

 gtg tca act ggt tct gta ttt gga aga agc acg act cta aat atg cag     5978
 Val Ser Thr Gly Ser Val Phe Gly Arg Ser Thr Thr Leu Asn Met Gln
1930                1935                1940                1945

 aca tct cag cta aat acc cca cag gat aca tca tgt act cat ata ctt     6026
 Thr Ser Gln Leu Asn Thr Pro Gln Asp Thr Ser Cys Thr His Ile Leu
1946                1951                1956                1961

 gtg ttt cct act tct gct tct gtg caa gta gct tca gct act tat acc     6074
 Val Phe Pro Thr Ser Ala Ser Val Gln Val Ala Ser Ala Thr Tyr Thr
1962                1967                1972                1977

 act gaa aat ttg gat tta gct ttc aat ccc aac aat gat gga gca gat     6122
 Thr Glu Asn Leu Asp Leu Ala Phe Asn Pro Asn Asn Asp Gly Ala Asp
1978                1983                1988                1993

 gga atg ggt atc ttt gat ttg tta gac aca gga gat gat ctt gac cct     6170
 Gly Met Gly Ile Phe Asp Leu Leu Asp Thr Gly Asp Asp Leu Asp Pro
1994                1999                2004                2009

 gat atc att aat atc ctt cct gct tct cca act ggt tct cct gta ctt     6218
 Asp Ile Ile Asn Ile Leu Pro Ala Ser Pro Thr Gly Ser Pro Val Leu
2010                2015                2020                2025

 tct cca gga tct cat tac ccc cat gga ggt gat gcg ggc aag ggt cag     6266
 Ser Pro Gly Ser His Tyr Pro His Gly Gly Asp Ala Gly Lys Gly Gln
2026                2031                2036                2041

 agt act gat cgg cta cta tca aca gaa cct cat gag gaa gta cct aat     6314
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 Ser Thr Asp Arg Leu Leu Ser Thr Glu Pro His Glu Glu Val Pro Asn
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 att ctt cag caa cca ttg gcc ctt ggt tac ttt gta tca act gcc aaa     6362
 Ile Leu Gln Gln Pro Leu Ala Leu Gly Tyr Phe Val Ser Thr Ala Lys
2058                2063                2068                2073

 gca ggt cca tta cct gac tgg ttc tgg tca gca tgt cct caa gca caa     6410
 Ala Gly Pro Leu Pro Asp Trp Phe Trp Ser Ala Cys Pro Gln Ala Gln
2074                2079                2084                2089

 tat cag tgt ccc ctt ttt ctt aag gcc tct ttg cac ctc cac gtg cct     6458
 Tyr Gln Cys Pro Leu Phe Leu Lys Ala Ser Leu His Leu His Val Pro
2090                2095                2100                2105

 tca gtg caa tct gac gag ctg ctt cac agt aaa cac tcc cac cca ctt     6506
 Ser Val Gln Ser Asp Glu Leu Leu His Ser Lys His Ser His Pro Leu
2106                2111                2116                2121

 gac tca aat cag act tca gat gtc ctc agg ttt gtt ttg gaa cag tac     6554
 Asp Ser Asn Gln Thr Ser Asp Val Leu Arg Phe Val Leu Glu Gln Tyr
2122                2127                2132                2137

 aat gca ctc tcc tgg cta acc tgt gac cct gca acc cag gac aga cgc     6602
 Asn Ala Leu Ser Trp Leu Thr Cys Asp Pro Ala Thr Gln Asp Arg Arg
2138                2143                2148                2153

 tca tgt ctc cca att cat ttt gtg gtg ctg aat cag tta tat aac ttt     6650
 Ser Cys Leu Pro Ile His Phe Val Val Leu Asn Gln Leu Tyr Asn Phe
2154                2159                2164                2169

 att atg aat atg ctg tga tcttca tttgatggaa ctgtgcaaga aaagaacaag     6704
 Ile Met Asn Met Leu  *
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Gln Gln Leu Leu Glu Asp Gly Ala Asp Pro Cys Ala Ala Asp Asp Lys
  7                  12                  17                  22

ggc cgc aca gct cta cac ttt gcc tca tgc aat ggc aat gac cag att      150
Gly Arg Thr Ala Leu His Phe Ala Ser Cys Asn Gly Asn Asp Gln Ile
 23                  28                  33                  38

gtg cag ctg ctc ctg gac cat ggt gct gat cct aac cag cga gat ggg      198
Val Gln Leu Leu Leu Asp His Gly Ala Asp Pro Asn Gln Arg Asp Gly
 39                  44                  49                  54

ctg ggg aac acg cca ctg cac ctg gcg gcc tgc acc aac cac gtt cct      246
Leu Gly Asn Thr Pro Leu His Leu Ala Ala Cys Thr Asn His Val Pro
 55                  60                  65                  70

gtc atc acc aca ctg cta cga gga ggg gcc cgt gta gat gcc ctg gac      294
Val Ile Thr Thr Leu Leu Arg Gly Gly Ala Arg Val Asp Ala Leu Asp
 71                  76                  81                  86

cga gct ggt cgc aca ccc ctg cac ctg gcc aag tca aag ctg aat atc      342
Arg Ala Gly Arg Thr Pro Leu His Leu Ala Lys Ser Lys Leu Asn Ile
 87                  92                  97                 102

ctg cag gag ggc cat gcc cag tgc cta gag gct gtg cgt ctg gag gtg      390
Leu Gln Glu Gly His Ala Gln Cys Leu Glu Ala Val Arg Leu Glu Val
103                 108                 113                 118

aag cag atc atc cat atg ctg agg gag tat ctg gag cgc cta ggg caa      438
Lys Gln Ile Ile His Met Leu Arg Glu Tyr Leu Glu Arg Leu Gly Gln
119                 124                 129                 134

cat gag cag cga gaa cgc ctg gat gac ctc tgc acc cgc ctg cag atg      486
His Glu Gln Arg Glu Arg Leu Asp Asp Leu Cys Thr Arg Leu Gln Met
135                 140                 145                 150

acc agt acc aaa gag cag gtg gat gaa gtg act gac ctc ctg gcc agc      534
Thr Ser Thr Lys Glu Gln Val Asp Glu Val Thr Asp Leu Leu Ala Ser
151                 156                 161                 166

ttc acc tcc ctc agt ctg cag atg cag agc atg gag aag agg tag caa      582
Phe Thr Ser Leu Ser Leu Gln Met Gln Ser Met Glu Lys Arg  *
167                 172                 177

gagaggctcc ctgccttcct gccactgccc caccctgccc cactgctgtc tcagtaccaa    642

gaaaaagccc aacatctggg acttggagct gcacttgtct ggtgaggacc ttgccctcac    702

ccgcagatgc cgtggggcag agatgctctc tctccacggc ctcagagcca ctcccagcca    762
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cagtttccag catctctgtg gacagggacc acagctccca gcttcttcca gttctcgcag 822

caccagacca gcctctgcag ctgcacttca gctccgcaga cctgcgctat ctcagcagac 882

ctcacttgcc ccatggcctt catggcgcgc tccaggcctc agacccttct ctgtgttccg 942

tcctggccat gggcttgttg cagtcagcag gtgtgggctt aggcgggcac cctgtggcca 1002

ggggtactgc gtgaggccct cagttggtcc tgtgcctctc accagcactt agacagacac 1062

gtcaccagac tttcaaggag atactgcagt gagtttctct ggttggaagg ggagggttgg 1122

tgagtcccag accttaaaaa tacaaggtta agagggaccc ccaaagcaaa aaattccaac 1182

ccttttcctc ccagtcattg aaacaccaaa actattatac cggagggtgt aatagttttg 1242

ctgcccagtt gtggtaggcc agtagtggcc tcccaagatg cccatgtcct aatcccagga 1302

acctgtcaaa attaccttgt atggcccaaa ggggctttgc agatgtaatg aagttaagga 1362

tctttcgcca ggaagattat cccagcttgt tcaggagggc ttgatgtcct cacccgggtc 1422

tgtataacag aagagcaggt gacgggagag gaggttggag gtgtagcgat ggagcaggaa 1482

actggagttg aggagggcag ctcaagccac agagtccagg ccacctcaga gccaggaaat 1542

gcatcctccc acgggcaagg aggtgcacgc tctgaaaaga ctgagggact cggccaatgc 1602

caatgatgtg gaaacagtgc agcagctgct ggaagatggc gcggatccct gtgcagctga 1662

tgacaagggc cgcacagctc tacactttgc ctcatgcaat ggcaatgacc agattgtgca 1722

gccctgctcc cacctggact ggctcagtga ggctaatttt ataattctgg ctgattttag 1782

aactctaacg gcctaaattt gtgttgtttt aagtccaat 1821

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<213> Homo sapiens

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ctccctgtgc cttgcttgga gctgacgccg acggtttatt gcagggaact gacaagatca 180

cattttgaga agaagttgga aagaatccca agtggatgaa ctgaatatct ggatgaggac 240

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aagatctgtg gggagagact gtaagataga atgagtccat ttaagtccca ggacggtgga     300

aactagctag tagattgcag cc atg ttg tgg aag ctg ctg ctg aga tcc cag      352
                          Met Leu Trp Lys Leu Leu Leu Arg Ser Gln
                            1               5

tcc tgc agg ctg tgt tct ttc aga aag atg cga tca cct cca aaa tac      400
Ser Cys Arg Leu Cys Ser Phe Arg Lys Met Arg Ser Pro Pro Lys Tyr
 11                  16                  21                  26

aga cct ttc tta gca tgc ttc acc tat aca act gat aaa cag tcg agc      448
Arg Pro Phe Leu Ala Cys Phe Thr Tyr Thr Thr Asp Lys Gln Ser Ser
 27                  32                  37                  42

aaa gaa aat aca aga aca gtg gaa aag ctc tat aaa tgt tca gtt gac      496
Lys Glu Asn Thr Arg Thr Val Glu Lys Leu Tyr Lys Cys Ser Val Asp
 43                  48                  53                  58

att agg aaa att cgt aga tta aaa gga tgg gta ctt tta gaa gat gaa      544
Ile Arg Lys Ile Arg Arg Leu Lys Gly Trp Val Leu Leu Glu Asp Glu
 59                  64                  69                  74

acc tat gtt gaa gaa att gcg aat att tta caa gaa cta ggt gcc gat      592
Thr Tyr Val Glu Glu Ile Ala Asn Ile Leu Gln Glu Leu Gly Ala Asp
 75                  80                  85                  90

gag act gct gta gcc agt att ttg gaa cgc tgc ccg gaa gca att gtc      640
Glu Thr Ala Val Ala Ser Ile Leu Glu Arg Cys Pro Glu Ala Ile Val
 91                  96                 101                 106

tgt agt cca acc gct gtt aac acc cag aga aaa ctc tgg cag ttg gtc      688
Cys Ser Pro Thr Ala Val Asn Thr Gln Arg Lys Leu Trp Gln Leu Val
107                 112                 117                 122

tgc aaa aat gag gaa gag tta atc aag tta ata gag cag ttt cca gaa      736
Cys Lys Asn Glu Glu Glu Leu Ile Lys Leu Ile Glu Gln Phe Pro Glu
123                 128                 133                 138

tct ttc ttt act att aaa gac caa gag aac cag aag ctg aat gtt cag      784
Ser Phe Phe Thr Ile Lys Asp Gln Glu Asn Gln Lys Leu Asn Val Gln
139                 144                 149                 154

ttc ttt caa gag ttg gga cta aaa aat gtg gtc att agc aga ctt ttg      832
Phe Phe Gln Glu Leu Gly Leu Lys Asn Val Val Ile Ser Arg Leu Leu
155                 160                 165                 170

aca gct gca cct aat gtt ttt cat aat cct gtt gag aag aat aag caa      880
Thr Ala Ala Pro Asn Val Phe His Asn Pro Val Glu Lys Asn Lys Gln
171                 176                 181                 186

atg gta aga att ctc caa gag agt tat cta gat gta ggt ggc tct gag      928
Met Val Arg Ile Leu Gln Glu Ser Tyr Leu Asp Val Gly Gly Ser Glu
187                 192                 197                 202

gcc aac atg aaa gtt tgg cta cta aaa ttg tta agc caa aac cca ttt      976
Ala Asn Met Lys Val Trp Leu Leu Lys Leu Leu Ser Gln Asn Pro Phe
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203                 208                 213                 218

att ttg tta aat tct ccc aca gct ata aag gaa aca cta gaa ttt ctc     1024
Ile Leu Leu Asn Ser Pro Thr Ala Ile Lys Glu Thr Leu Glu Phe Leu
219                 224                 229                 234

cag gag caa ggt ttc acc agc ttt gaa att ctc cag ctt cta tcc aaa     1072
Gln Glu Gln Gly Phe Thr Ser Phe Glu Ile Leu Gln Leu Leu Ser Lys
235                 240                 245                 250

ctc aaa gga ttt ctt ttt caa ctt tgc cca aga agt ata cag aat agt     1120
Leu Lys Gly Phe Leu Phe Gln Leu Cys Pro Arg Ser Ile Gln Asn Ser
251                 256                 261                 266

att tcc ttc tct aaa aat gct ttt aaa tgc aca gat cat gac ctg aag     1168
Ile Ser Phe Ser Lys Asn Ala Phe Lys Cys Thr Asp His Asp Leu Lys
267                 272                 277                 282

caa tta gtt ttg aaa tgt cct gcc ctt tta tat tat tct gtt cca gtt     1216
Gln Leu Val Leu Lys Cys Pro Ala Leu Leu Tyr Tyr Ser Val Pro Val
283                 288                 293                 298

tta gaa gag aga atg caa gga tta ttg aga gaa gga att tcc ata gct     1264
Leu Glu Glu Arg Met Gln Gly Leu Leu Arg Glu Gly Ile Ser Ile Ala
299                 304                 309                 314

cag ata aga gag acg cca atg gtt ctt gaa tta aca cca cag ata gta     1312
Gln Ile Arg Glu Thr Pro Met Val Leu Glu Leu Thr Pro Gln Ile Val
315                 320                 325                 330

cag tac agg ata agg aaa ctg aat tcc tca ggc tac aga ata aag gat     1360
Gln Tyr Arg Ile Arg Lys Leu Asn Ser Ser Gly Tyr Arg Ile Lys Asp
331                 336                 341                 346

gga cat cta gca aat cta aat gga tca aaa aaa gag ttt gaa gct aat     1408
Gly His Leu Ala Asn Leu Asn Gly Ser Lys Lys Glu Phe Glu Ala Asn
347                 352                 357                 362

ttt ggc aaa att cag gcc aaa aaa gta agg cca tta ttt aac cct gtg     1456
Phe Gly Lys Ile Gln Ala Lys Lys Val Arg Pro Leu Phe Asn Pro Val
363                 368                 373                 378

gca cca tta aat gtt gaa gaa tga cgtcgacgcg gccgcgaatt cggatcctcg    1510
Ala Pro Leu Asn Val Glu Glu  *
379                 384

agagatctct ttttttgggt ttggtggggt atcttcatca tcgaatagat agttatatac   1570

atgaccttcg attttagagt atcgcct                                      1597
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tccactagtc cagtgtggtg gaattccctt ggctggggaa gggtggc  atg gag cct      116
                                                     Met Glu Pro
                                                       1

ctc cgg ctg ctc atc tta ctc ttt gtc aca gag ctg tcc gga gcc cac      164
Leu Arg Leu Leu Ile Leu Leu Phe Val Thr Glu Leu Ser Gly Ala His
  4                   9                  14                  19

aac acc aca gtg ttc cag ggc gtg gcg ggc cag tcc ctg cag gtg tct      212
Asn Thr Thr Val Phe Gln Gly Val Ala Gly Gln Ser Leu Gln Val Ser
 20                  25                  30                  35

tgc ccc tat gac tcc atg aag cac tgg ggg agg cgc aag gcc tgg tgc      260
Cys Pro Tyr Asp Ser Met Lys His Trp Gly Arg Arg Lys Ala Trp Cys
 36                  41                  46                  51

cgc cag ctg gga gag aag ggc cca tgc cag cgt gtg gtc agc acg cac      308
Arg Gln Leu Gly Glu Lys Gly Pro Cys Gln Arg Val Val Ser Thr His
 52                  57                  62                  67

aac ttg tgg ctg ctg tcc ttc ctg agg agg tgg aat ggg agc aca gcc      356
Asn Leu Trp Leu Leu Ser Phe Leu Arg Arg Trp Asn Gly Ser Thr Ala
 68                  73                  78                  83

atc aca gac gat acc ctg ggt ggc act ctc acc att acg ctg cgg aat      404
Ile Thr Asp Asp Thr Leu Gly Gly Thr Leu Thr Ile Thr Leu Arg Asn
 84                  89                  94                  99

cta caa ccc cat gat gcg ggt ctc tac cag tgc cag agc ctc cat ggc      452
Leu Gln Pro His Asp Ala Gly Leu Tyr Gln Cys Gln Ser Leu His Gly
100                 105                 110                 115

agt gag gct gac acc ctc agg aag gtc ctg gtg gag gtg ctg gca gac      500
Ser Glu Ala Asp Thr Leu Arg Lys Val Leu Val Glu Val Leu Ala Asp
116                 121                 126                 131

ccc ctg gat cac cgg gat gct gga gat ctc tgg ttc ccc ggg gag tct      548
Pro Leu Asp His Arg Asp Ala Gly Asp Leu Trp Phe Pro Gly Glu Ser
132                 137                 142                 147

gag agc ttc gag gat gcc cat gtg gag cac agc atc tcc agg agc ctc      596
Glu Ser Phe Glu Asp Ala His Val Glu His Ser Ile Ser Arg Ser Leu
148                 153                 158                 163

ttg gaa gga gaa atc ccc ttc cca ccc act tcc atc ctt ctc ctc ctg      644
Leu Glu Gly Glu Ile Pro Phe Pro Pro Thr Ser Ile Leu Leu Leu Leu
164                 169                 174                 179

gcc tgc atc ttt ctc atc aag att cta gca gcc agc gcc ctc tgg gct      692
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Ala Cys Ile Phe Leu Ile Lys Ile Leu Ala Ala Ser Ala Leu Trp Ala
180                 185                 190                 195

gca gcc tgg cat gga cag aag cca ggg aca cat cca ccc agt gaa ctg      740
Ala Ala Trp His Gly Gln Lys Pro Gly Thr His Pro Pro Ser Glu Leu
196                 201                 206                 211

gac tgt ggc cat gac cca ggg tat cag ctc caa act ctg cca ggg ctg      788
Asp Cys Gly His Asp Pro Gly Tyr Gln Leu Gln Thr Leu Pro Gly Leu
212                 217                 222                 227

aga gac acg tga agg aagatgatgg gaggaaaagc ccaggagaag tcccaccagg      843
Arg Asp Thr  *
228

gaccagccca gcctgcatac ttgccacttg gccaccagga ctccttgttc tgctctggca    903

agagactact ctgcctgaac actgcttctc ctggaccctg gaagcaggga ctggttgagg    963

gagtggggag gtggtaagaa cacctgacaa cttctgaata ttggacattt taaacactta   1023

caaataaatc caagactgtc atatttagct ggaaaaaaaa aaaa                    1067
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US 2005/0260650 A1

<210> 15
<211> 3098
<212> DNA
<213> Homo sapiens

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<222> (194)..(2785)

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tttggtctgg gccaaactga aggggtttcc attctggcct gcaaaagctc taagggataa    120

agacgggcag gtcgatgccc gattctttgg acaacatgac agggcctggg ttccaataaa    180

taattgctac ctc   atg tct aaa gaa att cct ttt tct gtg aaa aag act      229
                 Met Ser Lys Glu Ile Pro Phe Ser Val Lys Lys Thr
                   1               5                  10

aag agc atc ttc aac agt gcc atg caa gag atg gag gtt tac gtg gag      277
Lys Ser Ile Phe Asn Ser Ala Met Gln Glu Met Glu Val Tyr Val Glu
 13                  18                  23                  28

aac atc cgc agg aag ttt ggg gtt ttt aat tac tct cca ttt agg aca      325
Asn Ile Arg Arg Lys Phe Gly Val Phe Asn Tyr Ser Pro Phe Arg Thr
 29                  34                  39                  44

ccc tac aca ccc aac agc cag tat caa atg ctg ctc gat ccc acc aac      373
Pro Tyr Thr Pro Asn Ser Gln Tyr Gln Met Leu Leu Asp Pro Thr Asn
 45                  50                  55                  60
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ccc agc gcc ggc act gcc aag ata gac aag cag gag aag gtc aag ctc      421
Pro Ser Ala Gly Thr Ala Lys Ile Asp Lys Gln Glu Lys Val Lys Leu
 61                  66                  71                  76

aac ttt gac atg acg gca tcc ccc aag atc ctg atg agc aag cct gtg      469
Asn Phe Asp Met Thr Ala Ser Pro Lys Ile Leu Met Ser Lys Pro Val
 77                  82                  87                  92

ctg agt ggg ggc aca ggc cgc cgg att tcc ttg tcg gat atg ccg cgc      517
Leu Ser Gly Gly Thr Gly Arg Arg Ile Ser Leu Ser Asp Met Pro Arg
 93                  98                 103                 108

tcc ccc atg agc aca aac tct tct gtg cac acg ggc tcc gac gtg gag      565
Ser Pro Met Ser Thr Asn Ser Ser Val His Thr Gly Ser Asp Val Glu
109                 114                 119                 124

cag gat gct gag aag aag gcc acg tcg agc cac ttc agt gcg agc gag      613
Gln Asp Ala Glu Lys Lys Ala Thr Ser Ser His Phe Ser Ala Ser Glu
125                 130                 135                 140

gag tcc atg gac ttc ctg gat aag agc aca gct tca cca gcc tcc acc      661
Glu Ser Met Asp Phe Leu Asp Lys Ser Thr Ala Ser Pro Ala Ser Thr
141                 146                 151                 156

aag acg gga caa gca ggg agt tta tcc ggc agc cca aag ccc ttc tct      709
Lys Thr Gly Gln Ala Gly Ser Leu Ser Gly Ser Pro Lys Pro Phe Ser
157                 162                 167                 172

cct caa ctg tca gct cct atc acg acg aaa acg gac aaa acc tcc acc      757
Pro Gln Leu Ser Ala Pro Ile Thr Thr Lys Thr Asp Lys Thr Ser Thr
173                 178                 183                 188

acc ggc agc atc ctg aat ctt aac ctg gat cga agc aaa gct gag atg      805
Thr Gly Ser Ile Leu Asn Leu Asn Leu Asp Arg Ser Lys Ala Glu Met
189                 194                 199                 204

gat ttg aag gag ctg agc gag tcg gtc cag caa cag tcc acc cct gtt      853
Asp Leu Lys Glu Leu Ser Glu Ser Val Gln Gln Gln Ser Thr Pro Val
205                 210                 215                 220

cct ctc atc tct ccc aag cgc cag att cgt agc agg ttc cag ctg aat      901
Pro Leu Ile Ser Pro Lys Arg Gln Ile Arg Ser Arg Phe Gln Leu Asn
221                 226                 231                 236

ctt gac aag acc ata gag agt tgc aaa gca caa tta ggc ata aat gaa      949
Leu Asp Lys Thr Ile Glu Ser Cys Lys Ala Gln Leu Gly Ile Asn Glu
237                 242                 247                 252

atc tcg gaa gat gtc tat acg gcc gta gag cac agc gat tcg gag gat      997
Ile Ser Glu Asp Val Tyr Thr Ala Val Glu His Ser Asp Ser Glu Asp
253                 258                 263                 268

tct gag aag tca gat agt agc gat agt gag tat atc agt gat gat gag     1045
Ser Glu Lys Ser Asp Ser Ser Asp Ser Glu Tyr Ile Ser Asp Asp Glu
269                 274                 279                 284
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cag aag tct aag aac gag cca gaa gac aca gag gac aaa gaa ggt tgt     1093
Gln Lys Ser Lys Asn Glu Pro Glu Asp Thr Glu Asp Lys Glu Gly Cys
285                 290                 295                 300

cag atg gac aaa gag cca tct gct gtt aaa aaa aag ccc aag cct aca     1141
Gln Met Asp Lys Glu Pro Ser Ala Val Lys Lys Lys Pro Lys Pro Thr
301                 306                 311                 316

aac cca gtg gag att aaa gag gag ctg aaa agc acg tca cca gcc agc     1189
Asn Pro Val Glu Ile Lys Glu Glu Leu Lys Ser Thr Ser Pro Ala Ser
317                 322                 327                 332

gag aag gca gac cct gga gca gtc aag gac aag gcc agc cct gag cct     1237
Glu Lys Ala Asp Pro Gly Ala Val Lys Asp Lys Ala Ser Pro Glu Pro
333                 338                 343                 348

gag aag gac ttt tcc gaa aag gca aaa cct tca cct cac ccc ata aag     1285
Glu Lys Asp Phe Ser Glu Lys Ala Lys Pro Ser Pro His Pro Ile Lys
349                 354                 359                 364

gat aaa ctg aag gga aaa gat gag acg gat tcc cca aca gtc cat ttg     1333
Asp Lys Leu Lys Gly Lys Asp Glu Thr Asp Ser Pro Thr Val His Leu
365                 370                 375                 380

ggc ctg gac tct gat tca gag agc gaa ctt gtc ata gat tta gga gaa     1381
Gly Leu Asp Ser Asp Ser Glu Ser Glu Leu Val Ile Asp Leu Gly Glu
381                 386                 391                 396

gac cat tct ggg cgg gag ggt cga aaa aat aag aag gaa ccc aaa gaa     1429
Asp His Ser Gly Arg Glu Gly Arg Lys Asn Lys Lys Glu Pro Lys Glu
397                 402                 407                 412

cca tct ccc aaa cag gat gtt gta ggt aaa act cca cca tcc acg acg     1477
Pro Ser Pro Lys Gln Asp Val Val Gly Lys Thr Pro Pro Ser Thr Thr
413                 418                 423                 428

gtg ggc agc cat tct ccc ccg gaa aca ccg gtg ctc acc cgc tct tcc     1525
Val Gly Ser His Ser Pro Pro Glu Thr Pro Val Leu Thr Arg Ser Ser
429                 434                 439                 444

gcc caa act tcc gcg gct ggc gcc aca gcc acc acc agc acg tcc tcc     1573
Ala Gln Thr Ser Ala Ala Gly Ala Thr Ala Thr Thr Ser Thr Ser Ser
445                 450                 455                 460

acg gtc acc gtc acg gcc ccg gcc ccc gcc gcc aca gga agc cca gtg     1621
Thr Val Thr Val Thr Ala Pro Ala Pro Ala Ala Thr Gly Ser Pro Val
461                 466                 471                 476

aaa aag cag agg ccg ctt tta ccg aag gag act gcc ccg gcc gtg cag     1669
Lys Lys Gln Arg Pro Leu Leu Pro Lys Glu Thr Ala Pro Ala Val Gln
477                 482                 487                 492

cgg gtc gtg tgg aac tca tca act aag ttt caa acg tcc tcc caa aag     1717
Arg Val Val Trp Asn Ser Ser Thr Lys Phe Gln Thr Ser Ser Gln Lys
493                 498                 503                 508

tgg cac atg cag aag atg cag cgt cag cag cag cag cag cag cag caa     1765
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Trp His Met Gln Lys Met Gln Arg Gln Gln Gln Gln Gln Gln Gln
509                 514                 519                 524

aac cag cag cag cag cct cag tct tcc cag ggg acg aga tat cag acc     1813
Asn Gln Gln Gln Gln Pro Gln Ser Ser Gln Gly Thr Arg Tyr Gln Thr
525                 530                 535                 540

aga cag gct gtg aaa gct gtc cag cag aag gag atc aca cag agc cca     1861
Arg Gln Ala Val Lys Ala Val Gln Gln Lys Glu Ile Thr Gln Ser Pro
541                 546                 551                 556

tcc acg tcc acc atc acc ctg gtg acc agc aca cag tca tcg ccc ctg     1909
Ser Thr Ser Thr Ile Thr Leu Val Thr Ser Thr Gln Ser Ser Pro Leu
557                 562                 567                 572

gtc acc agc tcg ggg tcc atg agc acc ctt gtg tcc tca gtc aac gct     1957
Val Thr Ser Ser Gly Ser Met Ser Thr Leu Val Ser Ser Val Asn Ala
573                 578                 583                 588

gac ctg ccc atc gcc act gcc tca gct gat gtc gcc gct gat att gcc     2005
Asp Leu Pro Ile Ala Thr Ala Ser Ala Asp Val Ala Ala Asp Ile Ala
589                 594                 599                 604

aag tac act agc aaa atg atg gat gca ata aaa gga aca atg aca gaa     2053
Lys Tyr Thr Ser Lys Met Met Asp Ala Ile Lys Gly Thr Met Thr Glu
605                 610                 615                 620

ata tac aac gat ctt tct aaa aac act act gga agc aca ata gct gag     2101
Ile Tyr Asn Asp Leu Ser Lys Asn Thr Thr Gly Ser Thr Ile Ala Glu
621                 626                 631                 636

att cgc agg ctg agg atc gag ata gag aag ctc cag tgg ctg cac cag     2149
Ile Arg Arg Leu Arg Ile Glu Ile Glu Lys Leu Gln Trp Leu His Gln
637                 642                 647                 652

caa gag ctc tcc gaa atg aaa cac aac tta gag ctg acc atg gcg gag     2197
Gln Glu Leu Ser Glu Met Lys His Asn Leu Glu Leu Thr Met Ala Glu
653                 658                 663                 668

atg cgg cag agc ctg gag cag gag cgg gac cgg ctc atc gcc gag gtg     2245
Met Arg Gln Ser Leu Glu Gln Glu Arg Asp Arg Leu Ile Ala Glu Val
669                 674                 679                 684

aag aag cag ctg gag ttg gag aag cag cag gcg gtg gat gag acc aag     2293
Lys Lys Gln Leu Glu Leu Glu Lys Gln Gln Ala Val Asp Glu Thr Lys
685                 690                 695                 700

aag aag cag tgg tgc gcc aac tgc aag aag gag gcc atc ttt tac tgc     2341
Lys Lys Gln Trp Cys Ala Asn Cys Lys Lys Glu Ala Ile Phe Tyr Cys
701                 706                 711                 716

tgt tgg aac acc agc tac tgt gac tac ccc tgc cag caa gcc cac tgg     2389
Cys Trp Asn Thr Ser Tyr Cys Asp Tyr Pro Cys Gln Gln Ala His Trp
717                 722                 727                 732

cct gag cac atg aag tcc tgc acc cag tca gct act gct cct cag cag     2437
Pro Glu His Met Lys Ser Cys Thr Gln Ser Ala Thr Ala Pro Gln Gln
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09/760,756

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733                 738                 743                 748

gaa gcg gat gct gag gtg aac aca gaa aca cta aat aag tcc tcc cag     2485
Glu Ala Asp Ala Glu Val Asn Thr Glu Thr Leu Asn Lys Ser Ser Gln
749                 754                 759                 764

ggg agc tcc tcg agc aca caa tca gca cct tca gaa acg gcc agc gcc     2533
Gly Ser Ser Ser Ser Thr Gln Ser Ala Pro Ser Glu Thr Ala Ser Ala
765                 770                 775                 780

tcc aaa gag aag gag acg tca gct gag aaa agc aag gag agt ggc tcg     2581
Ser Lys Glu Lys Glu Thr Ser Ala Glu Lys Ser Lys Glu Ser Gly Ser
781                 786                 791                 796

acc ctt gac ctt tct ggc tcc aga gag acg ccc tcc tcc att ctc tta     2629
Thr Leu Asp Leu Ser Gly Ser Arg Glu Thr Pro Ser Ser Ile Leu Leu
797                 802                 807                 812

ggc tcc aac caa ggc tct gac cat tcc cgg agt aat aaa tcc agt tgg     2677
Gly Ser Asn Gln Gly Ser Asp His Ser Arg Ser Asn Lys Ser Ser Trp
813                 818                 823                 828

agc agc agt gat gag aag agg gga tcg aca cgt tcc gat cac aac acc     2725
Ser Ser Ser Asp Glu Lys Arg Gly Ser Thr Arg Ser Asp His Asn Thr
829                 834                 839                 844

agt acc agc acg aag agc ctc ctc ccg aaa gag tct cgg ctg gac acc     2773
Ser Thr Ser Thr Lys Ser Leu Leu Pro Lys Glu Ser Arg Leu Asp Thr
845                 850                 855                 860

ttc tgg gac tag cag tgaatcggga cacaaaccac ccaccccatt gggagaaaaa     2828
Phe Trp Asp  *
861

cccagacgcc aggaaaagaa gaaacaacaa aggcaggaga acagccactt tcagacttga   2888

aaatgacaaa accctcagtt gagcctgagc ccccggcgcg ggggctgcta cactacagga   2948

cacccagcat cggctttgac tgcagactgt tcacccacac gagccctgtg cttttggtgt   3008

aaataatgta caatttgtgg atgtcattga atctagagga ctttcccctt tttatatttg   3068

tattaacttt aacttattaa aaaaaaaaaa                                    3098
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<211> 2960
<212> DNA
<213> Homo sapiens

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<221> CDS
<222> (194)..(2647)

<400> 16

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agacgggcag gtcgatgccc gattctttgg acaacatgac agggcctggg ttccaataaa    180

taattgctac ctc   atg tct aaa gaa att cct ttt tct gtg aaa aag act      229
                 Met Ser Lys Glu Ile Pro Phe Ser Val Lys Lys Thr
                   1               5                  10

aag agc atc ttc aac agt gcc atg caa gag atg gag gtt tac gtg gag      277
Lys Ser Ile Phe Asn Ser Ala Met Gln Glu Met Glu Val Tyr Val Glu
 13                  18                  23                  28

aac atc cgc agg aag ttt ggg gtt ttt aat tac tct cca ttt agg aca      325
Asn Ile Arg Arg Lys Phe Gly Val Phe Asn Tyr Ser Pro Phe Arg Thr
 29                  34                  39                  44

ccc tac aca ccc aac agc cag tat caa atg ctg ctc gat ccc acc aac      373
Pro Tyr Thr Pro Asn Ser Gln Tyr Gln Met Leu Leu Asp Pro Thr Asn
 45                  50                  55                  60

ccc agc gcc ggc act gcc aag ata gac aag cag gag aag gtc aag ctc      421
Pro Ser Ala Gly Thr Ala Lys Ile Asp Lys Gln Glu Lys Val Lys Leu
 61                  66                  71                  76

aac ttt gac atg acg gca tcc ccc aag atc ctg atg agc aag cct gtg      469
Asn Phe Asp Met Thr Ala Ser Pro Lys Ile Leu Met Ser Lys Pro Val
 77                  82                  87                  92

ctg agt ggg ggc aca ggc cgc cgg att tcc ttg tcg gat atg ccg cgc      517
Leu Ser Gly Gly Thr Gly Arg Arg Ile Ser Leu Ser Asp Met Pro Arg
 93                  98                 103                 108

tcc ccc atg agc aca aac tct tct gtg cac acg ggc tcc gac gtg gag      565
Ser Pro Met Ser Thr Asn Ser Ser Val His Thr Gly Ser Asp Val Glu
109                 114                 119                 124

cag gat gct gag aag aag gcc acg tcg agc cac ttc agt gcg agc gag      613
Gln Asp Ala Glu Lys Lys Ala Thr Ser Ser His Phe Ser Ala Ser Glu
125                 130                 135                 140

gag tcc atg gac ttc ctg gat aag agc aca gct tca cca gcc tcc acc      661
Glu Ser Met Asp Phe Leu Asp Lys Ser Thr Ala Ser Pro Ala Ser Thr
141                 146                 151                 156

aag acg gga caa gca ggg agt tta tcc ggc agc cca aag ccc ttc tct      709
Lys Thr Gly Gln Ala Gly Ser Leu Ser Gly Ser Pro Lys Pro Phe Ser
157                 162                 167                 172

cct caa ctg tca gct cct atc acg acg aaa acg gac aaa acc tcc acc      757
Pro Gln Leu Ser Ala Pro Ile Thr Thr Lys Thr Asp Lys Thr Ser Thr
173                 178                 183                 188

acc ggc agc atc ctg aat ctt aac ctg gat cga agc aaa gct gag atg      805
Thr Gly Ser Ile Leu Asn Leu Asn Leu Asp Arg Ser Lys Ala Glu Met
189                 194                 199                 204
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gat ttg aag gag ctg agc gag tcg gtc cag caa cag tcc acc cct gtt      853
Asp Leu Lys Glu Leu Ser Glu Ser Val Gln Gln Gln Ser Thr Pro Val
205                 210                 215                 220

cct ctc atc tct ccc aag cgc cag att cgt agc agg ttc cag ctg aat      901
Pro Leu Ile Ser Pro Lys Arg Gln Ile Arg Ser Arg Phe Gln Leu Asn
221                 226                 231                 236

ctt gac aag acc ata gag agt tgc aaa gca caa tta ggc ata aat gaa      949
Leu Asp Lys Thr Ile Glu Ser Cys Lys Ala Gln Leu Gly Ile Asn Glu
237                 242                 247                 252

atc tcg gaa gat gtc tat acg gcc gta gag cac agc gat tcg gag gat      997
Ile Ser Glu Asp Val Tyr Thr Ala Val Glu His Ser Asp Ser Glu Asp
253                 258                 263                 268

tct gag aag tca gat agt agc gat agt gag tat atc agt gat gat gag     1045
Ser Glu Lys Ser Asp Ser Ser Asp Ser Glu Tyr Ile Ser Asp Asp Glu
269                 274                 279                 284

cag aag tct aag aac gag cca gaa gac aca gag gac aaa gaa ggt tgt     1093
Gln Lys Ser Lys Asn Glu Pro Glu Asp Thr Glu Asp Lys Glu Gly Cys
285                 290                 295                 300

cag atg gac aaa gag cca tct gct gtt aaa aaa aag ccc aag cct aca     1141
Gln Met Asp Lys Glu Pro Ser Ala Val Lys Lys Lys Pro Lys Pro Thr
301                 306                 311                 316

aac cca gtg gag att aaa gag gag ctg aaa agc acg tca cca gcc agc     1189
Asn Pro Val Glu Ile Lys Glu Glu Leu Lys Ser Thr Ser Pro Ala Ser
317                 322                 327                 332

gag aag gca gac cct gga gca gtc aag gac aag gcc agc cct gag cct     1237
Glu Lys Ala Asp Pro Gly Ala Val Lys Asp Lys Ala Ser Pro Glu Pro
333                 338                 343                 348

gag aag gac ttt tcc gaa aag gca aaa cct tca cct cac ccc ata aag     1285
Glu Lys Asp Phe Ser Glu Lys Ala Lys Pro Ser Pro His Pro Ile Lys
349                 354                 359                 364

gat aaa ctg aag gga aaa gat gag acg gat tcc cca aca gtc cat ttg     1333
Asp Lys Leu Lys Gly Lys Asp Glu Thr Asp Ser Pro Thr Val His Leu
365                 370                 375                 380

ggc ctg gac tct gat tca gag agc gaa ctt gtc ata gat tta gga gaa     1381
Gly Leu Asp Ser Asp Ser Glu Ser Glu Leu Val Ile Asp Leu Gly Glu
381                 386                 391                 396

gac cat tct ggg cgg gag ggt cga aaa aat aag aag gaa ccc aaa gaa     1429
Asp His Ser Gly Arg Glu Gly Arg Lys Asn Lys Lys Glu Pro Lys Glu
397                 402                 407                 412

cca tct ccc aaa cag gat gtt gta ggt aaa act cca cca tcc acg acg     1477
Pro Ser Pro Lys Gln Asp Val Val Gly Lys Thr Pro Pro Ser Thr Thr
413                 418                 423                 428
```

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gtg ggc agc cat tct ccc ccg gaa aca ccg gtg ctc acc cgc tct tcc     1525
Val Gly Ser His Ser Pro Pro Glu Thr Pro Val Leu Thr Arg Ser Ser
429                 434                 439                 444

gcc caa act tcc gcg gct ggc gcc aca gcc acc acc agc acg tcc tcc     1573
Ala Gln Thr Ser Ala Ala Gly Ala Thr Ala Thr Thr Ser Thr Ser Ser
445                 450                 455                 460

acg gtc acc gtc acg gcc ccg gcc ccc gcc gcc aca gga agc cca gtg     1621
Thr Val Thr Val Thr Ala Pro Ala Pro Ala Ala Thr Gly Ser Pro Val
461                 466                 471                 476

aaa aag cag agg ccg ctt tta ccg aag gag act gcc ccg gcc gtg cag     1669
Lys Lys Gln Arg Pro Leu Leu Pro Lys Glu Thr Ala Pro Ala Val Gln
477                 482                 487                 492

cgg gtc gtg tgg aac tca tca act gtc cag cag aag gag atc aca cag     1717
Arg Val Val Trp Asn Ser Ser Thr Val Gln Gln Lys Glu Ile Thr Gln
493                 498                 503                 508

agc cca tcc acg tcc acc atc acc ctg gtg acc agc aca cag tca tcg     1765
Ser Pro Ser Thr Ser Thr Ile Thr Leu Val Thr Ser Thr Gln Ser Ser
509                 514                 519                 524

ccc ctg gtc acc agc tcg ggg tcc atg agc acc ctt gtg tcc tca gtc     1813
Pro Leu Val Thr Ser Ser Gly Ser Met Ser Thr Leu Val Ser Ser Val
525                 530                 535                 540

aac gct gac ctg ccc atc gcc act gcc tca gct gat gtc gcc gct gat     1861
Asn Ala Asp Leu Pro Ile Ala Thr Ala Ser Ala Asp Val Ala Ala Asp
541                 546                 551                 556

att gcc aag tac act agc aaa atg atg gat gca ata aaa gga aca atg     1909
Ile Ala Lys Tyr Thr Ser Lys Met Met Asp Ala Ile Lys Gly Thr Met
557                 562                 567                 572

aca gaa ata tac aac gat ctt tct aaa aac act act gga agc aca ata     1957
Thr Glu Ile Tyr Asn Asp Leu Ser Lys Asn Thr Thr Gly Ser Thr Ile
573                 578                 583                 588

gct gag att cgc agg ctg agg atc gag ata gag aag ctc cag tgg ctg     2005
Ala Glu Ile Arg Arg Leu Arg Ile Glu Ile Glu Lys Leu Gln Trp Leu
589                 594                 599                 604

cac cag caa gag ctc tcc gaa atg aaa cac aac tta gag ctg acc atg     2053
His Gln Gln Glu Leu Ser Glu Met Lys His Asn Leu Glu Leu Thr Met
605                 610                 615                 620

gcg gag atg cgg cag agc ctg gag cag gag cgg gac cgg ctc atc gcc     2101
Ala Glu Met Arg Gln Ser Leu Glu Gln Glu Arg Asp Arg Leu Ile Ala
621                 626                 631                 636

gag gtg aag aag cag ctg gag ttg gag aag cag cag gcg gtg gat gag     2149
Glu Val Lys Lys Gln Leu Glu Leu Glu Lys Gln Gln Ala Val Asp Glu
637                 642                 647                 652

acc aag aag aag cag tgg tgc gcc aac tgc aag aag gag gcc atc ttt     2197
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Thr Lys Lys Lys Gln Trp Cys Ala Asn Cys Lys Lys Glu Ala Ile Phe
653                 658                 663                 668

tac tgc tgt tgg aac acc agc tac tgt gac tac ccc tgc cag caa gcc     2245
Tyr Cys Cys Trp Asn Thr Ser Tyr Cys Asp Tyr Pro Cys Gln Gln Ala
669                 674                 679                 684

cac tgg cct gag cac atg aag tcc tgc acc cag tca gct act gct cct     2293
His Trp Pro Glu His Met Lys Ser Cys Thr Gln Ser Ala Thr Ala Pro
685                 690                 695                 700

cag cag gaa gcg gat gct gag gtg aac aca gaa aca cta aat aag tcc     2341
Gln Gln Glu Ala Asp Ala Glu Val Asn Thr Glu Thr Leu Asn Lys Ser
701                 706                 711                 716

tcc cag ggg agc tcc tcg agc aca caa tca gca cct tca gaa acg gcc     2389
Ser Gln Gly Ser Ser Ser Ser Thr Gln Ser Ala Pro Ser Glu Thr Ala
717                 722                 727                 732

agc gcc tcc aaa gag aag gag acg tca gct gag aaa agc aag gag agt     2437
Ser Ala Ser Lys Glu Lys Glu Thr Ser Ala Glu Lys Ser Lys Glu Ser
733                 738                 743                 748

ggc tcg acc ctt gac ctt tct ggc tcc aga gag acg ccc tcc tcc att     2485
Gly Ser Thr Leu Asp Leu Ser Gly Ser Arg Glu Thr Pro Ser Ser Ile
749                 754                 759                 764

ctc tta ggc tcc aac caa ggc tct gac cat tcc cgg agt aat aaa tcc     2533
Leu Leu Gly Ser Asn Gln Gly Ser Asp His Ser Arg Ser Asn Lys Ser
765                 770                 775                 780

agt tgg agc agc agt gat gag aag agg gga tcg aca cgt tcc gat cac     2581
Ser Trp Ser Ser Ser Asp Glu Lys Arg Gly Ser Thr Arg Ser Asp His
781                 786                 791                 796

aac acc agt acc agc acg aag agc ctc ctc ccg aaa gag tct cgg ctg     2629
Asn Thr Ser Thr Ser Thr Lys Ser Leu Leu Pro Lys Glu Ser Arg Leu
797                 802                 807                 812

gac acc ttc tgg gac tag cagtga atcgggacac aaaccaccca ccccattggg     2683
Asp Thr Phe Trp Asp  *
813                 818

agaaaaaccc agacgccagg aaaagaagaa acaacaaagg caggagaaca gccactttca   2743

gacttgaaaa tgacaaaacc ctcagttgag cctgagcccc cggcgcgggg gctgctacac   2803

tacaggacac ccagcatcgg ctttgactgc agactgttca cccacacgag ccctgtgctt   2863

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gctccatgga cgggcgcccg tccctgcaca gcccgccgca gaggtaaggc tggcctctct 120

gcagtcagag gtctgagctc tgccatgggg ataggggtgt ctttattact gcagttttct 180

ctaacacctg ggggctaccg gagtgtgggc cgaagcaggc gctgcagccg cggatagtat 240

ccccaggaac atccccaaga ggagctggaa aaagcctcat ccccagctct gcagtctcca 300

ggggagctca gtgtctgttt gtccagcttc tcagagttgc tgtgccagct cggatgtggc 360

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attttctggt gagtcctgtg gcaggaatgt ttgtgcattc agcactggag catttactcc 480

ctgtctgaca ctggggtagc tgccatgagg gggattctag tatcagagtc cctcccttct 540

ggaagtttcc agggcaacaa agacataaga caaacatcct tgaaatgtta tctaaaaacc 600

caagattgaa ataatacata ccacacaagg aaacaggaga gtagtctagc tccatgtccg 660

gggctctagg ggttcataga tggcagctcc tgtccggggc tgaggttggg aggggagaaa 720

caggggcaga gtgagttggt ctctggagtg actgtgcttt tccaccctca gcagaggaag 780

aaccg atg ctg gaa cgt cgt tgc agg ggc ccc ctg gcc atg ggc ccg 827
Met Leu Glu Arg Arg Cys Arg Gly Pro Leu Ala Met Gly Pro
1 5 10

gcc cag ccc cga ctc ctt tct ggg ccc tcc cag gag tca ccc cag acc 875
Ala Gln Pro Arg Leu Leu Ser Gly Pro Ser Gln Glu Ser Pro Gln Thr
15 20 25 30

ctg ggg aag gag tcc cgc ggg ctg agg caa caa ggc acg tca gtg gcc 923
Leu Gly Lys Glu Ser Arg Gly Leu Arg Gln Gln Gly Thr Ser Val Ala
31 36 41 46

cag tct ggt gcc caa gcc cca ggc agg gcc cat cgc tgt gcc cac tgt 971
Gln Ser Gly Ala Gln Ala Pro Gly Arg Ala His Arg Cys Ala His Cys
47 52 57 62

cga agg cac ttc cct ggc tgg gtg gct ctg tgg ctt cac acc cgc cgg 1019
Arg Arg His Phe Pro Gly Trp Val Ala Leu Trp Leu His Thr Arg Arg
63 68 73 78

tgc cag gcc cgg ctg ccc ttg ccc tgc cct gag tgt ggc cgt cgc ttt 1067
Cys Gln Ala Arg Leu Pro Leu Pro Cys Pro Glu Cys Gly Arg Arg Phe

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 79                  84                  89                  94

cgc cat gcc ccc ttc tta gca ctg cac cgc cag gtc cat gct gct gcc     1115
Arg His Ala Pro Phe Leu Ala Leu His Arg Gln Val His Ala Ala Ala
 95                 100                 105                 110

acc cca gac ctg ggc ttt gcc tgc cac ctc tgt ggg cag agc ttc cga     1163
Thr Pro Asp Leu Gly Phe Ala Cys His Leu Cys Gly Gln Ser Phe Arg
111                 116                 121                 126

ggc tgg gtg gcc ctg gtt ctg cat ctg cgg gcc cat tca gct gca aag     1211
Gly Trp Val Ala Leu Val Leu His Leu Arg Ala His Ser Ala Ala Lys
127                 132                 137                 142

cgg ccc atc gct tgt ccc aaa tgc gag aga cgc ttc tgg cga cga aag     1259
Arg Pro Ile Ala Cys Pro Lys Cys Glu Arg Arg Phe Trp Arg Arg Lys
143                 148                 153                 158

cag ctt cga gct cat ctg cgg cgg tgc cac cct ccc gcc ccg gca gcc     1307
Gln Leu Arg Ala His Leu Arg Arg Cys His Pro Pro Ala Pro Ala Ala
159                 164                 169                 174

cgg ccc ttc ata tgc ggc aac tgt ggc cgg agc ttt gcc cag tgg gac     1355
Arg Pro Phe Ile Cys Gly Asn Cys Gly Arg Ser Phe Ala Gln Trp Asp
175                 180                 185                 190

cag cta gtt gcc cac aag cgg gtg cac gta gct gag gcc ctg gag gag     1403
Gln Leu Val Ala His Lys Arg Val His Val Ala Glu Ala Leu Glu Glu
191                 196                 201                 206

gcc gca gcc aag gct ctg ggg ccc cgg ccc agg ggg cgc ccc gcg gtg     1451
Ala Ala Ala Lys Ala Leu Gly Pro Arg Pro Arg Gly Arg Pro Ala Val
207                 212                 217                 222

acc gcc ccc cgg ccc ggt gga gat gcc gtc gac cgc ccc ttc cag tgt     1499
Thr Ala Pro Arg Pro Gly Gly Asp Ala Val Asp Arg Pro Phe Gln Cys
223                 228                 233                 238

gcc tgt tgt ggc aag cgc ttc cgg cac aag ccc aac ttg atc gct cac     1547
Ala Cys Cys Gly Lys Arg Phe Arg His Lys Pro Asn Leu Ile Ala His
239                 244                 249                 254

cgc cgc gtg cac acg ggc gag cgg ccc cac cag tgc ccc gag tgc ggg     1595
Arg Arg Val His Thr Gly Glu Arg Pro His Gln Cys Pro Glu Cys Gly
255                 260                 265                 270

aag cgc ttt acc aat aag ccc tat ctg act tcg cac cgg cgc atc cac     1643
Lys Arg Phe Thr Asn Lys Pro Tyr Leu Thr Ser His Arg Arg Ile His
271                 276                 281                 286

acc ggc gag aag ccc tac ccg tgc aaa gag tgc ggc cgc cgc ttc cgg     1691
Thr Gly Glu Lys Pro Tyr Pro Cys Lys Glu Cys Gly Arg Arg Phe Arg
287                 292                 297                 302

cac aaa ccc aac ctg ctg tct cac agc aag att cac aag cga tcc gag     1739
His Lys Pro Asn Leu Leu Ser His Ser Lys Ile His Lys Arg Ser Glu
303                 308                 313                 318
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ggg tcg gcc cag gcc gcc ccc ggc ccg ggg agc ccc cag ctg cca gcc     1787
Gly Ser Ala Gln Ala Ala Pro Gly Pro Gly Ser Pro Gln Leu Pro Ala
319                 324                 329                 334

ggc ccc cag gag tcc gcg gcc gag ccc acc ccg gcg gta cct ctg aaa     1835
Gly Pro Gln Glu Ser Ala Ala Glu Pro Thr Pro Ala Val Pro Leu Lys
335                 340                 345                 350

ccg gcc cag gag ccg ccg cca ggg gcc ccg cca gag cac ccg cag gac     1883
Pro Ala Gln Glu Pro Pro Pro Gly Ala Pro Pro Glu His Pro Gln Asp
351                 356                 361                 366

ccg atc gaa gcc ccc ccc tcc ctc tac agc tgc gac gac tgc ggc agg     1931
Pro Ile Glu Ala Pro Pro Ser Leu Tyr Ser Cys Asp Asp Cys Gly Arg
367                 372                 377                 382

agc ttc cgg ctg gag cgc ttc ctg cgg gcc cac cag cgg cag cac acc     1979
Ser Phe Arg Leu Glu Arg Phe Leu Arg Ala His Gln Arg Gln His Thr
383                 388                 393                 398

ggg gag cgg ccc ttc acc tgc gcc gag tgc ggg aag aac ttc ggc aag     2027
Gly Glu Arg Pro Phe Thr Cys Ala Glu Cys Gly Lys Asn Phe Gly Lys
399                 404                 409                 414

aag acg cac ctg gtg gcg cac tcg cgc gtg cac tcc ggc gag cgg ccc     2075
Lys Thr His Leu Val Ala His Ser Arg Val His Ser Gly Glu Arg Pro
415                 420                 425                 430

ttc gcc tgc gag gag tgc ggc cgc cgc ttc tcc cag ggc agc cat ctg     2123
Phe Ala Cys Glu Glu Cys Gly Arg Arg Phe Ser Gln Gly Ser His Leu
431                 436                 441                 446

gcg gcg cat cgg cgg gac cac gcc ccc gat cgg ccc ttc gtg tgt ccc     2171
Ala Ala His Arg Arg Asp His Ala Pro Asp Arg Pro Phe Val Cys Pro
447                 452                 457                 462

gac tgc ggc aag gcc ttc cgc cac aaa ccc tac ctg gcg gcg cac cgg     2219
Asp Cys Gly Lys Ala Phe Arg His Lys Pro Tyr Leu Ala Ala His Arg
463                 468                 473                 478

cgc atc cac acc ggc gag aag ccc tac gtc tgc ccc gac tgc ggc aaa     2267
Arg Ile His Thr Gly Glu Lys Pro Tyr Val Cys Pro Asp Cys Gly Lys
479                 484                 489                 494

gcc ttc agc cag aag tcc aac ctg gtg tcg cac cgg cgc atc cac acg     2315
Ala Phe Ser Gln Lys Ser Asn Leu Val Ser His Arg Arg Ile His Thr
495                 500                 505                 510

ggc gag cgg ccc tac gcc tgt ccc gac tgc gac cgc agc ttc agc cag     2363
Gly Glu Arg Pro Tyr Ala Cys Pro Asp Cys Asp Arg Ser Phe Ser Gln
511                 516                 521                 526

aag tcc aac ctc atc acc cac cgc aag agc cac atc cgg gac ggc gcc     2411
Lys Ser Asn Leu Ile Thr His Arg Lys Ser His Ile Arg Asp Gly Ala
527                 532                 537                 542
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ttc tgc tgt gcc atc tgt ggc cag acc ttc gac gac gag gag aga ctc     2459
Phe Cys Cys Ala Ile Cys Gly Gln Thr Phe Asp Asp Glu Glu Arg Leu
543                 548                 553                 558

ctg gcc cac cag aag aag cac gat gtc tga g acggtgggcg gggccgtgtt     2510
Leu Ala His Gln Lys Lys His Asp Val  *
559                 564

ggctgagaga gggctggggt ccttcgtggt gggagtcgca gtgggctggg ggtgcctgcc   2570

tagtgctgga gtaggggaca atgggaatcc tagaggggat ggaagacgcg gggagtgagc   2630

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tggatgattc taattgttag aaattctaat tgttagaaat ccttccttat aatgaatgaa   3470

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cgagtgaggc ccatggactg gggagggctg tgcctgacga ctcctgtgtc cctctatgag 240

ggcccagcgc cctgaccctc ctgcctaggt ttctaccttt tctctctgtc tttggccagc 300

tgggggaggg ggtagaggcc gggtgagcaa c atg gca cag agc aag agg cac 352
Met Ala Gln Ser Lys Arg His
1 5

gtg tac agc cgg acg ccc agc ggc agc agg atg agt gcg gag gca agc 400
Val Tyr Ser Arg Thr Pro Ser Gly Ser Arg Met Ser Ala Glu Ala Ser
8 13 18 23

gcc cgg cct ctg cgg gtg ggc tcc cgt gta gag gtg att gga aaa ggc 448
Ala Arg Pro Leu Arg Val Gly Ser Arg Val Glu Val Ile Gly Lys Gly
24 29 34 39

cac cga ggc act gtg gcc tat gtt gga gcc aca ctg ttt gcc act ggc 496
His Arg Gly Thr Val Ala Tyr Val Gly Ala Thr Leu Phe Ala Thr Gly
40 45 50 55

aaa tgg gta ggc gtg att ctg gat gaa gca aag ggc aaa aat gat gga 544
Lys Trp Val Gly Val Ile Leu Asp Glu Ala Lys Gly Lys Asn Asp Gly
56 61 66 71

act gtt caa ggc agg aag tac ttc act tgt gat gaa ggg cat ggc atc 592
Thr Val Gln Gly Arg Lys Tyr Phe Thr Cys Asp Glu Gly His Gly Ile
72 77 82 87

ttt gtg cgc cag tcc cag atc cag gta ttt gaa gat gga gca gat act 640
Phe Val Arg Gln Ser Gln Ile Gln Val Phe Glu Asp Gly Ala Asp Thr
88 93 98 103

act tcc cca gag aca cct gat tct tct gct tca aaa gtc ctc aaa aga 688
Thr Ser Pro Glu Thr Pro Asp Ser Ser Ala Ser Lys Val Leu Lys Arg
104 109 114 119

gag gga act gat aca act gca aag act agc aaa ctg cgg gga ctg aag 736
Glu Gly Thr Asp Thr Thr Ala Lys Thr Ser Lys Leu Arg Gly Leu Lys
120 125 130 135

cct aag aag gca ccg aca gcc cga aag acc aca act cgg cga ccc aag 784
Pro Lys Lys Ala Pro Thr Ala Arg Lys Thr Thr Thr Arg Arg Pro Lys
136 141 146 151

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ccc acg cgc cca gcc agt act ggg gtg gct ggg gcc agt agc tcc ctg      832
Pro Thr Arg Pro Ala Ser Thr Gly Val Ala Gly Ala Ser Ser Ser Leu
152                 157                 162                 167

ggc ccc tct ggc tca gcg tca gca ggt gag ctg agc agc agt gag ccc      880
Gly Pro Ser Gly Ser Ala Ser Ala Gly Glu Leu Ser Ser Ser Glu Pro
168                 173                 178                 183

agc acc ccg gct cag act ccg ctg gca gca ccc atc atc ccc acg ccg      928
Ser Thr Pro Ala Gln Thr Pro Leu Ala Ala Pro Ile Ile Pro Thr Pro
184                 189                 194                 199

gtc ctc acc tct cct gga gca gtc ccc ccg ctt cct tcc cca tcc aag      976
Val Leu Thr Ser Pro Gly Ala Val Pro Pro Leu Pro Ser Pro Ser Lys
200                 205                 210                 215

gag gag gag gga cta agg gct cag gtg cgg gac ctg gag gag aaa cta     1024
Glu Glu Glu Gly Leu Arg Ala Gln Val Arg Asp Leu Glu Glu Lys Leu
216                 221                 226                 231

gag acc ctg aga ctg aaa cgg gca gaa gac aaa gca aag cta aaa gag     1072
Glu Thr Leu Arg Leu Lys Arg Ala Glu Asp Lys Ala Lys Leu Lys Glu
232                 237                 242                 247

ctg gag aaa cac aaa atc cag ctg gag cag gtg cag gaa tgg aag agc     1120
Leu Glu Lys His Lys Ile Gln Leu Glu Gln Val Gln Glu Trp Lys Ser
248                 253                 258                 263

aaa atg cag gag cag cag gcc gac ctg cag cgg cgc ctc aag gag gcg     1168
Lys Met Gln Glu Gln Gln Ala Asp Leu Gln Arg Arg Leu Lys Glu Ala
264                 269                 274                 279

aga aag gaa gcc aag gag gcg ctg gag gca aag gaa cgc tat atg gag     1216
Arg Lys Glu Ala Lys Glu Ala Leu Glu Ala Lys Glu Arg Tyr Met Glu
280                 285                 290                 295

gag atg gct gat act gct gat gcc att gag atg gcc act ttg gac aag     1264
Glu Met Ala Asp Thr Ala Asp Ala Ile Glu Met Ala Thr Leu Asp Lys
296                 301                 306                 311

gag atg gct gaa gag cgg gct gag tcc ctg cag cag gag gtg gag gca     1312
Glu Met Ala Glu Glu Arg Ala Glu Ser Leu Gln Gln Glu Val Glu Ala
312                 317                 322                 327

ctg aag gag cgg gtg gac gag ctc act act gac tta gag atc ctc aag     1360
Leu Lys Glu Arg Val Asp Glu Leu Thr Thr Asp Leu Glu Ile Leu Lys
328                 333                 338                 343

gct gag att gaa gag aag ggc tca gat ggc gct gca tcc agt tat cag     1408
Ala Glu Ile Glu Glu Lys Gly Ser Asp Gly Ala Ala Ser Ser Tyr Gln
344                 349                 354                 359

ctc aag cag ctt gag gag cag aat gcc cgc ctg aag gat gcc ctg gtg     1456
Leu Lys Gln Leu Glu Glu Gln Asn Ala Arg Leu Lys Asp Ala Leu Val
360                 365                 370                 375

agg atg cgg gat ctt tct tcc tca gag aag cag gag cat gtg aag ctc     1504
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Arg Met Arg Asp Leu Ser Ser Ser Glu Lys Gln Glu His Val Lys Leu
376                 381                 386                 391

cag aag ctc atg gaa aag aag aac caa gag ctg gaa gtt gtg agg caa     1552
Gln Lys Leu Met Glu Lys Lys Asn Gln Glu Leu Glu Val Val Arg Gln
392                 397                 402                 407

cag cgg gag cgt ctg cag gag gag cta agc cag gca gag agc acc att     1600
Gln Arg Glu Arg Leu Gln Glu Glu Leu Ser Gln Ala Glu Ser Thr Ile
408                 413                 418                 423

gat gag ctc aag gag cag gtg gat gct gct ctg ggt gct gag gag atg     1648
Asp Glu Leu Lys Glu Gln Val Asp Ala Ala Leu Gly Ala Glu Glu Met
424                 429                 434                 439

gtg gag atg ctg aca gat cgg aac ctg aat ctg gaa gag aaa gtg cgc     1696
Val Glu Met Leu Thr Asp Arg Asn Leu Asn Leu Glu Glu Lys Val Arg
440                 445                 450                 455

gag ttg agg gag act gtg gga gac ttg gaa gcg atg aat gag atg aac     1744
Glu Leu Arg Glu Thr Val Gly Asp Leu Glu Ala Met Asn Glu Met Asn
456                 461                 466                 471

gat gag ctg cag gag aat gca cgt gag aca gaa ctg gag ctg cgg gag     1792
Asp Glu Leu Gln Glu Asn Ala Arg Glu Thr Glu Leu Glu Leu Arg Glu
472                 477                 482                 487

cag ctg gac atg gca ggc gcg cgg gtt cgt gag gcc cag aag cgt gtg     1840
Gln Leu Asp Met Ala Gly Ala Arg Val Arg Glu Ala Gln Lys Arg Val
488                 493                 498                 503

gag gca gcc cag gag acg gtt gca gac tac cag cag acc atc aag aag     1888
Glu Ala Ala Gln Glu Thr Val Ala Asp Tyr Gln Gln Thr Ile Lys Lys
504                 509                 514                 519

tac cgc cag ctg acc gcc cat cta cag gat gtg aat cgg gaa ctg aca     1936
Tyr Arg Gln Leu Thr Ala His Leu Gln Asp Val Asn Arg Glu Leu Thr
520                 525                 530                 535

aac cag cag gaa gca tct gtg gag agg caa cag cag cca cct cca gag     1984
Asn Gln Gln Glu Ala Ser Val Glu Arg Gln Gln Gln Pro Pro Pro Glu
536                 541                 546                 551

acc ttt gac ttc aaa atc aag ttt gct gag act aag gcc cat gcc aag     2032
Thr Phe Asp Phe Lys Ile Lys Phe Ala Glu Thr Lys Ala His Ala Lys
552                 557                 562                 567

gca att gag atg gaa ttg agg cag atg gag gtg gcc cag gcc aat cga     2080
Ala Ile Glu Met Glu Leu Arg Gln Met Glu Val Ala Gln Ala Asn Arg
568                 573                 578                 583

cac atg tcc ctg ctg aca gcc ttc atg cct gac agc ttc ctt cgg cca     2128
His Met Ser Leu Leu Thr Ala Phe Met Pro Asp Ser Phe Leu Arg Pro
584                 589                 594                 599

ggt ggg gac cat gac tgc gtt ctg gtg ctg ttg ctc atg cct cgt ctc     2176
Gly Gly Asp His Asp Cys Val Leu Val Leu Leu Leu Met Pro Arg Leu
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600                 605                 610                 615

att tgc aag gca gag ctg atc cgg aag cag gcc cag gag aag ttt gaa     2224
Ile Cys Lys Ala Glu Leu Ile Arg Lys Gln Ala Gln Glu Lys Phe Glu
616                 621                 626                 631

cta agt gag aac tgt tca gag cgg cct ggg ctg cga gga gct gct ggg     2272
Leu Ser Glu Asn Cys Ser Glu Arg Pro Gly Leu Arg Gly Ala Ala Gly
632                 637                 642                 647

gag caa ctc agc ttt gct gct gga ctg gtg tac tcg ctg agc ctg ctg     2320
Glu Gln Leu Ser Phe Ala Ala Gly Leu Val Tyr Ser Leu Ser Leu Leu
648                 653                 658                 663

cag gcc acg cta cac cgc tat gag cat gcc ctc tct cag tgc agt gtg     2368
Gln Ala Thr Leu His Arg Tyr Glu His Ala Leu Ser Gln Cys Ser Val
664                 669                 674                 679

gat gtg tat aag aaa gtg ggc agc ctg tac cct gag atg agt gcc cat     2416
Asp Val Tyr Lys Lys Val Gly Ser Leu Tyr Pro Glu Met Ser Ala His
680                 685                 690                 695

gag cgc tcc ttg gat ttc ctc att gaa ctg ctg cac aag gat cag ctg     2464
Glu Arg Ser Leu Asp Phe Leu Ile Glu Leu Leu His Lys Asp Gln Leu
696                 701                 706                 711

gat gag act gtc aat gtg gag cct ctc acc aag gcc atc aag tac tat     2512
Asp Glu Thr Val Asn Val Glu Pro Leu Thr Lys Ala Ile Lys Tyr Tyr
712                 717                 722                 727

cag cat ctg tac agc atc cac ctt gcc gaa cag cct gag gac tgt act     2560
Gln His Leu Tyr Ser Ile His Leu Ala Glu Gln Pro Glu Asp Cys Thr
728                 733                 738                 743

atg cag ctg gct gac cac att aag ttc acg cag agt gct ctg gac tgc     2608
Met Gln Leu Ala Asp His Ile Lys Phe Thr Gln Ser Ala Leu Asp Cys
744                 749                 754                 759

atg agt gtg gag gta gga cgg ctg cgt gcc ttc ttg cag ggt ggg cag     2656
Met Ser Val Glu Val Gly Arg Leu Arg Ala Phe Leu Gln Gly Gly Gln
760                 765                 770                 775

gag gct aca gat att gcc ctc ctg ctc cgg gat ctg gaa act tca tgc     2704
Glu Ala Thr Asp Ile Ala Leu Leu Leu Arg Asp Leu Glu Thr Ser Cys
776                 781                 786                 791

agt gac atc cgc cag ttc tgc aag aag atc cga agg cga atg cca ggg     2752
Ser Asp Ile Arg Gln Phe Cys Lys Lys Ile Arg Arg Arg Met Pro Gly
792                 797                 802                 807

aca gat gct cct ggg atc cca gct gca ctg gcc ttt gga cca cag gta     2800
Thr Asp Ala Pro Gly Ile Pro Ala Ala Leu Ala Phe Gly Pro Gln Val
808                 813                 818                 823

tct gac acg ctc cta gac tgc agg aaa cac ttg acg tgg gtc gtg gct     2848
Ser Asp Thr Leu Leu Asp Cys Arg Lys His Leu Thr Trp Val Val Ala
824                 829                 834                 839
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gtg ctg cag gag gtg gca gct gct gct gcc cag ctc att gcc cca ctg     2896
Val Leu Gln Glu Val Ala Ala Ala Ala Ala Gln Leu Ile Ala Pro Leu
840                 845                 850                 855

gca gag aat gag ggg cta ctt gtg gct gct ctg gag gaa ctg gct ttc     2944
Ala Glu Asn Glu Gly Leu Leu Val Ala Ala Leu Glu Glu Leu Ala Phe
856                 861                 866                 871

aaa gca agc gag cag atc tat ggg acc ccc tcc agc agc ccc tat gag     2992
Lys Ala Ser Glu Gln Ile Tyr Gly Thr Pro Ser Ser Ser Pro Tyr Glu
872                 877                 882                 887

tgt ctg cgc cag tca tgc aac atc ctc atc agt acc atg aac aag ctg     3040
Cys Leu Arg Gln Ser Cys Asn Ile Leu Ile Ser Thr Met Asn Lys Leu
888                 893                 898                 903

gcc aca gcc atg cag gag ggg gag tat gat gca gag cgg ccc ccc agc     3088
Ala Thr Ala Met Gln Glu Gly Glu Tyr Asp Ala Glu Arg Pro Pro Ser
904                 909                 914                 919

aag cct cca ccg gtt gaa ctg cgg gct gct gcc ctt cgt gca gag atc     3136
Lys Pro Pro Pro Val Glu Leu Arg Ala Ala Ala Leu Arg Ala Glu Ile
920                 925                 930                 935

aca gat gct gaa ggc ctg ggt ttg aag ctc gaa gat cga gag aca gtt     3184
Thr Asp Ala Glu Gly Leu Gly Leu Lys Leu Glu Asp Arg Glu Thr Val
936                 941                 946                 951

att aag gag ttg aag aag tca ctc aag att aag gga gag gag cta agt     3232
Ile Lys Glu Leu Lys Lys Ser Leu Lys Ile Lys Gly Glu Glu Leu Ser
952                 957                 962                 967

gag gcc aat gtg cgg ctg agc ctc ctg gag aag aag ttg gac agt gct     3280
Glu Ala Asn Val Arg Leu Ser Leu Leu Glu Lys Lys Leu Asp Ser Ala
968                 973                 978                 983

gcc aag gat gca gat gag cgc atc gag aaa gtc cag act cgg ctg gag     3328
Ala Lys Asp Ala Asp Glu Arg Ile Glu Lys Val Gln Thr Arg Leu Glu
984                 989                 994                 999

gag acc cag gca ctg ctg cga aag aag gag aaa gag ttt gag gag aca     3376
Glu Thr Gln Ala Leu Leu Arg Lys Lys Glu Lys Glu Phe Glu Glu Thr
1000                1005                1010                1015

atg gat gca ctc cag gct gac atc gac cag ctg gag gca gag aag gca     3424
Met Asp Ala Leu Gln Ala Asp Ile Asp Gln Leu Glu Ala Glu Lys Ala
1016                1021                1026                1031

gaa cta aag cag cgt ctg aac agc cag tcc aaa cgc acg att gag gga     3472
Glu Leu Lys Gln Arg Leu Asn Ser Gln Ser Lys Arg Thr Ile Glu Gly
1032                1037                1042                1047

ctc cgg ggc cct cct cct tca ggc att gct act ctg gtc tct ggc att     3520
Leu Arg Gly Pro Pro Pro Ser Gly Ile Ala Thr Leu Val Ser Gly Ile
1048                1053                1058                1063
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 gct ggt gaa gaa cag cag cga gga gcc atc cct ggg cag gct cca ggg     3568
 Ala Gly Glu Glu Gln Gln Arg Gly Ala Ile Pro Gly Gln Ala Pro Gly
1064                1069                1074                1079

 tct gtg cca ggc cca ggg ctg gtg aag gac tca cca ctg ctg ctt cag     3616
 Ser Val Pro Gly Pro Gly Leu Val Lys Asp Ser Pro Leu Leu Leu Gln
1080                1085                1090                1095

 cag atc tct gcc atg agg ctg cac atc tcc cag ctc cag cat gag aac     3664
 Gln Ile Ser Ala Met Arg Leu His Ile Ser Gln Leu Gln His Glu Asn
1096                1101                1106                1111

 agc atc ctc aag gga gcc cag atg aag gca tcc ttg gca tcc ctg ccc     3712
 Ser Ile Leu Lys Gly Ala Gln Met Lys Ala Ser Leu Ala Ser Leu Pro
1112                1117                1122                1127

 cct ctg cat gtt gca aag cta tcc cat gag ggc cct ggc agt gag tta     3760
 Pro Leu His Val Ala Lys Leu Ser His Glu Gly Pro Gly Ser Glu Leu
1128                1133                1138                1143

 cca gct gga gcg ctg tat cgt aag acc agc cag ctg ctg gag aca ttg     3808
 Pro Ala Gly Ala Leu Tyr Arg Lys Thr Ser Gln Leu Leu Glu Thr Leu
1144                1149                1154                1159

 aat caa ttg agc aca cac acg cac gta gta gac atc act cgc acc agc     3856
 Asn Gln Leu Ser Thr His Thr His Val Val Asp Ile Thr Arg Thr Ser
1160                1165                1170                1175

 cct gct gcc aag agc ccg tcg gcc caa ctt atg gag caa gtg gct cag     3904
 Pro Ala Ala Lys Ser Pro Ser Ala Gln Leu Met Glu Gln Val Ala Gln
1176                1181                1186                1191

 ctt aag tcc ctg agt gac acc gtc gag aag ctc aag gat gag gtc ctc     3952
 Leu Lys Ser Leu Ser Asp Thr Val Glu Lys Leu Lys Asp Glu Val Leu
1192                1197                1202                1207

 aag gag aca gta tct cag cgc cct gga gcc aca gta ccc act gac ttt     4000
 Lys Glu Thr Val Ser Gln Arg Pro Gly Ala Thr Val Pro Thr Asp Phe
1208                1213                1218                1223

 gcc acc ttc cct tca tca gcc ttc ctc agg gcc aag gag gag cag cag     4048
 Ala Thr Phe Pro Ser Ser Ala Phe Leu Arg Ala Lys Glu Glu Gln Gln
1224                1229                1234                1239

 gat gac aca gtc tac atg ggc aaa gtg acc ttc tca tgt gcg gct ggt     4096
 Asp Asp Thr Val Tyr Met Gly Lys Val Thr Phe Ser Cys Ala Ala Gly
1240                1245                1250                1255

 ttt gga cag cga cac cgg ctg gtg ctg acc cag gag cag ctg cac cag     4144
 Phe Gly Gln Arg His Arg Leu Val Leu Thr Gln Glu Gln Leu His Gln
1256                1261                1266                1271

 ctt cac agt cgc ctc atc tcc taa gcactccttt cccctgctgt ccccttcgac    4198
 Leu His Ser Arg Leu Ile Ser  *
1272                1277

 cctcagccct ctggtgccgc tctgcccgat gcacagccac ctcagccagc ccccaggtag   4258
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aaacgtgggt taagctcttc ctgccccgtt cagcttcact cccacccttt cagcgtcctg   4318

ccccttcacc ttgacccggg ttcccccact cccattccct ggcctctgcc ataatttgtt   4378

gttcaactgc tccctccttc ctgaggggcc tcagggcttg tgggggggtag gctgagaccc   4438

caccaccaaa ggttaagtga ggtccccttg attgaggact tcacccccttg attaaagcaa   4498

cttctgcttc agtgcaaaaa aaaaaaaaag gggggccctt ttaaaagaac ccttgggggg   4558

cccaaattta accggggatg gcaaggaaaa attttttttct ttatgggggg cctattaaaa   4618

acctacttgg gaattttgga aaggaacctt ttttttgggg gggggacaaa ttggcccacc   4678

ctccctccaa aatttaaagc ttttagggaa aataaaaatt tttaagggga aaaggggggaa   4738

aaacaacctg catttt                                                   4753
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<210> 19
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<212> DNA
<213> Homo sapiens

<220>
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<222> (106)..(693)

<400> 19

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gttgatcgcc tgcggtaccg gcccggaatt cccgggtcga cccacgcgtc cgggctttcg     60

cccgctgctg ccgccgccgc cgccggccgc ggctgcactc ccaag    atg gcg gct     114
                                                     Met Ala Ala
                                                       1

cct ccg ggc gag tac ttc agc gtt ggg agc cag gtg tcg tgc cgg acg      162
Pro Pro Gly Glu Tyr Phe Ser Val Gly Ser Gln Val Ser Cys Arg Thr
  4                   9                  14                  19

tgc cag gag cag cgg ctg cag ggc gag gtg gta gcc ttt gac tac caa      210
Cys Gln Glu Gln Arg Leu Gln Gly Glu Val Val Ala Phe Asp Tyr Gln
 20                  25                  30                  35

tcc aaa atg ctg gct tta aaa tgt ccc tct tcc agt gga aag ccc aac      258
Ser Lys Met Leu Ala Leu Lys Cys Pro Ser Ser Ser Gly Lys Pro Asn
 36                  41                  46                  51

cat gca gac atc ttg ctc ata aac tta cag tat gtt tca gaa gtg gaa      306
His Ala Asp Ile Leu Leu Ile Asn Leu Gln Tyr Val Ser Glu Val Glu
 52                  57                  62                  67

ata att aat gac cga aca gaa acc cct cct ccc cta gct tca ctc aat      354
Ile Ile Asn Asp Arg Thr Glu Thr Pro Pro Pro Leu Ala Ser Leu Asn
 68                  73                  78                  83
```

```
gtt agt aag ctt gcc agc aaa gca cgg aca gag aag gag gag aag ctg      402
Val Ser Lys Leu Ala Ser Lys Ala Arg Thr Glu Lys Glu Glu Lys Leu
 84                  89                  94                  99

agc cag gcc tat gca atc agt gct ggt gtc tct cta gag ggc cag cag      450
Ser Gln Ala Tyr Ala Ile Ser Ala Gly Val Ser Leu Glu Gly Gln Gln
100                 105                 110                 115

ctc ttc cag acc att cac aag acc att aaa gac tgt aaa tgg caa gaa      498
Leu Phe Gln Thr Ile His Lys Thr Ile Lys Asp Cys Lys Trp Gln Glu
116                 121                 126                 131

aaa aac atc gta gtc atg gaa gaa gtt gtt att aca ccc cca tat caa      546
Lys Asn Ile Val Val Met Glu Glu Val Val Ile Thr Pro Pro Tyr Gln
132                 137                 142                 147

gtg gaa aac tgt aaa ggc aaa gag ggg agt gca ctg agc cat gta cgc      594
Val Glu Asn Cys Lys Gly Lys Glu Gly Ser Ala Leu Ser His Val Arg
148                 153                 158                 163

aaa ata gtt gaa aaa cat ttt aga gac gtg gaa agc caa aag ata ctg      642
Lys Ile Val Glu Lys His Phe Arg Asp Val Glu Ser Gln Lys Ile Leu
164                 169                 174                 179

caa cgt tca caa gcc cag caa cca cag aag gag gct gcc ctg tca tcc      690
Gln Arg Ser Gln Ala Gln Gln Pro Gln Lys Glu Ala Ala Leu Ser Ser
180                 185                 190                 195

tga gtccgtacac atgg                                                 707
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196
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6,956,120

<210> 20
<211> 1483
<212> DNA
<213> Homo sapiens

<220>
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<222> (129)..(1175)

<400> 20

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ctttgcaggg gtagaagaag gaagtgtagc gggccctcag attcatcgct accccgaggc    120

taagcgcc atg cct cat att gac aac gat gtg aaa ctg gac ttc aag gat     170
         Met Pro His Ile Asp Asn Asp Val Lys Leu Asp Phe Lys Asp
           1               5                  10

gtc ctt ttg agg ccc aaa cgc agt acc ctt aag tct cga agt gag gtg      218
Val Leu Leu Arg Pro Lys Arg Ser Thr Leu Lys Ser Arg Ser Glu Val
```

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 15                  20                  25                  30

gat ctc aca aga tcc ttt tca ttt cgg aac tca aag cag aca tac tct      266
Asp Leu Thr Arg Ser Phe Ser Phe Arg Asn Ser Lys Gln Thr Tyr Ser
 31                  36                  41                  46

ggg gtt ccc atc att gct gcc aat atg gat act gtg ggc acc ttt gag      314
Gly Val Pro Ile Ile Ala Ala Asn Met Asp Thr Val Gly Thr Phe Glu
 47                  52                  57                  62

atg gcc aag gtt ctc tgt aag ttc tct ctc ttc act gct gtc cat aag      362
Met Ala Lys Val Leu Cys Lys Phe Ser Leu Phe Thr Ala Val His Lys
 63                  68                  73                  78

cac tat agc ctc gtt cag tgg caa gag ttt gct ggc cag aat cct gac      410
His Tyr Ser Leu Val Gln Trp Gln Glu Phe Ala Gly Gln Asn Pro Asp
 79                  84                  89                  94

tgt ctt gag cat ctg gct gcc agc tca ggc aca ggc tct tct gac ttt      458
Cys Leu Glu His Leu Ala Ala Ser Ser Gly Thr Gly Ser Ser Asp Phe
 95                 100                 105                 110

gag cag ctg gaa cag atc ctg gaa gct att ccc cag gtg aag tat ata      506
Glu Gln Leu Glu Gln Ile Leu Glu Ala Ile Pro Gln Val Lys Tyr Ile
111                 116                 121                 126

tgc ctg gat gtg gca aat ggc tac tct gaa cac ttt gtt gaa ttt gta      554
Cys Leu Asp Val Ala Asn Gly Tyr Ser Glu His Phe Val Glu Phe Val
127                 132                 137                 142

aaa gat gta cgg aag cgc ttc ccc cag cac acc atc atg gca ggg aat      602
Lys Asp Val Arg Lys Arg Phe Pro Gln His Thr Ile Met Ala Gly Asn
143                 148                 153                 158

gtg gta aca gga gag atg gta gaa aag ctc atc ctt tct ggg gct gac      650
Val Val Thr Gly Glu Met Val Glu Lys Leu Ile Leu Ser Gly Ala Asp
159                 164                 169                 174

atc atc aaa gtg gga att ggg cca ggc tct gtg tgt act act cgg aag      698
Ile Ile Lys Val Gly Ile Gly Pro Gly Ser Val Cys Thr Thr Arg Lys
175                 180                 185                 190

aaa act gga gtg ggg tat cca cag ctc agc gca gtg atg gag tgt gca      746
Lys Thr Gly Val Gly Tyr Pro Gln Leu Ser Ala Val Met Glu Cys Ala
191                 196                 201                 206

gat gct gct cat ggc ctc aaa ggc cac atc att tca gat gga ggt tgc      794
Asp Ala Ala His Gly Leu Lys Gly His Ile Ile Ser Asp Gly Gly Cys
207                 212                 217                 222

agc tgt cct ggg gat gtg gcc aag gct ttt ggg gca gga gct gac ttc      842
Ser Cys Pro Gly Asp Val Ala Lys Ala Phe Gly Ala Gly Ala Asp Phe
223                 228                 233                 238

gtg atg ctg ggt ggc atg ctg gct ggg cac agt gag tca ggt ggt gag      890
Val Met Leu Gly Gly Met Leu Ala Gly His Ser Glu Ser Gly Gly Glu
239                 244                 249                 254
```

```
ctc atc gag agg gat ggc aag aag tac aag ctc ttc tat gga atg agt      938
Leu Ile Glu Arg Asp Gly Lys Lys Tyr Lys Leu Phe Tyr Gly Met Ser
255                 260                 265                 270

tct gaa atg gcc atg aag aag tat gct ggg ggc gtg gct gag tac aga      986
Ser Glu Met Ala Met Lys Lys Tyr Ala Gly Gly Val Ala Glu Tyr Arg
271                 276                 281                 286

gcc tca gag gga aag aca gtg gaa gtt cct ttt aaa gga gat gtg gaa     1034
Ala Ser Glu Gly Lys Thr Val Glu Val Pro Phe Lys Gly Asp Val Glu
287                 292                 297                 302

cat acc atc cga gac atc cta gga ggg atc cgc tct acg tgt acc tat     1082
His Thr Ile Arg Asp Ile Leu Gly Gly Ile Arg Ser Thr Cys Thr Tyr
303                 308                 313                 318

gtg gga gca gct aag ctc aaa gag ttg agc agg aga act acc ttc atc     1130
Val Gly Ala Ala Lys Leu Lys Glu Leu Ser Arg Arg Thr Thr Phe Ile
319                 324                 329                 334

cga gtc acc cag cag gtg aat cca atc ttc agt gag gcg tgc tag acc     1178
Arg Val Thr Gln Gln Val Asn Pro Ile Phe Ser Glu Ala Cys  *
335                 340                 345

tgagcagttc taccctccca aggcactcac tggggaggaa gcaaggaagc aaacagtctg   1238

agaaaatgat gcaagaaaat caaatgggaa tctggggacc caacacaaca tcctgaagat   1298

tattaaaagg aaaagatgct gattggtaca taaatctttt acatggcctt ggtctagagg   1358

aggcaggctt ttagaatcat gttttgttaa tccgcttcac taaattggac cttcacatat   1418

ctaaaaagct ctgaagtgtt tgtatatttg aaatacctca ataaagagag agctcattga   1478

ctgta                                                               1483
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<210> 21
<211> 1525
<212> DNA
<213> Homo sapiens

<220>
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<222> (129)..(1358)

<400> 21

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ctttgcaggg gtagaagaag gaagtgtagc gggccctcag attcatcgct accccgaggc    120

taagcgcc atg cct cat att gac aac gat gtg aaa ctg gac ttc aag gat     170
         Met Pro His Ile Asp Asn Asp Val Lys Leu Asp Phe Lys Asp
           1               5                  10
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gtc ctt ttg agg ccc aaa cgc agt acc ctt aag tct cga agt gag gtg      218
Val Leu Leu Arg Pro Lys Arg Ser Thr Leu Lys Ser Arg Ser Glu Val
 15                  20                  25                  30

gat ctc aca aga tcc ttt tca ttt cgg aac tca aag cag aca tac tct      266
Asp Leu Thr Arg Ser Phe Ser Phe Arg Asn Ser Lys Gln Thr Tyr Ser
 31                  36                  41                  46

ggg gtt ccc atc att gct gcc aat atg gat act gtg ggc acc ttt gag      314
Gly Val Pro Ile Ile Ala Ala Asn Met Asp Thr Val Gly Thr Phe Glu
 47                  52                  57                  62

atg gcc aag gtt ctc tgt aag ttc tct ctc ttc act gct gtc cat aag      362
Met Ala Lys Val Leu Cys Lys Phe Ser Leu Phe Thr Ala Val His Lys
 63                  68                  73                  78

cac tat agc ctc gtt cag tgg caa gag ttt gct ggc cag aat cct gac      410
His Tyr Ser Leu Val Gln Trp Gln Glu Phe Ala Gly Gln Asn Pro Asp
 79                  84                  89                  94

tgt ctt gag cat ctg gct gcc agc tca ggc aca ggc tct tct gac ttt      458
Cys Leu Glu His Leu Ala Ala Ser Ser Gly Thr Gly Ser Ser Asp Phe
 95                 100                 105                 110

gag cag ctg gaa cag atc ctg gaa gct att ccc cag gtg aag tat ata      506
Glu Gln Leu Glu Gln Ile Leu Glu Ala Ile Pro Gln Val Lys Tyr Ile
111                 116                 121                 126

tgc ctg gat gtg gca aat ggc tac tct gaa cac ttt gtt gaa ttt gta      554
Cys Leu Asp Val Ala Asn Gly Tyr Ser Glu His Phe Val Glu Phe Val
127                 132                 137                 142

aaa gat gta cgg aag cgc ttc ccc cag cac acc atc atg gca ggg aat      602
Lys Asp Val Arg Lys Arg Phe Pro Gln His Thr Ile Met Ala Gly Asn
143                 148                 153                 158

gtg gta aca gga gag atg gta gaa aag ctc atc ctt tct ggg gct gac      650
Val Val Thr Gly Glu Met Val Glu Lys Leu Ile Leu Ser Gly Ala Asp
159                 164                 169                 174

atc atc aaa gtg gga att ggg cca ggc tct gtg tgt act act cgg aag      698
Ile Ile Lys Val Gly Ile Gly Pro Gly Ser Val Cys Thr Thr Arg Lys
175                 180                 185                 190

aaa act gga gtg ggg tat cca cag ctc agc gca gtg atg gag tgt gca      746
Lys Thr Gly Val Gly Tyr Pro Gln Leu Ser Ala Val Met Glu Cys Ala
191                 196                 201                 206

gat gct gct cat ggc ctc aaa ggc cac atc att tca gat gga ggt tgc      794
Asp Ala Ala His Gly Leu Lys Gly His Ile Ile Ser Asp Gly Gly Cys
207                 212                 217                 222

agc tgt cct ggg gat gtg gcc aag gct ttt ggg gca gga gct gac ttc      842
Ser Cys Pro Gly Asp Val Ala Lys Ala Phe Gly Ala Gly Ala Asp Phe
223                 228                 233                 238
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gtg atg ctg ggt ggc atg ctg gct ggg cac agt gag tca ggt ggt gag      890
Val Met Leu Gly Gly Met Leu Ala Gly His Ser Glu Ser Gly Gly Glu
239                 244                 249                 254

ctc atc gag agg gat ggc aag aag tac aag ctc ttc tat gga atg agt      938
Leu Ile Glu Arg Asp Gly Lys Lys Tyr Lys Leu Phe Tyr Gly Met Ser
255                 260                 265                 270

tct gaa atg gcc atg aag aag tat gct ggg ggc gtg gct gag tac agg      986
Ser Glu Met Ala Met Lys Lys Tyr Ala Gly Gly Val Ala Glu Tyr Arg
271                 276                 281                 286

tat gtg tgg agg ccc agg agc tta gta ata gta tgg agg cag aac tca     1034
Tyr Val Trp Arg Pro Arg Ser Leu Val Ile Val Trp Arg Gln Asn Ser
287                 292                 297                 302

tgg ctg ctg aga ggg gga tgg tac agt tct cag aga agc atg gtg aac     1082
Trp Leu Leu Arg Gly Gly Trp Tyr Ser Ser Gln Arg Ser Met Val Asn
303                 308                 313                 318

cgg ggc tca atg cta ggg tct gtg gaa aag tcc ctg ggc tta agg aat     1130
Arg Gly Ser Met Leu Gly Ser Val Glu Lys Ser Leu Gly Leu Arg Asn
319                 324                 329                 334

cca gaa gga gaa gat aat aaa gtt ttt cct act tta aga gcc tca gag     1178
Pro Glu Gly Glu Asp Asn Lys Val Phe Pro Thr Leu Arg Ala Ser Glu
335                 340                 345                 350

gga aag aca gtg gaa gtt cct ttt aaa gga gat gtg gaa cat acc atc     1226
Gly Lys Thr Val Glu Val Pro Phe Lys Gly Asp Val Glu His Thr Ile
351                 356                 361                 366

cga gac atc cta gga ggg atc cgc tct acg tgt acc tat gtg gga gca     1274
Arg Asp Ile Leu Gly Gly Ile Arg Ser Thr Cys Thr Tyr Val Gly Ala
367                 372                 377                 382

gct aag ctc aaa gag ttg agc agg aga act acc ttc atc cga gtc acc     1322
Ala Lys Leu Lys Glu Leu Ser Arg Arg Thr Thr Phe Ile Arg Val Thr
383                 388                 393                 398

cag cag gtg aat cca atc ttc agt gag gcg tgc tag acct gagcagttct     1372
Gln Gln Val Asn Pro Ile Phe Ser Glu Ala Cys  *
399                 404                 409

accctcccaa ggcaccagta ctctaccatg gggcatccca agtggggtcc tcacccatcc   1432

cagctactgc atgctctgta ttactttgtc atttcctgtt gtctcactcc tgaagggctc   1492

ctgcagtaac tctgtacttc tctaatctgc aaa                                1525
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ggagcccatg tggctccgct gccggatggg agtgccccag tgtgctggat gaagctggcg 120

catgcacc atg tca tca tgt gtc tct agc cag ccc agc agc aac cgg gcc 170
Met Ser Ser Cys Val Ser Ser Gln Pro Ser Ser Asn Arg Ala
1 5 10

gcc ccc cag gat gag ctg ggg ggc agg ggc agc agc agc agc gaa agc 218
Ala Pro Gln Asp Glu Leu Gly Gly Arg Gly Ser Ser Ser Ser Glu Ser
15 20 25 30

cag aag ccc tgt gag gcc ctg cgg ggc ctc tca tcc ttg agc atc cac 266
Gln Lys Pro Cys Glu Ala Leu Arg Gly Leu Ser Ser Leu Ser Ile His
31 36 41 46

ctg ggc atg gag tcc ttc att gtg gtc acc gag tgt gag ccg ggc tgt 314
Leu Gly Met Glu Ser Phe Ile Val Val Thr Glu Cys Glu Pro Gly Cys
47 52 57 62

gct gtg gac ctc ggc ttg gcg cgg gac cgg ccc ctg gag gcc gat ggc 362
Ala Val Asp Leu Gly Leu Ala Arg Asp Arg Pro Leu Glu Ala Asp Gly
63 68 73 78

caa gag gtc ccc ctt gac acc tcc ggg tcc cag gcc cgg ccc cac ctc 410
Gln Glu Val Pro Leu Asp Thr Ser Gly Ser Gln Ala Arg Pro His Leu
79 84 89 94

tcc ggt cgc aag ctg tct ctg caa gag cgg tcc cag ggt ggg ctg gca 458
Ser Gly Arg Lys Leu Ser Leu Gln Glu Arg Ser Gln Gly Gly Leu Ala
95 100 105 110

gcc ggt ggc agc ctg gac atg aac gga cgc tgc atc tgc ccg tcc ctg 506
Ala Gly Gly Ser Leu Asp Met Asn Gly Arg Cys Ile Cys Pro Ser Leu
111 116 121 126

ccc tac tca ccc gtc agc tcc ccg cag tcc tcg cct cgg ctg ccc cgg 554
Pro Tyr Ser Pro Val Ser Ser Pro Gln Ser Ser Pro Arg Leu Pro Arg
127 132 137 142

cgg ccg aca gtg gag tct cac cac gtc tcc atc acg ggt atg cag gac 602
Arg Pro Thr Val Glu Ser His His Val Ser Ile Thr Gly Met Gln Asp
143 148 153 158

tgt gtg cag ctg aat cag tat acc ctg aag gat gaa att gga aag ggc 650
Cys Val Gln Leu Asn Gln Tyr Thr Leu Lys Asp Glu Ile Gly Lys Gly
159 164 169 174

tcc tat ggt gtc gtc aag ttg gcc tac aat gaa aat gac aat acc tac 698
Ser Tyr Gly Val Val Lys Leu Ala Tyr Asn Glu Asn Asp Asn Thr Tyr
175 180 185 190

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tat gca atg aag gtg ctg tcc aaa aag aag ctg atc cgg cag gcc gct      746
Tyr Ala Met Lys Val Leu Ser Lys Lys Lys Leu Ile Arg Gln Ala Ala
191                 196                 201                 206

ttt cca cgt cgc cct cca ccc cga ggc acc cgg cca gct cct gga ggc      794
Phe Pro Arg Arg Pro Pro Pro Arg Gly Thr Arg Pro Ala Pro Gly Gly
207                 212                 217                 222

tgc atc cag ccc agg ggc ccc att gag cag gtg tac cag gaa att gcc      842
Cys Ile Gln Pro Arg Gly Pro Ile Glu Gln Val Tyr Gln Glu Ile Ala
223                 228                 233                 238

atc ctc aag aag ctg gac cac ccc aat gtg gtg aag ctg gtg gag gtc      890
Ile Leu Lys Lys Leu Asp His Pro Asn Val Val Lys Leu Val Glu Val
239                 244                 249                 254

ctg gat gac ccc aat gag gac cat ctg tac atg gtg ttc gaa ctg gtc      938
Leu Asp Asp Pro Asn Glu Asp His Leu Tyr Met Val Phe Glu Leu Val
255                 260                 265                 270

aac caa ggg ccc gtg atg gaa gtg ccc acc ctc aaa cca ctc tct gaa      986
Asn Gln Gly Pro Val Met Glu Val Pro Thr Leu Lys Pro Leu Ser Glu
271                 276                 281                 286

gac cag gcc cgt ttc tac ttc cag gat ctg atc aaa ggc atc gag tac     1034
Asp Gln Ala Arg Phe Tyr Phe Gln Asp Leu Ile Lys Gly Ile Glu Tyr
287                 292                 297                 302

tta cac tac cag aag atc atc cac cgt gac atc aaa cct tcc aac ctc     1082
Leu His Tyr Gln Lys Ile Ile His Arg Asp Ile Lys Pro Ser Asn Leu
303                 308                 313                 318

ctg gtc gga gaa gat ggg cac atc aag atc gct gac ttt ggt gtg agc     1130
Leu Val Gly Glu Asp Gly His Ile Lys Ile Ala Asp Phe Gly Val Ser
319                 324                 329                 334

aat gaa ttc aag ggc agt gac gcg ctc ctc tcc aac tac gtg ggc acg     1178
Asn Glu Phe Lys Gly Ser Asp Ala Leu Leu Ser Asn Tyr Val Gly Thr
335                 340                 345                 350

ccc gcc ttc atg gct ccc gag tcg ctc tct gag acc cgc aag ata ttc     1226
Pro Ala Phe Met Ala Pro Glu Ser Leu Ser Glu Thr Arg Lys Ile Phe
351                 356                 361                 366

tct ggg aag gcc ttg gat gtt tgg gcc atg ggt gtg aca cta tac tgc     1274
Ser Gly Lys Ala Leu Asp Val Trp Ala Met Gly Val Thr Leu Tyr Cys
367                 372                 377                 382

ttt gtc ttt ggc cag tgc cca ttc atg gac gag cgg atc atg tgt tta     1322
Phe Val Phe Gly Gln Cys Pro Phe Met Asp Glu Arg Ile Met Cys Leu
383                 388                 393                 398

cac agt aag atc aag agt cag gcc ctg gaa ttt cca gac cag ccc gac     1370
His Ser Lys Ile Lys Ser Gln Ala Leu Glu Phe Pro Asp Gln Pro Asp
399                 404                 409                 414
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ata gct gag gac ttg aag gac ctg atc acc cgt atg ctg gac aag aac     1418
Ile Ala Glu Asp Leu Lys Asp Leu Ile Thr Arg Met Leu Asp Lys Asn
415                 420                 425                 430

ccc gag tcg agg atc gtg gtg ccg gaa atc aag ctg cac ccc tgg gtc     1466
Pro Glu Ser Arg Ile Val Val Pro Glu Ile Lys Leu His Pro Trp Val
431                 436                 441                 446

acg agg cat ggg gcg gag ccg ttg ccg tcg gag gat gag aac tgc acg     1514
Thr Arg His Gly Ala Glu Pro Leu Pro Ser Glu Asp Glu Asn Cys Thr
447                 452                 457                 462

ctg gtc gaa gtg act gaa gag gag gtc gag aac tca gtc aaa cac att     1562
Leu Val Glu Val Thr Glu Glu Glu Val Glu Asn Ser Val Lys His Ile
463                 468                 473                 478

ccc agc ttg gca acc gtg atc ctg gtg aag acc atg ata cgt aaa cgc     1610
Pro Ser Leu Ala Thr Val Ile Leu Val Lys Thr Met Ile Arg Lys Arg
479                 484                 489                 494

tcc ttt ggg aac cca ttc gag ggc agc cgg cgg gag gaa cgc tca ctg     1658
Ser Phe Gly Asn Pro Phe Glu Gly Ser Arg Arg Glu Glu Arg Ser Leu
495                 500                 505                 510

tca gcg cct gga aac ttg ctc acc aaa aaa cca acc agg gaa tgt gag     1706
Ser Ala Pro Gly Asn Leu Leu Thr Lys Lys Pro Thr Arg Glu Cys Glu
511                 516                 521                 526

tcc ctg tct gag ctc aag gaa gca agg cag cga aga caa cct cca ggg     1754
Ser Leu Ser Glu Leu Lys Glu Ala Arg Gln Arg Arg Gln Pro Pro Gly
527                 532                 537                 542

cac cga ccc gcc ccc cgt ggg gga gga gga agt gct ctt gtg aga ggc     1802
His Arg Pro Ala Pro Arg Gly Gly Gly Gly Ser Ala Leu Val Arg Gly
543                 548                 553                 558

agt ccc tgc gtg gaa agt tgc tgg gcc ccc gcc ccc ggc tcc ccc gca     1850
Ser Pro Cys Val Glu Ser Cys Trp Ala Pro Ala Pro Gly Ser Pro Ala
559                 564                 569                 574

cgc atg cat cca ctg cgg ccg gag gag gcc atg gag ccc gag tag ctg     1898
Arg Met His Pro Leu Arg Pro Glu Glu Ala Met Glu Pro Glu  *
575                 580                 585

cctggatcgc tcgacctcgc atggccgccg cgtcgcctct ggggggctgc tgcaccgcgt   1958

ttccatagca gcatgtccta cggaaaccca gcacgtgtgt agagcctcga tcgtcatctc   2018

tggttatttg ttttttcctt tgttgtttta aaggggac                          2056
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ggagcccatg tggctccgct gccggatggg agtgccccag tgtgctggat gaagctggcg 120

catgcacc atg tca tca tgt gtc tct agc cag ccc agc agc aac cgg gcc 170
Met Ser Ser Cys Val Ser Ser Gln Pro Ser Ser Asn Arg Ala
1 5 10

gcc ccc cag gat gag ctg ggg ggc agg ggc agc agc agc agc gaa agc 218
Ala Pro Gln Asp Glu Leu Gly Gly Arg Gly Ser Ser Ser Ser Glu Ser
15 20 25 30

cag aag ccc tgt gag gcc ctg cgg ggc ctc tca tcc ttg agc atc cac 266
Gln Lys Pro Cys Glu Ala Leu Arg Gly Leu Ser Ser Leu Ser Ile His
31 36 41 46

ctg ggc atg gag tcc ttc att gtg gtc acc gag tgt gag ccg ggc tgt 314
Leu Gly Met Glu Ser Phe Ile Val Val Thr Glu Cys Glu Pro Gly Cys
47 52 57 62

gct gtg gac ctc ggc ttg gcg cgg gac cgg ccc ctg gag gcc gat ggc 362
Ala Val Asp Leu Gly Leu Ala Arg Asp Arg Pro Leu Glu Ala Asp Gly
63 68 73 78

caa gag gtc ccc ctt gac acc tcc ggg tcc cag gcc cgg ccc cac ctc 410
Gln Glu Val Pro Leu Asp Thr Ser Gly Ser Gln Ala Arg Pro His Leu
79 84 89 94

tcc ggt cgc aag ctg tct ctg caa gag cgg tcc cag ggt ggg ctg gca 458
Ser Gly Arg Lys Leu Ser Leu Gln Glu Arg Ser Gln Gly Gly Leu Ala
95 100 105 110

gcc ggt ggc agc ctg gac atg aac gga cgc tgc atc tgc ccg tcc ctg 506
Ala Gly Gly Ser Leu Asp Met Asn Gly Arg Cys Ile Cys Pro Ser Leu
111 116 121 126

ccc tac tca ccc gtc agc tcc ccg cag tcc tcg cct cgg ctg ccc cgg 554
Pro Tyr Ser Pro Val Ser Ser Pro Gln Ser Ser Pro Arg Leu Pro Arg
127 132 137 142

cgg ccg aca gtg gag tct cac cac gtc tcc atc acg ggt atg cag gac 602
Arg Pro Thr Val Glu Ser His His Val Ser Ile Thr Gly Met Gln Asp
143 148 153 158

tgt gtg cag ctg aat cag tat acc ctg aag gat gaa att gga aag ggc 650
Cys Val Gln Leu Asn Gln Tyr Thr Leu Lys Asp Glu Ile Gly Lys Gly
159 164 169 174

tcc tat ggt gtc gtc aag ttg gcc tac aat gaa aat gac aat acc tac 698
Ser Tyr Gly Val Val Lys Leu Ala Tyr Asn Glu Asn Asp Asn Thr Tyr
175 180 185 190

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tat gca atg aag gtg ctg tcc aaa aag aag ctg atc cgg cag gcc gct      746
Tyr Ala Met Lys Val Leu Ser Lys Lys Lys Leu Ile Arg Gln Ala Ala
191                 196                 201                 206

ttt cca cgt cgc cct cca ccc cga ggc acc cgg cca gct cct gga ggc      794
Phe Pro Arg Arg Pro Pro Pro Arg Gly Thr Arg Pro Ala Pro Gly Gly
207                 212                 217                 222

tgc atc cag ccc agg ggc ccc att gag cag gtg tac cag gaa att gcc      842
Cys Ile Gln Pro Arg Gly Pro Ile Glu Gln Val Tyr Gln Glu Ile Ala
223                 228                 233                 238

atc ctc aag aag ctg gac cac ccc aat gtg gtg aag ctg gtg gag gtc      890
Ile Leu Lys Lys Leu Asp His Pro Asn Val Val Lys Leu Val Glu Val
239                 244                 249                 254

ctg gat gac ccc aat gag gac cat ctg tac atg gtg ttc gaa ctg gtc      938
Leu Asp Asp Pro Asn Glu Asp His Leu Tyr Met Val Phe Glu Leu Val
255                 260                 265                 270

aac caa ggg ccc gtg atg gaa gtg ccc acc ctc aaa cca ctc tct gaa      986
Asn Gln Gly Pro Val Met Glu Val Pro Thr Leu Lys Pro Leu Ser Glu
271                 276                 281                 286

gac cag gcc cgt ttc tac ttc cag gat ctg atc aaa ggc atc gag tac     1034
Asp Gln Ala Arg Phe Tyr Phe Gln Asp Leu Ile Lys Gly Ile Glu Tyr
287                 292                 297                 302

tta cac tac cag aag atc atc cac cgt gac atc aaa cct tcc aac ctc     1082
Leu His Tyr Gln Lys Ile Ile His Arg Asp Ile Lys Pro Ser Asn Leu
303                 308                 313                 318

ctg gtc gga gaa gat ggg cac atc aag atc gct gac ttt ggt gtg agc     1130
Leu Val Gly Glu Asp Gly His Ile Lys Ile Ala Asp Phe Gly Val Ser
319                 324                 329                 334

aat gaa ttc aag ggc agt gac gcg ctc ctc tcc aac tac gtg ggc acg     1178
Asn Glu Phe Lys Gly Ser Asp Ala Leu Leu Ser Asn Tyr Val Gly Thr
335                 340                 345                 350

ccc gcc ttc atg gct ccc gag tcg ctc tct gag acc cgc aag ata ttc     1226
Pro Ala Phe Met Ala Pro Glu Ser Leu Ser Glu Thr Arg Lys Ile Phe
351                 356                 361                 366

tct ggg aag gcc ttg gat gtt tgg gcc atg ggt gtg aca cta tac tgc     1274
Ser Gly Lys Ala Leu Asp Val Trp Ala Met Gly Val Thr Leu Tyr Cys
367                 372                 377                 382

ttt gtc ttt ggc cag tgc cca ttc atg gac gag cgg atc atg tgt tta     1322
Phe Val Phe Gly Gln Cys Pro Phe Met Asp Glu Arg Ile Met Cys Leu
383                 388                 393                 398

cac agt aag atc aag agt cag gcc ctg gaa ttt cca gac cag ccc gac     1370
His Ser Lys Ile Lys Ser Gln Ala Leu Glu Phe Pro Asp Gln Pro Asp
399                 404                 409                 414
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ata gct gag gac ttg aag gac ctg atc acc cgt atg ctg gac aag aac     1418
Ile Ala Glu Asp Leu Lys Asp Leu Ile Thr Arg Met Leu Asp Lys Asn
415                 420                 425                 430

ccc gag tcg agg atc gtg gtg ccg gaa atc aag atc ctg gtg aag acc     1466
Pro Glu Ser Arg Ile Val Val Pro Glu Ile Lys Ile Leu Val Lys Thr
431                 436                 441                 446

atg ata cgt aaa cgc tcc ttt ggg aac cca ttc gag ggc agc cgg cgg     1514
Met Ile Arg Lys Arg Ser Phe Gly Asn Pro Phe Glu Gly Ser Arg Arg
447                 452                 457                 462

gag gaa cgc tca ctg tca gcg cct gga aac ttg ctc acc aaa aaa cca     1562
Glu Glu Arg Ser Leu Ser Ala Pro Gly Asn Leu Leu Thr Lys Lys Pro
463                 468                 473                 478

acc agg gaa tgt gag tcc ctg tct gag ctc aag gaa gca agg cag cga     1610
Thr Arg Glu Cys Glu Ser Leu Ser Glu Leu Lys Glu Ala Arg Gln Arg
479                 484                 489                 494

aga caa cct cca ggg cac cga ccc gcc ccc cgt ggg gga gga gga agt     1658
Arg Gln Pro Pro Gly His Arg Pro Ala Pro Arg Gly Gly Gly Gly Ser
495                 500                 505                 510

gct ctt gtg aga ggc agt ccc tgc gtg gaa agt tgc tgg gcc ccc gcc     1706
Ala Leu Val Arg Gly Ser Pro Cys Val Glu Ser Cys Trp Ala Pro Ala
511                 516                 521                 526

ccc ggc tcc ccc gca cgc atg cat cca ctg cgg ccg gag gag gcc atg     1754
Pro Gly Ser Pro Ala Arg Met His Pro Leu Arg Pro Glu Glu Ala Met
527                 532                 537                 542

gag ccc gag tag ctg cctggatcgc tcgacctcgc atggccgccg cgtcgcctct     1809
Glu Pro Glu  *
543

gggggggctgc tgcaccgcgt ttccatagca gcatgtccta cggaaaccca gcacgtgtgt   1869

agagcctcga tcgtcatctc tggttatttg ttttttcctt tgttgtttta aaggggac     1927
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<220>
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<220>
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<222> (1)...(1661)
<223> n = a,t,c or g

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acccacgcgt ccgcgcgagg tgaggggcgc gaggttccca gcaggatgcc ccggctctgc 120

aggaagctga agtgagaggc ccggagaggg cccagcccgc ccggggcagg atg acc 176
Met Thr
1

aag gcc cgg ctg ttc cgg ctg tgg ctg gtg ctg ggg tcg gtg ttc atg 224
Lys Ala Arg Leu Phe Arg Leu Trp Leu Val Leu Gly Ser Val Phe Met
3 8 13 18

atc ctg ctg atc atc gtg tac tgg gac agc gca ggc gcc gcg cac ttc 272
Ile Leu Leu Ile Ile Val Tyr Trp Asp Ser Ala Gly Ala Ala His Phe
19 24 29 34

tac ttg cac acg tcc ttc tct agg ccg cac acg ggg ccg ccg ctg ccc 320
Tyr Leu His Thr Ser Phe Ser Arg Pro His Thr Gly Pro Pro Leu Pro
35 40 45 50

acg ccc ggg ccg gac agg gac agg gag ctc acg gcc gac tcc gat gtc 368
Thr Pro Gly Pro Asp Arg Asp Arg Glu Leu Thr Ala Asp Ser Asp Val
51 56 61 66

gac gag ttt ctg gac aag ttt ctc agt gct ggc gtg aag cag agc gac 416
Asp Glu Phe Leu Asp Lys Phe Leu Ser Ala Gly Val Lys Gln Ser Asp
67 72 77 82

ctt ccc aga aag gag acg gag cag ccg cct gcg ccg ggg agc atg gag 464
Leu Pro Arg Lys Glu Thr Glu Gln Pro Pro Ala Pro Gly Ser Met Glu
83 88 93 98

gag agc gtg aga ggc tac gac tgg tcc ccg cgc gac gcc cgg cgc agc 512
Glu Ser Val Arg Gly Tyr Asp Trp Ser Pro Arg Asp Ala Arg Arg Ser
99 104 109 114

cca gac cag ggc cgg cag cag gcg gag cgg agg agc gtg ctg cgg ggc 560
Pro Asp Gln Gly Arg Gln Gln Ala Glu Arg Arg Ser Val Leu Arg Gly
115 120 125 130

ttc tgc gcc aac tcc agc ctg gcc ttc ccc acc aag gag cgc cca ttc 608
Phe Cys Ala Asn Ser Ser Leu Ala Phe Pro Thr Lys Glu Arg Pro Phe
131 136 141 146

gac gac atc ccc aac tcg gag ctg agc cac ctg atc gtg gac gac cgg 656
Asp Asp Ile Pro Asn Ser Glu Leu Ser His Leu Ile Val Asp Asp Arg
147 152 157 162

cac ggg gcc atc tac tgc tac gtg ccc aag gtg gcc tgc acc aac tgg 704
His Gly Ala Ile Tyr Cys Tyr Val Pro Lys Val Ala Cys Thr Asn Trp
163 168 173 178

aag cgc gtg atg atc gtg ctg agc gga agc ctg ctg cac cgc ggt gcg 752
Lys Arg Val Met Ile Val Leu Ser Gly Ser Leu Leu His Arg Gly Ala
179 184 189 194

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ccc tac cgc gac ccg ctg cgc atc ccg cgc gag cac gtg cac aac gcc      800
Pro Tyr Arg Asp Pro Leu Arg Ile Pro Arg Glu His Val His Asn Ala
195                 200                 205                 210

agc gcg cac ctg acc ttc aac aag ttc tgg cgc cgc tac ggg aag ctc      848
Ser Ala His Leu Thr Phe Asn Lys Phe Trp Arg Arg Tyr Gly Lys Leu
211                 216                 221                 226

tcc cgc cac ctc atg aag gtc aag ctc aag aag tac acc aag ttc ctc      896
Ser Arg His Leu Met Lys Val Lys Leu Lys Lys Tyr Thr Lys Phe Leu
227                 232                 237                 242

ttc gtg cgc gac ccc ttc gtg cgc ctg atc tcc gcc ttc cgc agc aag      944
Phe Val Arg Asp Pro Phe Val Arg Leu Ile Ser Ala Phe Arg Ser Lys
243                 248                 253                 258

ttc gag ctg gag aac gag gag ttc tac cgc aag ttc gcc gtg ccc atg      992
Phe Glu Leu Glu Asn Glu Glu Phe Tyr Arg Lys Phe Ala Val Pro Met
259                 264                 269                 274

ctg cgg ctg tac gcc aac cac acc agc ctg ccc gcc tcg gcg cgc gag     1040
Leu Arg Leu Tyr Ala Asn His Thr Ser Leu Pro Ala Ser Ala Arg Glu
275                 280                 285                 290

gcc ttc cgc gct ggc ctc aag gtg tcc ttc gcc aac ttc atc cag tac     1088
Ala Phe Arg Ala Gly Leu Lys Val Ser Phe Ala Asn Phe Ile Gln Tyr
291                 296                 301                 306

ctg ctg gac ccg cac acg gag aag ctg gcg ccc ttc aac gag cac tgg     1136
Leu Leu Asp Pro His Thr Glu Lys Leu Ala Pro Phe Asn Glu His Trp
307                 312                 317                 322

cgg cag gtg tac cgc ctc tgc cac ccg tgc cag atc gac tac gac ttc     1184
Arg Gln Val Tyr Arg Leu Cys His Pro Cys Gln Ile Asp Tyr Asp Phe
323                 328                 333                 338

gtg ggg aag ctg gag act ctg gac gag gac gcc gcg cag ctg ctg cag     1232
Val Gly Lys Leu Glu Thr Leu Asp Glu Asp Ala Ala Gln Leu Leu Gln
339                 344                 349                 354

cta ctc cag gtg gac cgg cag ctc cgc ttc ccc ccg agc tac cgg aac     1280
Leu Leu Gln Val Asp Arg Gln Leu Arg Phe Pro Pro Ser Tyr Arg Asn
355                 360                 365                 370

agg acc gcc agc agc tgg gag gag gac tgg ttc gcc aag atc ccc ctg     1328
Arg Thr Ala Ser Ser Trp Glu Glu Asp Trp Phe Ala Lys Ile Pro Leu
371                 376                 381                 386

gcc tgg agg cag cag ctg tat aaa ctc tac gag gcc gac ttt gtt ctc     1376
Ala Trp Arg Gln Gln Leu Tyr Lys Leu Tyr Glu Ala Asp Phe Val Leu
387                 392                 397                 402

ttc ggc tac ccc aag ccc gaa aac ctc ctc cga gac tga aagctttcgc      1425
Phe Gly Tyr Pro Lys Pro Glu Asn Leu Leu Arg Asp  *
403                 408                 413

gttgcttttt ctcgcgtgcc tggaacctga cgcacgcgca ctccagtttt tttatgacct   1485
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acgattttgc aatctgggtc gacgcggccg cgaattccag atctatgaat cgtagatact   1545

gaaaaacccc gcaagttcac ttcaactgtg catcgtgcac catctcaatt tctttcattt   1605

atacatcgtt ttgccttctt ttatgtaact atactcctct aagtttcaat cttggg       1661
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<210> 25
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tgagtggaac gtctcttggg gtgtcggaat tcaaaacgga cctggagg atg ttg atc     117
                                                      Met Leu Ile
                                                        1

tcc aag aac atg ccc tgg cgg cgg ctg cag ggc att tcc ttc ggg atg      165
Ser Lys Asn Met Pro Trp Arg Arg Leu Gln Gly Ile Ser Phe Gly Met
  4                   9                  14                  19

tat tcg gct gaa gag ctc aag aaa tta agt gtt aaa tcc att acg aac      213
Tyr Ser Ala Glu Glu Leu Lys Lys Leu Ser Val Lys Ser Ile Thr Asn
 20                  25                  30                  35

cct cga tac ctg gac agc ctg ggg aac cca tcg gca aac ggc ctg tac      261
Pro Arg Tyr Leu Asp Ser Leu Gly Asn Pro Ser Ala Asn Gly Leu Tyr
 36                  41                  46                  51

gat tta gct ttg ggc cct gca gat tcc aaa gag gtg tgc tcc acc tgc      309
Asp Leu Ala Leu Gly Pro Ala Asp Ser Lys Glu Val Cys Ser Thr Cys
 52                  57                  62                  67

gtg cag gac ttc agc aac tgt tct ggg cac ctg ggc cac att gag ctc      357
Val Gln Asp Phe Ser Asn Cys Ser Gly His Leu Gly His Ile Glu Leu
 68                  73                  78                  83

cca ctc aca gtg tat aac cct ctc ctc ttc gat aag ctg tac ctg ctg      405
Pro Leu Thr Val Tyr Asn Pro Leu Leu Phe Asp Lys Leu Tyr Leu Leu
 84                  89                  94                  99

ctt cgg ggc tct tgt tta aac tgc cac atg ctg act tgt ccc cgg gcc      453
Leu Arg Gly Ser Cys Leu Asn Cys His Met Leu Thr Cys Pro Arg Ala
100                 105                 110                 115

gtg att cac ctc tta ctc tgc cag ctg agg gtt ctg gaa gtc ggg gcc      501
Val Ile His Leu Leu Leu Cys Gln Leu Arg Val Leu Glu Val Gly Ala
116                 121                 126                 131
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cta caa gca gtc tac gag ctt gag aga att ctg aac agg ttt ctg gaa      549
Leu Gln Ala Val Tyr Glu Leu Glu Arg Ile Leu Asn Arg Phe Leu Glu
132                 137                 142                 147

gaa aat gcc gat ccc tct gcc tct gaa att cgg gag gaa tta gaa caa      597
Glu Asn Ala Asp Pro Ser Ala Ser Glu Ile Arg Glu Glu Leu Glu Gln
148                 153                 158                 163

tac aca act gaa att gtg cag aac aac ctc ctg ggg tcc cag ggc gca      645
Tyr Thr Thr Glu Ile Val Gln Asn Asn Leu Leu Gly Ser Gln Gly Ala
164                 169                 174                 179

cat gta aag aac gtg tgt gag agc aag agc aag ctc att gct ctc ttc      693
His Val Lys Asn Val Cys Glu Ser Lys Ser Lys Leu Ile Ala Leu Phe
180                 185                 190                 195

tgg aag gca cat atg aat gct aag cgc tgt ccc cac tgc aag acc ggg      741
Trp Lys Ala His Met Asn Ala Lys Arg Cys Pro His Cys Lys Thr Gly
196                 201                 206                 211

cga tcc gtt gtc cga aag gaa cac aac agc aag ttg act atc aca ttt      789
Arg Ser Val Val Arg Lys Glu His Asn Ser Lys Leu Thr Ile Thr Phe
212                 217                 222                 227

cca gcc atg gtg cac agg aca gct ggc cag aag gac tct gag ccc ctg      837
Pro Ala Met Val His Arg Thr Ala Gly Gln Lys Asp Ser Glu Pro Leu
228                 233                 238                 243

gga att gag gaa gct cag ata gga aaa cga gga tac tta aca ccc acc      885
Gly Ile Glu Glu Ala Gln Ile Gly Lys Arg Gly Tyr Leu Thr Pro Thr
244                 249                 254                 259

agt gcc cgc gaa cac ctt tct gcc ctg tgg aag aat gaa gga ttc ttt      933
Ser Ala Arg Glu His Leu Ser Ala Leu Trp Lys Asn Glu Gly Phe Phe
260                 265                 270                 275

ctg aac tac ctt ttt tcg gga atg gat gat gat ggt atg gaa tcc aga      981
Leu Asn Tyr Leu Phe Ser Gly Met Asp Asp Asp Gly Met Glu Ser Arg
276                 281                 286                 291

ttc aat ccc agt gtg ttc ttt cta gat ttc ttg gtg gtg ccg ccc tca     1029
Phe Asn Pro Ser Val Phe Phe Leu Asp Phe Leu Val Val Pro Pro Ser
292                 297                 302                 307

agg tat cgc cca gtc agt cgc cta gga gac cag atg ttt act aat ggc     1077
Arg Tyr Arg Pro Val Ser Arg Leu Gly Asp Gln Met Phe Thr Asn Gly
308                 313                 318                 323

cag acg gtg aac ttg cag gct gtc atg aag gat gta gtt ctg att cga     1125
Gln Thr Val Asn Leu Gln Ala Val Met Lys Asp Val Val Leu Ile Arg
324                 329                 334                 339

aaa ctt ctg gca ttg atg gcc caa gaa cag aag ttg cca gag gaa gtg     1173
Lys Leu Leu Ala Leu Met Ala Gln Glu Gln Lys Leu Pro Glu Glu Val
340                 345                 350                 355
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gcc aca ccc act aca gat gag gaa aaa gac tct ttg att gct att gac     1221
Ala Thr Pro Thr Thr Asp Glu Glu Lys Asp Ser Leu Ile Ala Ile Asp
356                 361                 366                 371

cga tcc ttt ttg agt aca ctt cca ggc cag tcc ctc ata gac aaa ctt     1269
Arg Ser Phe Leu Ser Thr Leu Pro Gly Gln Ser Leu Ile Asp Lys Leu
372                 377                 382                 387

tac aac att tgg att cgc ctt cag agc cac gtc aat att gtg ttt gat     1317
Tyr Asn Ile Trp Ile Arg Leu Gln Ser His Val Asn Ile Val Phe Asp
388                 393                 398                 403

agc gag atg gac aaa cta atg atg gac aag tac cca ggc att agg cag     1365
Ser Glu Met Asp Lys Leu Met Met Asp Lys Tyr Pro Gly Ile Arg Gln
404                 409                 414                 419

atc ctg gag aag aaa gaa ggc ctg ttc cga aaa cac atg atg gga aag     1413
Ile Leu Glu Lys Lys Glu Gly Leu Phe Arg Lys His Met Met Gly Lys
420                 425                 430                 435

cga gtg gac tac gct gcg cgc tca gtc atc tgc cca gac atg tac atc     1461
Arg Val Asp Tyr Ala Ala Arg Ser Val Ile Cys Pro Asp Met Tyr Ile
436                 441                 446                 451

aac acc aac gaa att gga att ccc atg gtg ttt gcc aca aaa ctg acc     1509
Asn Thr Asn Glu Ile Gly Ile Pro Met Val Phe Ala Thr Lys Leu Thr
452                 457                 462                 467

tac cca cag cca gtt acc cca tgg aat gtt cag gaa ctt agg caa gcg     1557
Tyr Pro Gln Pro Val Thr Pro Trp Asn Val Gln Glu Leu Arg Gln Ala
468                 473                 478                 483

gtc atc aac ggc cct aat gtg cac cca gga gcc tcc atg gtc atc aat     1605
Val Ile Asn Gly Pro Asn Val His Pro Gly Ala Ser Met Val Ile Asn
484                 489                 494                 499

gag gac ggc agc cgc aca gcc ctg agc gct gtg gac atg acc cag cga     1653
Glu Asp Gly Ser Arg Thr Ala Leu Ser Ala Val Asp Met Thr Gln Arg
500                 505                 510                 515

gag gcc gtg gcc aag cag ctt ctg acc cca gcc acg ggg gca cct aag     1701
Glu Ala Val Ala Lys Gln Leu Leu Thr Pro Ala Thr Gly Ala Pro Lys
516                 521                 526                 531

ccc cag ggg aca aaa att gtg tgc cgg cat gtg aag aat ggg gac att     1749
Pro Gln Gly Thr Lys Ile Val Cys Arg His Val Lys Asn Gly Asp Ile
532                 537                 542                 547

ctg cta ctg aac cga cag ccc aca ctg cac aga ccc tcc atc cag gcc     1797
Leu Leu Leu Asn Arg Gln Pro Thr Leu His Arg Pro Ser Ile Gln Ala
548                 553                 558                 563

cac cgt gcc cgc atc ctg cct gaa gag aaa gtg ctg cgg ctc cac tat     1845
His Arg Ala Arg Ile Leu Pro Glu Glu Lys Val Leu Arg Leu His Tyr
564                 569                 574                 579

gcc aac tgc aag gcc tat aat gcc gac ttt gat gga gac gag atg aat     1893
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Ala Asn Cys Lys Ala Tyr Asn Ala Asp Phe Asp Gly Asp Glu Met Asn
580                 585                 590                 595

gcc cat ttc ccc cag agt gag ctg ggc cgg gcc gag gcc tac gtc ctg     1941
Ala His Phe Pro Gln Ser Glu Leu Gly Arg Ala Glu Ala Tyr Val Leu
596                 601                 606                 611

gcc tgc act gat cag cag tac ctt gtt ccc aag gat ggc caa cca ttg     1989
Ala Cys Thr Asp Gln Gln Tyr Leu Val Pro Lys Asp Gly Gln Pro Leu
612                 617                 622                 627

gcg gga ctg atc cag gat cac atg gtt tca ggg gca agc atg act act     2037
Ala Gly Leu Ile Gln Asp His Met Val Ser Gly Ala Ser Met Thr Thr
628                 633                 638                 643

cgg ggt tgc ttt ttc acc cgg gag cac tat atg gag ctg gtg tac cga     2085
Arg Gly Cys Phe Phe Thr Arg Glu His Tyr Met Glu Leu Val Tyr Arg
644                 649                 654                 659

gga ctc acg gac aaa gtg ggg cgc gtg aag ctc ctt tct cct tcc atc     2133
Gly Leu Thr Asp Lys Val Gly Arg Val Lys Leu Leu Ser Pro Ser Ile
660                 665                 670                 675

ctg aag ccc ttt ccg ctg tgg aca gga aaa cag gtt gtg tca acg ctg     2181
Leu Lys Pro Phe Pro Leu Trp Thr Gly Lys Gln Val Val Ser Thr Leu
676                 681                 686                 691

ctc ata aat ata atc cca gag gac cac atc cca ctg aac tta tct gga     2229
Leu Ile Asn Ile Ile Pro Glu Asp His Ile Pro Leu Asn Leu Ser Gly
692                 697                 702                 707

aag gcg aaa atc act ggg aaa gcc tgg gtg aag gaa act cct cga tcc     2277
Lys Ala Lys Ile Thr Gly Lys Ala Trp Val Lys Glu Thr Pro Arg Ser
708                 713                 718                 723

gtt cct ggc ttt aac cct gac tcg atg tgc gag tcc cag gtg atc atc     2325
Val Pro Gly Phe Asn Pro Asp Ser Met Cys Glu Ser Gln Val Ile Ile
724                 729                 734                 739

agg gaa ggg gag ctg ctc tgc gga gtg ctg gac aag gcg cac tat ggg     2373
Arg Glu Gly Glu Leu Leu Cys Gly Val Leu Asp Lys Ala His Tyr Gly
740                 745                 750                 755

agc tcc gcc tac ggc ctg gtc cac tgc tgc tat gag atc tat gga ggc     2421
Ser Ser Ala Tyr Gly Leu Val His Cys Cys Tyr Glu Ile Tyr Gly Gly
756                 761                 766                 771

gag acc agc ggc aag gtt cta acc tgc ctg gcc cgc ctc ttc acc gcc     2469
Glu Thr Ser Gly Lys Val Leu Thr Cys Leu Ala Arg Leu Phe Thr Ala
772                 777                 782                 787

tac ctg cag ctc tac aga ggc ttc acc ttg ggc gtg gaa gac att ttg     2517
Tyr Leu Gln Leu Tyr Arg Gly Phe Thr Leu Gly Val Glu Asp Ile Leu
788                 793                 798                 803

gtg aag cca aag gca gat gtc aag agg caa cgt atc att gaa gaa tcc     2565
Val Lys Pro Lys Ala Asp Val Lys Arg Gln Arg Ile Ile Glu Glu Ser
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804                 809                 814                 819

acc cac tgc ggg ccc cag gct gtc agg gct gca tta aac ctg cca gaa     2613
Thr His Cys Gly Pro Gln Ala Val Arg Ala Ala Leu Asn Leu Pro Glu
820                 825                 830                 835

gcc gca tca tat gat gag gtc cga gga aaa tgg cag gat gcc cat ctg     2661
Ala Ala Ser Tyr Asp Glu Val Arg Gly Lys Trp Gln Asp Ala His Leu
836                 841                 846                 851

ggc aag gac cag agg gat ttt aac atg att gat ctg aag ttc aag gag     2709
Gly Lys Asp Gln Arg Asp Phe Asn Met Ile Asp Leu Lys Phe Lys Glu
852                 857                 862                 867

gaa gtg aac cat tac agc aat gag att aac aag gca tgc atg cct ttt     2757
Glu Val Asn His Tyr Ser Asn Glu Ile Asn Lys Ala Cys Met Pro Phe
868                 873                 878                 883

ggc cta cac aga cag ttc cca gag aac acg ctg cag ctg atg gtg cag     2805
Gly Leu His Arg Gln Phe Pro Glu Asn Thr Leu Gln Leu Met Val Gln
884                 889                 894                 899

tcg gga gcc aaa ggt tca act gtg aac acg atg cag atc tcg tgc ctg     2853
Ser Gly Ala Lys Gly Ser Thr Val Asn Thr Met Gln Ile Ser Cys Leu
900                 905                 910                 915

ctg ggc cag att gaa ctg gaa ggt cgg agc acc ccg ctg atg gcg tct     2901
Leu Gly Gln Ile Glu Leu Glu Gly Arg Ser Thr Pro Leu Met Ala Ser
916                 921                 926                 931

ggc aag tca ctg ccc tgc ttt gag cct tat gag ttc acc ccc agg gct     2949
Gly Lys Ser Leu Pro Cys Phe Glu Pro Tyr Glu Phe Thr Pro Arg Ala
932                 937                 942                 947

ggt ggc ttt gtc act ggc agg ttc ctc acc ggc atc aaa cct cct gag     2997
Gly Gly Phe Val Thr Gly Arg Phe Leu Thr Gly Ile Lys Pro Pro Glu
948                 953                 958                 963

ttc ttc ttc cac tgc atg gca gga cga gag ggc ctg gtg gac act gct     3045
Phe Phe Phe His Cys Met Ala Gly Arg Glu Gly Leu Val Asp Thr Ala
964                 969                 974                 979

gtg aaa acc agc cgc tca ggc tat ctc caa agg tgc atc atc aag cac     3093
Val Lys Thr Ser Arg Ser Gly Tyr Leu Gln Arg Cys Ile Ile Lys His
980                 985                 990                 995

cta gag ggg ctg gtc gtg cag tat gat ctc acg gtc cgt gac agt gac     3141
Leu Glu Gly Leu Val Val Gln Tyr Asp Leu Thr Val Arg Asp Ser Asp
996                1001                1006                1011

ggc agt gtg gtg cag ttc ctg tat ggg gag gat ggc ctg gac atc ccc     3189
Gly Ser Val Val Gln Phe Leu Tyr Gly Glu Asp Gly Leu Asp Ile Pro
1012                1017                1022                1027

aag aca cag ttc ctg cag ccc aag cag ttc ccc ttc ctg gcc agc aac     3237
Lys Thr Gln Phe Leu Gln Pro Lys Gln Phe Pro Phe Leu Ala Ser Asn
1028                1033                1038                1043
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 tac gag gtg ata atg aaa tca cag cat ctc cat gaa gtt tta tcc aga     3285
 Tyr Glu Val Ile Met Lys Ser Gln His Leu His Glu Val Leu Ser Arg
1044                1049                1054                1059

 gca gat ccc aaa aaa gct ctc cac cac ttc aga gct atc aaa aaa tgg     3333
 Ala Asp Pro Lys Lys Ala Leu His His Phe Arg Ala Ile Lys Lys Trp
1060                1065                1070                1075

 caa agc aag cac ccc aac acc ctg ctg aga aga ggc gcc ttc ttg agt     3381
 Gln Ser Lys His Pro Asn Thr Leu Leu Arg Arg Gly Ala Phe Leu Ser
1076                1081                1086                1091

 tat tcc cag aaa att cag gaa gct gtg aaa gcc ctg aaa ctt gag agt     3429
 Tyr Ser Gln Lys Ile Gln Glu Ala Val Lys Ala Leu Lys Leu Glu Ser
1092                1097                1102                1107

 gaa aac cgc aat ggc cgc aga ccc tgg gac tca ggg agg atg ctg agg     3477
 Glu Asn Arg Asn Gly Arg Arg Pro Trp Asp Ser Gly Arg Met Leu Arg
1108                1113                1118                1123

 atg tgg tat gag ttg gat gag gaa agc cga agg aaa tac cag aag aag     3525
 Met Trp Tyr Glu Leu Asp Glu Glu Ser Arg Arg Lys Tyr Gln Lys Lys
1124                1129                1134                1139

 gcg gcc gct tgt cct gac ccc agt ctg tct gtc tgg cgt cct gac atc     3573
 Ala Ala Ala Cys Pro Asp Pro Ser Leu Ser Val Trp Arg Pro Asp Ile
1140                1145                1150                1155

 tac ttt gca tca gtg tca gaa aca ttt gaa aca aag gtt gat gac tac     3621
 Tyr Phe Ala Ser Val Ser Glu Thr Phe Glu Thr Lys Val Asp Asp Tyr
1156                1161                1166                1171

 agt caa gag tgg gca gct caa aca gag aag agt tat gag aaa tca gag     3669
 Ser Gln Glu Trp Ala Ala Gln Thr Glu Lys Ser Tyr Glu Lys Ser Glu
1172                1177                1182                1187

 ctt tct ctc gac agg ttg agg acc ttg ctg cag ctg aag tgg cag cgc     3717
 Leu Ser Leu Asp Arg Leu Arg Thr Leu Leu Gln Leu Lys Trp Gln Arg
1188                1193                1198                1203

 tca ctg tgt gag ccg ggc gag gct gtg ggc ctg ctg gct gcc cag agc     3765
 Ser Leu Cys Glu Pro Gly Glu Ala Val Gly Leu Leu Ala Ala Gln Ser
1204                1209                1214                1219

 atc gga gag ccc tcc acc cag atg acc ctc aac acc ttc cac ttt gca     3813
 Ile Gly Glu Pro Ser Thr Gln Met Thr Leu Asn Thr Phe His Phe Ala
1220                1225                1230                1235

 ggc aga ggc gag atg aac gtc acc ctg ggc att cca agg ttg cgg gag     3861
 Gly Arg Gly Glu Met Asn Val Thr Leu Gly Ile Pro Arg Leu Arg Glu
1236                1241                1246                1251

 att ctc atg gtg gcc agc gcc aac atc aag aca ccc atg atg agc gtg     3909
 Ile Leu Met Val Ala Ser Ala Asn Ile Lys Thr Pro Met Met Ser Val
1252                1257                1262                1267
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 ccc gtg ctc aac acc aag aaa gcc ctg aag aga gtg aaa agc ctg aag     3957
 Pro Val Leu Asn Thr Lys Lys Ala Leu Lys Arg Val Lys Ser Leu Lys
1268                1273                1278                1283

 aag caa ctc acc agg gtg tgc ttg ggg gag gtg ttg cag aaa att gac     4005
 Lys Gln Leu Thr Arg Val Cys Leu Gly Glu Val Leu Gln Lys Ile Asp
1284                1289                1294                1299

 gtc cag gag tcc ttc tgt atg gaa gaa aaa cag aac aaa ttc cag gtg     4053
 Val Gln Glu Ser Phe Cys Met Glu Glu Lys Gln Asn Lys Phe Gln Val
1300                1305                1310                1315

 tac cag ctg cgg ttt cag ttc ctg cca cat gca tat tac cag cag gag     4101
 Tyr Gln Leu Arg Phe Gln Phe Leu Pro His Ala Tyr Tyr Gln Gln Glu
1316                1321                1326                1331

 aag tgc ctg aga ccc gag gac atc ctg cgc ttc atg gaa aca aga ttc     4149
 Lys Cys Leu Arg Pro Glu Asp Ile Leu Arg Phe Met Glu Thr Arg Phe
1332                1337                1342                1347

 ttt aaa ctt ctg atg gaa tcc atc aaa aag aag aat aat aaa gca tca     4197
 Phe Lys Leu Leu Met Glu Ser Ile Lys Lys Lys Asn Asn Lys Ala Ser
1348                1353                1358                1363

 gct ttc agg aac gta aac act cga aga gct aca cag cgg gat ctg gac     4245
 Ala Phe Arg Asn Val Asn Thr Arg Arg Ala Thr Gln Arg Asp Leu Asp
1364                1369                1374                1379

 aac gct ggg gag ttg ggg agg agt cgg gga gag cag gag ggt gat gag     4293
 Asn Ala Gly Glu Leu Gly Arg Ser Arg Gly Glu Gln Glu Gly Asp Glu
1380                1385                1390                1395

 gaa gag gag ggg cac att gtg gat gct gaa gct gag gag gga gac gcc     4341
 Glu Glu Glu Gly His Ile Val Asp Ala Glu Ala Glu Glu Gly Asp Ala
1396                1401                1406                1411

 gat gcc tct gat gcc aaa cgc aag gag aag cag gag gag gag gtt gat     4389
 Asp Ala Ser Asp Ala Lys Arg Lys Glu Lys Gln Glu Glu Glu Val Asp
1412                1417                1422                1427

 tat gag agt gag gaa gag gag gag agg gag ggc gag gag aac gac gat     4437
 Tyr Glu Ser Glu Glu Glu Glu Glu Arg Glu Gly Glu Glu Asn Asp Asp
1428                1433                1438                1443

 gaa gac atg cag gag gaa cga aat ccc cac agg gaa ggt gct cga aag     4485
 Glu Asp Met Gln Glu Glu Arg Asn Pro His Arg Glu Gly Ala Arg Lys
1444                1449                1454                1459

 acc caa gag caa gat gaa gag gtg ggc tta ggc act gag gag gac ccg     4533
 Thr Gln Glu Gln Asp Glu Glu Val Gly Leu Gly Thr Glu Glu Asp Pro
1460                1465                1470                1475

 tcc ctt ccc gcc ctc ctg acg cag ccc cgg aaa ccc acc cac agc cag     4581
 Ser Leu Pro Ala Leu Leu Thr Gln Pro Arg Lys Pro Thr His Ser Gln
1476                1481                1486                1491

 gag ccc cag ggg ccc gag gcc atg gag cgc cgg gtc cag gct gtg cgt     4629
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 Glu Pro Gln Gly Pro Glu Ala Met Glu Arg Arg Val Gln Ala Val Arg
1492                1497                1502                1507

 gag atc cac ccg ttc ata gat gac tac cag tac gac acc gag gag agc     4677
 Glu Ile His Pro Phe Ile Asp Asp Tyr Gln Tyr Asp Thr Glu Glu Ser
1508                1513                1518                1523

 ctg tgg tgc cag gtg aca gtg aag ctc cct ctg atg aag atc aac ttt     4725
 Leu Trp Cys Gln Val Thr Val Lys Leu Pro Leu Met Lys Ile Asn Phe
1524                1529                1534                1539

 gac atg agc tcc ctg gta gta tct ttg gcc cat ggt gcc gtc atc tat     4773
 Asp Met Ser Ser Leu Val Val Ser Leu Ala His Gly Ala Val Ile Tyr
1540                1545                1550                1555

 gcg acc aag ggc atc act cgg tgc ctc ctg aat gaa aca acc aac aat     4821
 Ala Thr Lys Gly Ile Thr Arg Cys Leu Leu Asn Glu Thr Thr Asn Asn
1556                1561                1566                1571

 aag aac gag aag gag ctt gtg cta aac aca gaa gga atc aac ctc cca     4869
 Lys Asn Glu Lys Glu Leu Val Leu Asn Thr Glu Gly Ile Asn Leu Pro
1572                1577                1582                1587

 gag cta ttc aag tat gca gag gtc ctg gat ctg cgc cgc ctc tac tcc     4917
 Glu Leu Phe Lys Tyr Ala Glu Val Leu Asp Leu Arg Arg Leu Tyr Ser
1588                1593                1598                1603

 aac gac atc cac gcc ata gcc aac acg tat ggc att gag gcc gcg ctg     4965
 Asn Asp Ile His Ala Ile Ala Asn Thr Tyr Gly Ile Glu Ala Ala Leu
1604                1609                1614                1619

 cgg gtg atc gag aag gag atc aag gat gtg ttt gcc gtg tat ggc atc     5013
 Arg Val Ile Glu Lys Glu Ile Lys Asp Val Phe Ala Val Tyr Gly Ile
1620                1625                1630                1635

 gcg gtc gac cct cgc cat ctc tcc ctg gtt gct gat tat atg tgc ttc     5061
 Ala Val Asp Pro Arg His Leu Ser Leu Val Ala Asp Tyr Met Cys Phe
1636                1641                1646                1651

 gag ggt gtt tac aag cca ctg aat cgc ttt ggg atc cgg tca aac tct     5109
 Glu Gly Val Tyr Lys Pro Leu Asn Arg Phe Gly Ile Arg Ser Asn Ser
1652                1657                1662                1667

 tcc ccg cta cag cag atg aca ttt gaa acc agc ttc cag ttt ctg aag     5157
 Ser Pro Leu Gln Gln Met Thr Phe Glu Thr Ser Phe Gln Phe Leu Lys
1668                1673                1678                1683

 caa gcc acc atg ctg gga tcc cac gat gag ctg agg tct cct tct gcc     5205
 Gln Ala Thr Met Leu Gly Ser His Asp Glu Leu Arg Ser Pro Ser Ala
1684                1689                1694                1699

 tgc ctt gtg gtc ggg aag gtc gtc agg ggc ggg aca ggc ctg ttc gag     5253
 Cys Leu Val Val Gly Lys Val Val Arg Gly Gly Thr Gly Leu Phe Glu
1700                1705                1710                1715

 ctc aag cag cct ctg aga tag ca gctaccccgg caccatctgc ccagctccaa     5306
 Leu Lys Gln Pro Leu Arg  *
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1716 1721

ggacccttgg tgagggcgtg gcccagcctg ccttctgcat gagaggacca ggagactgga 5366

atccagggca gttccaagtg acagtacaga gcacagcagc gaccttgggc ctgaaagcag 5426

tgggcctctg agctgggcca gcttcacctg gaaagtgaca gagttgctca tccttgcccc 5486

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cccatacacc ccacaggccc tgcttatggg aaggaacaca ggcctccagc ccagaggact 6146

gtgccgccct gttcttggcc gtccacgttt cctctccctc tagcaccagc aatacatttc 6206

cctggcatgg acagaaaaga cagagaggac ttgtacaaag gctttgtaaa accagaggct 6266

agcttctatc tttgtctact gttatttcag ctcagggcgg gtaattaaca tcattggaac 6326

tagctattag gaaagaaaaa aaacttggtt ttttttacaa caaaaaaaaa aaaa 6380

<210> 26
<211> 1775
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (397)..(1176)

<400> 26
acgactgact cgaattttta cgactcacta tagggaattt ggccctcgag gccaagaatt 60

cggcacgaga ttggctgact ttggctatag aaaaaagaaa ggaacgaaaa gagacagttt 120

tttttggaaa gctaagtctt ccctttatcg agtcaagaaa ccccccccttc ttgagctatt 180

```
tacagctttt aacaattgag taaagtacgc tccggtcaca attggagaaa ctggttattt    240

aacaagggtt tgactcgagt ggcatgcttt caaatataaa cagacttctt taaggaatta    300

aagttgacta atagagccaa taaaagcctc ttggaaaaac tggccttgta ccttgtgtat    360

gaagtccctg tatagggttc ctgacctgtg gtcacc  atg ggg aca gcc gcc ctg     414
                                        Met Gly Thr Ala Ala Leu
                                          1

ggt ccc gtc tgg gca gcg ctc ctg ctc ttt ctc ctg atg tgt gag atc      462
Gly Pro Val Trp Ala Ala Leu Leu Leu Phe Leu Leu Met Cys Glu Ile
  7                  12                  17                  22

cct atg gtg gag ctc acc ttt gac aga gct gtg gcc agc ggc tgc caa      510
Pro Met Val Glu Leu Thr Phe Asp Arg Ala Val Ala Ser Gly Cys Gln
 23                  28                  33                  38

cgg tgc tgt gac tct gag gac ccc ctg gat cct gcc cat gta tcc tca      558
Arg Cys Cys Asp Ser Glu Asp Pro Leu Asp Pro Ala His Val Ser Ser
 39                  44                  49                  54

gcc tct tcc tcc ggc cgc ccc cac gcc ctg cct gag atc aga ccc tac      606
Ala Ser Ser Ser Gly Arg Pro His Ala Leu Pro Glu Ile Arg Pro Tyr
 55                  60                  65                  70

att aat atc acc atc ctg aag ggt gac aaa ggg gac cca ggc cca atg      654
Ile Asn Ile Thr Ile Leu Lys Gly Asp Lys Gly Asp Pro Gly Pro Met
 71                  76                  81                  86

ggc ctg cca ggg tac atg ggc agg gag ggt ccc caa ggg gag cct ggc      702
Gly Leu Pro Gly Tyr Met Gly Arg Glu Gly Pro Gln Gly Glu Pro Gly
 87                  92                  97                 102

cct cag ggc agc aag ggt gac aag ggg gag atg ggc agc ccc ggc gcc      750
Pro Gln Gly Ser Lys Gly Asp Lys Gly Glu Met Gly Ser Pro Gly Ala
103                 108                 113                 118

ccg tgc cag aag cgc ttc ttc gcc ttc tca gtg ggc cgc aag acg gcc      798
Pro Cys Gln Lys Arg Phe Phe Ala Phe Ser Val Gly Arg Lys Thr Ala
119                 124                 129                 134

ctg cac agc ggc gag gac ttc cag acg ctg ctc ttc gaa agg gtc ttt      846
Leu His Ser Gly Glu Asp Phe Gln Thr Leu Leu Phe Glu Arg Val Phe
135                 140                 145                 150

gtg aac ctt gat ggg tgc ttt gac atg gcg acc ggc cag ttt gct gct      894
Val Asn Leu Asp Gly Cys Phe Asp Met Ala Thr Gly Gln Phe Ala Ala
151                 156                 161                 166

ccc ctg cgt ggc atc tac ttc ttc agc ctc aat gtg cac agc tgg aat      942
Pro Leu Arg Gly Ile Tyr Phe Phe Ser Leu Asn Val His Ser Trp Asn
167                 172                 177                 182

tac aag gag acg tac gtg cac att atg cat aac cag aaa gag gct gtc      990
Tyr Lys Glu Thr Tyr Val His Ile Met His Asn Gln Lys Glu Ala Val
183                 188                 193                 198
```

```
atc ctg tac gcg cag ccc agc gag cgc agc atc atg cag agc cag agt     1038
Ile Leu Tyr Ala Gln Pro Ser Glu Arg Ser Ile Met Gln Ser Gln Ser
199                 204                 209                 214

gtg atg ctg gac ctg gcc tac ggg gac cgc gtc tgg gtg cgg ctc ttc     1086
Val Met Leu Asp Leu Ala Tyr Gly Asp Arg Val Trp Val Arg Leu Phe
215                 220                 225                 230

aag cgc cag cgc gag aac gcc atc tac agc aac gac ttc gac acc tac     1134
Lys Arg Gln Arg Glu Asn Ala Ile Tyr Ser Asn Asp Phe Asp Thr Tyr
231                 236                 241                 246

atc acc ttc agc ggc cac ctc atc aag gcc gag gac gac tga gggcctc     1183
Ile Thr Phe Ser Gly His Leu Ile Lys Ala Glu Asp Asp  *
247                 252                 257

tgggccaccc tcccggctgg agagctcagg tgctggtccc gtcccctgca gggctcagtt   1243

tgcactgctg tgaagcagga aggccaggga ggtccccggg gacctggcat tctggggaga   1303

ccctgcttct atcttggctg ccatcatccc tcccagccta tttctgctcc tctcttctct   1363

cttggaccta ttttaagaag cttgctaacc taaatattct agaactttcc cagcctcgta   1423

gcccagcact tctcaaactt ggaaatgcat gcgaatcacc cggggttcgt gttaaatgca   1483

gattctgact cagcaggtct gagtgggtcc aggattctgt gtttctcata tgttcctggg   1543

tgatgctgat ggggtcagtc tatgaaccac actggagcaa ccaggttcta ggactttctc   1603

aatattctag tactttctga acattctgga atcctcccca cattctagaa ttctcccaac   1663

tactagggag gctgaggcag gagaatcgct tgagcacagg aggcgttggc tgcagtgagc   1723

caagatcacg ccactgcact ccagcctggg taacaagagc gaaactatcg cc            1775
```

<210> 27
<211> 635
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (99)..(569)

<400> 27

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caccgcccct ttgagatcat cgagacccaa gctggctagc gtttaaactt aagcttggta     60

ccgagctcgg atccactagt ccagtgtggt ggaattcg    atg gcg ccg aaa gcg     113
                                             Met Ala Pro Lys Ala
                                               1

aag aag gaa gct cct gcc cct cct aaa gct gaa gcc aaa gcg aag gct      161
```

```
Lys Lys Glu Ala Pro Ala Pro Pro Lys Ala Glu Ala Lys Ala Lys Ala
  6                  11                  16                  21

tta aag gcc aag aag gca gtg ttg aaa ggt gtc cac agc cac aaa aag      209
Leu Lys Ala Lys Lys Ala Val Leu Lys Gly Val His Ser His Lys Lys
 22                  27                  32                  37

aag aag atc cgc acg tca ccc acc ttc cgg cgg ccg aag aca ctg cga      257
Lys Lys Ile Arg Thr Ser Pro Thr Phe Arg Arg Pro Lys Thr Leu Arg
 38                  43                  48                  53

ctc cgg aga cag ccc aaa tat cct cgg aag agc gct ccc agg aga aac      305
Leu Arg Arg Gln Pro Lys Tyr Pro Arg Lys Ser Ala Pro Arg Arg Asn
 54                  59                  64                  69

aag ctt gac cac tat gct atc atc aag ttt ccg ctg acc act gag tct      353
Lys Leu Asp His Tyr Ala Ile Ile Lys Phe Pro Leu Thr Thr Glu Ser
 70                  75                  80                  85

gcc atg aag aag ata gaa gac aac aac aca ctt gtg ttc att gtg gat      401
Ala Met Lys Lys Ile Glu Asp Asn Asn Thr Leu Val Phe Ile Val Asp
 86                  91                  96                 101

gtt aaa gcc aac aag cac cag att aaa cag gct gtg aag aag ctg tat      449
Val Lys Ala Asn Lys His Gln Ile Lys Gln Ala Val Lys Lys Leu Tyr
102                 107                 112                 117

gac att gat gtg gcc aag gtc aac acc ctg att cgg cct gat gga gag      497
Asp Ile Asp Val Ala Lys Val Asn Thr Leu Ile Arg Pro Asp Gly Glu
118                 123                 128                 133

aag aag gca tat gtt cga ctg gct cct gat tac gat gct ttg gat gtt      545
Lys Lys Ala Tyr Val Arg Leu Ala Pro Asp Tyr Asp Ala Leu Asp Val
134                 139                 144                 149

gcc aac aaa att ggg atc atc taa actgagtcca gctgcctaat tctgaatata     599
Ala Asn Lys Ile Gly Ile Ile  *
150                 155

tatatatata tatcttttca ccataaaaaa aaaaaa                              635
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Sequence Listing.ST25.txt

<210> 28
<211> 572
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (15)..(572)

<400> 28

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tttcgtgggg cgtg  atg tat ata act atc tat tcg atg atg aag ata ccc      50
                 Met Tyr Ile Thr Ile Tyr Ser Met Met Lys Ile Pro
                   1               5                  10
```

```
cac caa acc caa aaa aag aga tct ctc gag gat ccg aat tcg cgg ccg        98
His Gln Thr Gln Lys Lys Arg Ser Leu Glu Asp Pro Asn Ser Arg Pro
 13                  18                  23                  28

cgt cga ccg ccg aaa gcg aag aag gaa gct cct gcc cct cct aaa gct       146
Arg Arg Pro Pro Lys Ala Lys Lys Glu Ala Pro Ala Pro Pro Lys Ala
 29                  34                  39                  44

gaa gcc aaa gcg aag gct tta aag gcc aag aag gca gtg ttg aaa ggt       194
Glu Ala Lys Ala Lys Ala Leu Lys Ala Lys Lys Ala Val Leu Lys Gly
 45                  50                  55                  60

gtc cac agc cac aaa aag aag aag atc cgc acg tca ccc acc ttc cgg       242
Val His Ser His Lys Lys Lys Lys Ile Arg Thr Ser Pro Thr Phe Arg
 61                  66                  71                  76

cgg ccg aag aca ctg cga ctc cgg aga cag ccc aaa tat cct cgg aag       290
Arg Pro Lys Thr Leu Arg Leu Arg Arg Gln Pro Lys Tyr Pro Arg Lys
 77                  82                  87                  92

agc gct ccc agg aga aac aag ctt gac cac tat gct atc atc aag ttt       338
Ser Ala Pro Arg Arg Asn Lys Leu Asp His Tyr Ala Ile Ile Lys Phe
 93                  98                 103                 108

ccg ctg acc act gag tct gcc atg aag aag ata gga gac agc aac aca       386
Pro Leu Thr Thr Glu Ser Ala Met Lys Lys Ile Gly Asp Ser Asn Thr
109                 114                 119                 124

ctt gtg ttc ata gtg gat gtt aaa gcc aac aag cac cag atc aaa cag       434
Leu Val Phe Ile Val Asp Val Lys Ala Asn Lys His Gln Ile Lys Gln
125                 130                 135                 140

gct gtg aag aag ctc tat gat att gac atg gcc aag gtc aac acc ctg       482
Ala Val Lys Lys Leu Tyr Asp Ile Asp Met Ala Lys Val Asn Thr Leu
141                 146                 151                 156

att cgg cct gat gga gag aag aag gca tat gtt cca ctg gct cct gat       530
Ile Arg Pro Asp Gly Glu Lys Lys Ala Tyr Val Pro Leu Ala Pro Asp
157                 162                 167                 172

tat gat gct ttg gat gtt gcc aac aaa att ggg atc atc taa               572
Tyr Asp Ala Leu Asp Val Ala Asn Lys Ile Gly Ile Ile  *
173                 178                 183
```

<210> 29
<211> 3195
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (2)..(2164)

<400> 29

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t    atg gaa agc tgg tac gcc tgc agg tac cgg tcc gga tat tcc cgg      46
     Met Glu Ser Trp Tyr Ala Cys Arg Tyr Arg Ser Gly Tyr Ser Arg
       1               5                  10

gtc gac tcc acg cgt ccg gcg gct tgc gga ggg tgc tgg ttt gct ctc      94
Val Asp Ser Thr Arg Pro Ala Ala Cys Gly Gly Cys Trp Phe Ala Leu
 16                  21                  26                  31

ggt gaa cgg cgc gcg ggg tct ctc ctg agt gcg agc tac ggg acc ttc     142
Gly Glu Arg Arg Ala Gly Ser Leu Leu Ser Ala Ser Tyr Gly Thr Phe
 32                  37                  42                  47

gcc atg ccg ggg atg gta ctc ttc ggc cgg cgc tgg gcc atc gcc agc     190
Ala Met Pro Gly Met Val Leu Phe Gly Arg Arg Trp Ala Ile Ala Ser
 48                  53                  58                  63

gac gac ttg gtc ttc cca ggg ttc ttc gag ctg gtc gtg cga gtg ctg     238
Asp Asp Leu Val Phe Pro Gly Phe Phe Glu Leu Val Val Arg Val Leu
 64                  69                  74                  79

tgg tgg att ggc att ctg acg ttg tat ctc atg cac aga gga aag ctg     286
Trp Trp Ile Gly Ile Leu Thr Leu Tyr Leu Met His Arg Gly Lys Leu
 80                  85                  90                  95

gac tgt gct ggt gga gcc ttg ctc agc agt tac ttg atc gtc ctc atg     334
Asp Cys Ala Gly Gly Ala Leu Leu Ser Ser Tyr Leu Ile Val Leu Met
 96                 101                 106                 111

att ctc ctg gca gtt gtc ata tgt act gtg tca gcc atc atg tgt gtc     382
Ile Leu Leu Ala Val Val Ile Cys Thr Val Ser Ala Ile Met Cys Val
112                 117                 122                 127

agc atg aga gga acg att tgt aac cct gga ccg cgg aag tct atg tct     430
Ser Met Arg Gly Thr Ile Cys Asn Pro Gly Pro Arg Lys Ser Met Ser
128                 133                 138                 143

aag ctg ctt tac atc cgc ctg gcg ctg ttt ttt cca gag atg gtc tgg     478
Lys Leu Leu Tyr Ile Arg Leu Ala Leu Phe Phe Pro Glu Met Val Trp
144                 149                 154                 159

gcc tct ctg ggg gct gcc tgg gtg gca gat ggt gtt cag tgc gac agg     526
Ala Ser Leu Gly Ala Ala Trp Val Ala Asp Gly Val Gln Cys Asp Arg
160                 165                 170                 175

aca gtt gta aac ggc atc atc gca acc gtc gtg gtc agt tgg atc atc     574
Thr Val Val Asn Gly Ile Ile Ala Thr Val Val Val Ser Trp Ile Ile
176                 181                 186                 191

atc gct gcc aca gtg gtt tcc att atc att gtc ttt gac cct ctt ggg     622
Ile Ala Ala Thr Val Val Ser Ile Ile Ile Val Phe Asp Pro Leu Gly
192                 197                 202                 207

ggg aaa atg gct cca tat tcc tct gcc ggc ccc agc cac ctg gat agt     670
Gly Lys Met Ala Pro Tyr Ser Ser Ala Gly Pro Ser His Leu Asp Ser
208                 213                 218                 223
```

```
cat gat tca agc cag tta ctt aat ggc ctc aag aca gca gct aca agc      718
His Asp Ser Ser Gln Leu Leu Asn Gly Leu Lys Thr Ala Ala Thr Ser
224                 229                 234                 239

gtg tgg gaa acc aga atc aag ctc ttg tgc tgt tgc att ggg aaa gac      766
Val Trp Glu Thr Arg Ile Lys Leu Leu Cys Cys Cys Ile Gly Lys Asp
240                 245                 250                 255

gac cat act cgg gtt gct ttt tcg agt acg gca gag ctt ttc tca acc      814
Asp His Thr Arg Val Ala Phe Ser Ser Thr Ala Glu Leu Phe Ser Thr
256                 261                 266                 271

tac ttt tca gac aca gat ctg gtg ccc agc gac att gcg gcg ggc ctc      862
Tyr Phe Ser Asp Thr Asp Leu Val Pro Ser Asp Ile Ala Ala Gly Leu
272                 277                 282                 287

gcc ctg ctt cat cag caa cag gac aat atc agg aac aac caa gag cct      910
Ala Leu Leu His Gln Gln Gln Asp Asn Ile Arg Asn Asn Gln Glu Pro
288                 293                 298                 303

gcc cag gtg gtc tgc cat gcc cca ggg agc tcc cag gaa gct gat ctg      958
Ala Gln Val Val Cys His Ala Pro Gly Ser Ser Gln Glu Ala Asp Leu
304                 309                 314                 319

gat gca gaa tta gaa aac tgc cat cat tac atg cag ttt gca gca gcg     1006
Asp Ala Glu Leu Glu Asn Cys His His Tyr Met Gln Phe Ala Ala Ala
320                 325                 330                 335

gcc tat ggg tgg ccc ctc tac atc tac aga aac ccc ctc acg ggg ctg     1054
Ala Tyr Gly Trp Pro Leu Tyr Ile Tyr Arg Asn Pro Leu Thr Gly Leu
336                 341                 346                 351

tgc agg att ggt ggt gac tgc tgc aga agc aga acc aca gac tat gac     1102
Cys Arg Ile Gly Gly Asp Cys Cys Arg Ser Arg Thr Thr Asp Tyr Asp
352                 357                 362                 367

ttg gtc gga ggc gat cag ctc aac tgt cac ttc ggc tcc atc ctg cac     1150
Leu Val Gly Gly Asp Gln Leu Asn Cys His Phe Gly Ser Ile Leu His
368                 373                 378                 383

acc aca ggg ctg cag tac agg gac ttc atc cac gtc agc ttc cat gac     1198
Thr Thr Gly Leu Gln Tyr Arg Asp Phe Ile His Val Ser Phe His Asp
384                 389                 394                 399

aag gtt tac gag ctg ccg ttt tta gtg gct ctg gat cac agg aaa gag     1246
Lys Val Tyr Glu Leu Pro Phe Leu Val Ala Leu Asp His Arg Lys Glu
400                 405                 410                 415

tct gtt gtg gtc gct gtg agg ggg acc atg tct ctg cag gat gtc ctt     1294
Ser Val Val Val Ala Val Arg Gly Thr Met Ser Leu Gln Asp Val Leu
416                 421                 426                 431

acg gac ctg tca gcg gag agt gag gtg ctg gac gtg gag tgt gag gtg     1342
Thr Asp Leu Ser Ala Glu Ser Glu Val Leu Asp Val Glu Cys Glu Val
432                 437                 442                 447
```

```
cag gac cgc ctg gca cac aag ggt att tct caa gct gcc aga tac gtt     1390
Gln Asp Arg Leu Ala His Lys Gly Ile Ser Gln Ala Ala Arg Tyr Val
448                 453                 458                 463

tac caa cga ctc atc aac gac ggg att ttg agc caa gcc ttc agc att     1438
Tyr Gln Arg Leu Ile Asn Asp Gly Ile Leu Ser Gln Ala Phe Ser Ile
464                 469                 474                 479

gct cct gag tac cgg ctg gtc ata gtg ggc cac agc ctc ggg gga ggg     1486
Ala Pro Glu Tyr Arg Leu Val Ile Val Gly His Ser Leu Gly Gly Gly
480                 485                 490                 495

gcg gcc gcc ctg ctg gcc acc atg gtc aga gcc gcc tac ccg cag gtc     1534
Ala Ala Ala Leu Leu Ala Thr Met Val Arg Ala Ala Tyr Pro Gln Val
496                 501                 506                 511

agg tgc tac gcc ttc tcc cca ccc cgg ggg ctg tgg agc aaa gct ctg     1582
Arg Cys Tyr Ala Phe Ser Pro Pro Arg Gly Leu Trp Ser Lys Ala Leu
512                 517                 522                 527

cag gaa tat tct cag agc ttc atc gtg tca ctc gtc ctg ggg aag gat     1630
Gln Glu Tyr Ser Gln Ser Phe Ile Val Ser Leu Val Leu Gly Lys Asp
528                 533                 538                 543

gtg att ccc agg ctc agt gtg acc aac ttg gaa gat ctg aag aga aga     1678
Val Ile Pro Arg Leu Ser Val Thr Asn Leu Glu Asp Leu Lys Arg Arg
544                 549                 554                 559

atc ttg cga gtg gtc gcg cac tgc aat aaa ccc aag tac aag atc ttg     1726
Ile Leu Arg Val Val Ala His Cys Asn Lys Pro Lys Tyr Lys Ile Leu
560                 565                 570                 575

ctg cac ggt ttg tgg tac gaa ctg ttt gga gga aac ccc aac aac ttg     1774
Leu His Gly Leu Trp Tyr Glu Leu Phe Gly Gly Asn Pro Asn Asn Leu
576                 581                 586                 591

ccc acg gag ctg gac ggg ggc gac cag gaa gtc ctg aca cag cct ctt     1822
Pro Thr Glu Leu Asp Gly Gly Asp Gln Glu Val Leu Thr Gln Pro Leu
592                 597                 602                 607

ctg ggg gag cag agc cta ctg acg cgc tgg tcc ccg gcc tac agc ttc     1870
Leu Gly Glu Gln Ser Leu Leu Thr Arg Trp Ser Pro Ala Tyr Ser Phe
608                 613                 618                 623

tcc agc gac tcc cca ctg gac tct tct ccc aag tac ccc cct ctc tac     1918
Ser Ser Asp Ser Pro Leu Asp Ser Ser Pro Lys Tyr Pro Pro Leu Tyr
624                 629                 634                 639

cct ccc ggc agg atc atc cac ctg cag gag gag ggc gcc tcg ggg cgg     1966
Pro Pro Gly Arg Ile Ile His Leu Gln Glu Glu Gly Ala Ser Gly Arg
640                 645                 650                 655

ttt ggc tgc tgc tct gct gct cac tat agc gcc aag tgg tca cac gaa     2014
Phe Gly Cys Cys Ser Ala Ala His Tyr Ser Ala Lys Trp Ser His Glu
656                 661                 666                 671

gcg gaa ttc agc aaa ata ctc ata ggt ccg aag atg ctc acc gac cac     2062
```

```
Ala Glu Phe Ser Lys Ile Leu Ile Gly Pro Lys Met Leu Thr Asp His
672                 677                 682                 687

atg cca gac atc ctg atg cgg gcc ttg gac agc gtg gtc tcc gac aga     2110
Met Pro Asp Ile Leu Met Arg Ala Leu Asp Ser Val Val Ser Asp Arg
688                 693                 698                 703

gcg gcc tgc gtc tcc tgt cca gca caa ggg gtc tcc agt gtg gac gtg     2158
Ala Ala Cys Val Ser Cys Pro Ala Gln Gly Val Ser Ser Val Asp Val
704                 709                 714                 719

gcc tga ccagggccac tggaaactgt cccaggaacg atggactcac gcttttgtcc      2214
Ala  *
720

ttaaactgac ttaccatccg aggagttccc atgacgccaa aacagcgaat gtccatcaac   2274

aggaatcgga tgggaacaga attccatggt ctcaatgact taagtttatg ggaagtcatt   2334

gtggccataa tggtagcaga agtagtgagc acgctcaggt gataggacga ctcctgagac   2394

ccagcgaccg tggagacagc ctcgggaagc cctggcccgt ggatggatcc cttggctgtc   2454

tgaggactgc tccagaagtg cgggaatcca gggcccaccc agaagaccgt gaacagttcc   2514

ttagcctccc acccccaagg cagctctttt catccaactc agtttacagg cgtggtttgt   2574

ttttcaaact gggcttcctg gatgtacaaa tggaactgtg gtgagggtgc gggctggggt   2634

tttctcctgg gcgtcaccaa gggcagccct gggctctggc tggggatgaa gacgaaaccc   2694

gatcgggaaa gtaagtggag cccccggccc cgccgagcca cagcccccca actgcctatt   2754

cccactgccc agttgtttgt ccacatcagg agttgctgat tgaattcttg ctactcttct   2814

ggctctgggg tcggccagtg gattcaggag ttgaaacaat aaagcgcgcg tcacgatagt   2874

gcttgtgtgt acagctgcgt gctctcttat tggggatttc caggtagcgc tactatactg   2934

ggtggttgta gagcaatgat gtttccacgt ttttttaaa ccctggggtt ctggctacag   2994

atggaagatt gcccaagctc tgatttcacc ccctctcccc ccggaagccc aacagaatga   3054

caggagggag atttctccaa aaaagcagag acccacagga tgggaaaaga cactccaaca   3114

acagtcagag gacgctcagt acagatcctt aaggggggaag gaaagacatg aactgacccc   3174

agcgctagag caagcgagcg t                                             3195
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<210> 30
<211> 1637
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (245)..(841)

<400> 30
cggcacgagc gcggtcgcgt cataggccga acaaccaaac agaaaagttt aataaacagc 60

ggacggaggg gccggcggtg gcggacggag gcaagcaggg gttcggcggc attacctgta 120

cccattcacc ggcggctacc ggcggcggcg cgcagcgtgt caggcggaga gacccgccgc 180

cagatcaaaa gacactgact tagctgctta ccagaagggg aacttgggtg tgcaactgag 240

gaac atg gct caa gaa act aat cac agc caa gtg cct atg ctt tgt tcc 289
Met Ala Gln Glu Thr Asn His Ser Gln Val Pro Met Leu Cys Ser
1 5 10

act ggc tgt gga ttt tat gga aac cct cgt aca aat ggc atg tgt tca 337
Thr Gly Cys Gly Phe Tyr Gly Asn Pro Arg Thr Asn Gly Met Cys Ser
16 21 26 31

gta tgc tat aaa gaa cat ctt caa aga cag aat agt agt aat ggt aga 385
Val Cys Tyr Lys Glu His Leu Gln Arg Gln Asn Ser Ser Asn Gly Arg
32 37 42 47

ata agc cca cct gca acc tct gtc agt agt ctg tct gaa tct tta cca 433
Ile Ser Pro Pro Ala Thr Ser Val Ser Ser Leu Ser Glu Ser Leu Pro
48 53 58 63

gtt caa tgc aca gat ggc agt gtg cca gaa gcc cag tca gca tta gac 481
Val Gln Cys Thr Asp Gly Ser Val Pro Glu Ala Gln Ser Ala Leu Asp
64 69 74 79

tct aca tct tca tct atg cag ccc agc cct gta tca aat cag tca ctt 529
Ser Thr Ser Ser Ser Met Gln Pro Ser Pro Val Ser Asn Gln Ser Leu
80 85 90 95

tta tca gaa tct gta gca tct tct caa ttg gac agt aca tct gtg gac 577
Leu Ser Glu Ser Val Ala Ser Ser Gln Leu Asp Ser Thr Ser Val Asp
96 101 106 111

aaa gca gta cct gaa aca gaa gat gtg cag gct tca gta tca gac aca 625
Lys Ala Val Pro Glu Thr Glu Asp Val Gln Ala Ser Val Ser Asp Thr
112 117 122 127

gca cag cag cca tct gaa gag caa agc aag tct ctt gat aac cga aac 673
Ala Gln Gln Pro Ser Glu Glu Gln Ser Lys Ser Leu Asp Asn Arg Asn
128 133 138 143

aaa aaa aga atc gct gtt tca tgt gca gga aga aag tgg gac tta ctg 721
Lys Lys Arg Ile Ala Val Ser Cys Ala Gly Arg Lys Trp Asp Leu Leu
144 149 154 159

ggt ttg aat gcc ggt gtg gaa atg ttt act gtg gtg tac acc gtt act 769
Gly Leu Asn Ala Gly Val Glu Met Phe Thr Val Val Tyr Thr Val Thr
160 165 170 175

```
cag atg tac aca att gct ctt aca att aca aag ccg atg ctg ctg aga      817
Gln Met Tyr Thr Ile Ala Leu Thr Ile Thr Lys Pro Met Leu Leu Arg
176                 181                 186                 191

aaa tca gaa aag aaa atc cag tag ttgttggtaa aaagatccaa aagatttgaa     871
Lys Ser Glu Lys Lys Ile Gln  *
192                 197

ctcctgctgg aatacaaaat tcttgagcat ctgcaaacta aaaattgact tgaggttttt    931

tttttcctag tcattgggaa tgtagagcag tgtatcttgc atttcatcgg aagaatagat    991

ttttgttttg gttttgtttt gaaaatgact ctgaacattt atttccattg caatttctgt   1051

ggctgaggag acttaaactt tacaagtatt atccttttaa gatcatttta attttagttg   1111

agtgcagagg gcttttataa caaacgtgca gaaattttgg agggctgtga tttttccagt   1171

attaaacatg catgcattaa tcttgcagtt tattttctca ttgtgtatgt atatatcgct   1231

tttctctgca gcacgatttc tcttttgata atgcccttta gggcacaact agttatcagt   1291

aactgaatgt atcttaatca ttatggctgc ttctgttttt tcattaacaa aggttattca   1351

tatgttaggc atatagtttc tttgcaccca ctatttatgt ctggaatcat ttgtcacaag   1411

aggagtgtgt gctgatggag attgtaagtt tgtgtgttta aacttttttt tgagcgaggg   1471

aagaaaaagc tgtatgcatt tcattgctgt ctacaggttt ctttcagatt atgttcatgg   1531

gtttgtgtgt atacaatatg aagaatgatc tgaagtaatt gtgctgtatt tatgtttatt   1591

caccagtctt tgattaaata aaaaggaaaa cccgaaaaaa aaaaaa                  1637
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Application Number: 10/560,950

<210> 31
<211> 1599
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (245)..(805)

<400> 31

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cggcacgagc gcggtcgcgt cataggccga acaaccaaac agaaaagttt aataaacagc     60

ggacggaggg gccggcggtg gcggacggag gcaagcaggg gttcggcggc attacctgta    120

cccattcacc ggcggctacc ggcggcggcg cgcagcgtgt caggcggaga gacccgccgc    180

cagatcaaaa gacactgact tagctgctta ccagaagggg aacttgggtg tgcaactgag    240

gaac atg gct caa gaa act aat cac agc caa gtg cct atg ctt tgt tcc     289
     Met Ala Gln Glu Thr Asn His Ser Gln Val Pro Met Leu Cys Ser
```

```
      1               5                  10

act ggc tgt gga ttt tat gga aac cct cgt aca aat ggc atg tgt tca      337
Thr Gly Cys Gly Phe Tyr Gly Asn Pro Arg Thr Asn Gly Met Cys Ser
 16                  21                  26                  31

gta tgc tat aaa gaa cat ctt caa aga cag aat agt agt aat ggt aga      385
Val Cys Tyr Lys Glu His Leu Gln Arg Gln Asn Ser Ser Asn Gly Arg
 32                  37                  42                  47

ata agc cca cct gtt caa tgc aca gat ggc agt gtg cca gaa gcc cag      433
Ile Ser Pro Pro Val Gln Cys Thr Asp Gly Ser Val Pro Glu Ala Gln
 48                  53                  58                  63

tca gca tta gac tct aca tct tca tct atg cag ccc agc cct gta tca      481
Ser Ala Leu Asp Ser Thr Ser Ser Ser Met Gln Pro Ser Pro Val Ser
 64                  69                  74                  79

aat cag tca ctt tta tca gaa tct gta gca tct tct caa ttg gac agt      529
Asn Gln Ser Leu Leu Ser Glu Ser Val Ala Ser Ser Gln Leu Asp Ser
 80                  85                  90                  95

aca tct gtg gac aaa gca gta cct gaa aca gaa gat gtg cag gct tca      577
Thr Ser Val Asp Lys Ala Val Pro Glu Thr Glu Asp Val Gln Ala Ser
 96                 101                 106                 111

gta tca gac aca gca cag cag cca tct gaa gag caa agc aag tct ctt      625
Val Ser Asp Thr Ala Gln Gln Pro Ser Glu Glu Gln Ser Lys Ser Leu
112                 117                 122                 127

gat aac cga aac aaa aaa aga atc gct gtt tca tgt gca gga aga aag      673
Asp Asn Arg Asn Lys Lys Arg Ile Ala Val Ser Cys Ala Gly Arg Lys
128                 133                 138                 143

tgg gac tta ctg ggt ttg aat gcc ggt gtg gaa atg ttt act gtg gtg      721
Trp Asp Leu Leu Gly Leu Asn Ala Gly Val Glu Met Phe Thr Val Val
144                 149                 154                 159

tac acc gtt act cag atg tac aca att gct ctt aca att aca aag ccg      769
Tyr Thr Val Thr Gln Met Tyr Thr Ile Ala Leu Thr Ile Thr Lys Pro
160                 165                 170                 175

atg ctg ctg aga aaa tca gaa aag aaa atc cag tag ttgt tggtaaaaag      819
Met Leu Leu Arg Lys Ser Glu Lys Lys Ile Gln  *
176                 181                 186

atccaaaaga tttgaactcc tgctggaata caaaattctt gagcatctgc aaactaaaaa    879

ttgacttgag gtttttttt tcctagtcat tgggaatgta gagcagtgta tcttgcattt    939

catcggaaga atagattttt gttttggttt tgttttgaaa atgactctga acatttattt    999

ccattgcaat ttctgtggct gaggagactt aaactttaca agtattatcc ttttaagatc   1059

attttaattt tagttgagtg cagagggctt ttataacaaa cgtgcagaaa ttttggaggg   1119

ctgtgatttt tccagtatta aacatgcatg cattaatctt gcagtttatt ttctcattgt   1179
```

gtatgtatat atcgcttttc tctgcagcac gatttctctt ttgataatgc cctttagggc 1239

acaactagtt atcagtaact gaatgtatct taatcattat ggctgcttct gttttttcat 1299

taacaaaggt tattcatatg ttaggcatat agtttctttg cacccactat ttatgtctgg 1359

aatcatttgt cacaagagga gtgtgtgctg atggagattg taagtttgtg tgtttaaact 1419

ttttttgag cgagggaaga aaaagctgta tgcatttcat tgctgtctac aggtttcttt 1479

cagattatgt tcatgggttt gtgtgtatac aatatgaaga atgatctgaa gtaattgtgc 1539

tgtatttatg tttattcacc agtctttgat taaataaaaa ggaaaacccg aaaaaaaaaa 1599

<210> 32
<211> 1662
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (307)..(1362)

<400> 32
atttggccct cgaggccaag aattcggcac gaggtctaaa cacttctttc cctgaggact 60

ggaagacatt agaataagct ccagacaatt caaacattga gattcctggg aactaccaga 120

tagtagcatc agttcaccaa gaaatgaagc tggtgaggca gtgaaaatcc agggcctaga 180

aagctgggaa tgccatgacg tgggcacatt gaaagacaag aggcaggcat gatcagcctt 240

gaactttagg aagatcccag gaagctgatg gaagacaaga tgtggagtga atgtgaaggt 300

ccagaa atg tcc ttg gtg tgt ctg aca gac ttt cag gcc cat gcg cga 348
Met Ser Leu Val Cys Leu Thr Asp Phe Gln Ala His Ala Arg
1 5 10

gag cag ctg tct aag tca act cgg gat ttt att gaa ggt gga gca gat 396
Glu Gln Leu Ser Lys Ser Thr Arg Asp Phe Ile Glu Gly Gly Ala Asp
15 20 25 30

gac agc atc acg cgg gat gac aac att gca gca ttt aaa aga att cgc 444
Asp Ser Ile Thr Arg Asp Asp Asn Ile Ala Ala Phe Lys Arg Ile Arg
31 36 41 46

ctc cgt ccg cgg tac ctg aga gat gtg tct gag gtg gac acc aga acc 492
Leu Arg Pro Arg Tyr Leu Arg Asp Val Ser Glu Val Asp Thr Arg Thr
47 52 57 62

aca atc caa ggg gag gag atc agt gcc cct att tgt atc gca ccc aca 540
Thr Ile Gln Gly Glu Glu Ile Ser Ala Pro Ile Cys Ile Ala Pro Thr
63 68 73 78

```
ggg ttc cac tgc ctt gtc tgg cct gat ggg gaa atg agc aca gca aga      588
Gly Phe His Cys Leu Val Trp Pro Asp Gly Glu Met Ser Thr Ala Arg
 79                  84                  89                  94

gct gcc caa gcg gct ggt atc tgc tac atc acc agc aca ttt gcc agc      636
Ala Ala Gln Ala Ala Gly Ile Cys Tyr Ile Thr Ser Thr Phe Ala Ser
 95                 100                 105                 110

tgt agc ctt gaa gac att gtc att gca gct ccc gaa ggc ctc cga tgg      684
Cys Ser Leu Glu Asp Ile Val Ile Ala Ala Pro Glu Gly Leu Arg Trp
111                 116                 121                 126

ttc caa ctc tat gtg cat cca gac ctg cag ctg aac aaa cag ttg atc      732
Phe Gln Leu Tyr Val His Pro Asp Leu Gln Leu Asn Lys Gln Leu Ile
127                 132                 137                 142

cag agg gta gaa tcc cta ggt ttc aaa gct ttg gta ata act ttg gat      780
Gln Arg Val Glu Ser Leu Gly Phe Lys Ala Leu Val Ile Thr Leu Asp
143                 148                 153                 158

aca cct gta tgt ggc aac agg cga cat gac att cga aac cag ttg agg      828
Thr Pro Val Cys Gly Asn Arg Arg His Asp Ile Arg Asn Gln Leu Arg
159                 164                 169                 174

agg aac tta aca cta aca gat ctt caa tca cct aaa aag gga aat gca      876
Arg Asn Leu Thr Leu Thr Asp Leu Gln Ser Pro Lys Lys Gly Asn Ala
175                 180                 185                 190

ata cct tat ttc cag atg act cct atc agc act tct ctc tgc tgg aat      924
Ile Pro Tyr Phe Gln Met Thr Pro Ile Ser Thr Ser Leu Cys Trp Asn
191                 196                 201                 206

gat ctc tcc tgg ttt cag agc ata act cga ttg ccc atc atc ctg aaa      972
Asp Leu Ser Trp Phe Gln Ser Ile Thr Arg Leu Pro Ile Ile Leu Lys
207                 212                 217                 222

ggg att ttg aca aaa gag gat gca gag tta gct gtg aag cac aat gtc     1020
Gly Ile Leu Thr Lys Glu Asp Ala Glu Leu Ala Val Lys His Asn Val
223                 228                 233                 238

cag ggt atc att gtt tcc aac cat ggt ggg agg cag ctt gat gag gtt     1068
Gln Gly Ile Ile Val Ser Asn His Gly Gly Arg Gln Leu Asp Glu Val
239                 244                 249                 254

ctt gct tca att gat gct ttg aca gaa gtg gtg gct gct gta aag ggg     1116
Leu Ala Ser Ile Asp Ala Leu Thr Glu Val Val Ala Ala Val Lys Gly
255                 260                 265                 270

aaa att gaa gtc tac ctg gat ggc ggg gtc cga act ggc aat gat gtg     1164
Lys Ile Glu Val Tyr Leu Asp Gly Gly Val Arg Thr Gly Asn Asp Val
271                 276                 281                 286

ctg aag gct ctg gcc ctt gga gct aag tgc att ttt ctt ggg aga cca     1212
Leu Lys Ala Leu Ala Leu Gly Ala Lys Cys Ile Phe Leu Gly Arg Pro
287                 292                 297                 302
```

```
atc cta tgg ggc ctt gcc tgc aag ggt gaa cat ggt gtt aag gaa gtt     1260
Ile Leu Trp Gly Leu Ala Cys Lys Gly Glu His Gly Val Lys Glu Val
303                 308                 313                 318

ttg aac att tta aca aat gag ttc cac act tcc atg gcc ctt aca ggc     1308
Leu Asn Ile Leu Thr Asn Glu Phe His Thr Ser Met Ala Leu Thr Gly
319                 324                 329                 334

tgc cgg tcg gtc gct gag atc aat cga aac ttg gtc cag ttt tcc agg     1356
Cys Arg Ser Val Ala Glu Ile Asn Arg Asn Leu Val Gln Phe Ser Arg
335                 340                 345                 350

ctg taa gaaaaaaggg ccaataacca gactgctgag gttgcccaca ggaggatcac      1412
Leu  *
351

aaactcacag cacagtgtgt gatgctgtcc ttcctggacc ccattctgtc cggaggctca   1472

tggcccatat ttcccacatt tctaatacca ccacccctgt gcttcaggcc ctccaaaccc   1532

ctgtgttccc caaatgttcc atgcccttct ttgtatcact gactattata tgttgctctc   1592

ttgcctaaat cttcctctga agtaaaagat ctcaaaagga cagatcatta atgactggaa   1652

aaaaaaaaaa                                                          1662
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<210> 33
<211> 1320
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (103)..(963)

<400> 33

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acggcgggag gacagcgctg cgaggaggcg cccgggacag tc   atg gag cgc cgc     114
                                                 Met Glu Arg Arg
                                                   1

ctg gga gtg agg gcc tgg gtg aag gag aac cgg ggc tcc ttc cag ccc      162
Leu Gly Val Arg Ala Trp Val Lys Glu Asn Arg Gly Ser Phe Gln Pro
  5                  10                  15                  20

ccg gtc tgc aac aag ctc atg cac cag gag cag ctc aaa gtc atg ttc      210
Pro Val Cys Asn Lys Leu Met His Gln Glu Gln Leu Lys Val Met Phe
 21                  26                  31                  36

atc gga ggc ccc aac acc agg aag gac tat cac atc gaa gag ggt gaa      258
Ile Gly Gly Pro Asn Thr Arg Lys Asp Tyr His Ile Glu Glu Gly Glu
 37                  42                  47                  52
```

```
gag gta ttt tac cag ctg gag gga gac atg gtt ctc cga gtc ctg gag      306
Glu Val Phe Tyr Gln Leu Glu Gly Asp Met Val Leu Arg Val Leu Glu
 53                  58                  63                  68

caa ggg aaa cac cgg gat gtg gtc att cgg cag gga gag ata ttc ctc      354
Gln Gly Lys His Arg Asp Val Val Ile Arg Gln Gly Glu Ile Phe Leu
 69                  74                  79                  84

ctg cct gcc agg gtg ccc cac tca cca cag agg ttt gcc aac acc gtg      402
Leu Pro Ala Arg Val Pro His Ser Pro Gln Arg Phe Ala Asn Thr Val
 85                  90                  95                 100

ggg ctg gtg gtt gag cga agg cgg ctg gag acc gag cta gat ggg ctc      450
Gly Leu Val Val Glu Arg Arg Arg Leu Glu Thr Glu Leu Asp Gly Leu
101                 106                 111                 116

agg tac tat gtg ggc gac acc atg gac gtt ctg ttt gag aag tgg ttc      498
Arg Tyr Tyr Val Gly Asp Thr Met Asp Val Leu Phe Glu Lys Trp Phe
117                 122                 127                 132

tac tgc aag gac ctc ggc acg cag ttg gcc ccc atc atc cag gag ttc      546
Tyr Cys Lys Asp Leu Gly Thr Gln Leu Ala Pro Ile Ile Gln Glu Phe
133                 138                 143                 148

ttc agc tct gag cag tac aga aca gga aag ccc atc cct gac cag ctg      594
Phe Ser Ser Glu Gln Tyr Arg Thr Gly Lys Pro Ile Pro Asp Gln Leu
149                 154                 159                 164

ctc aag gag cca cca ttc cct ctg agc aca cga tcc atc atg gag ccc      642
Leu Lys Glu Pro Pro Phe Pro Leu Ser Thr Arg Ser Ile Met Glu Pro
165                 170                 175                 180

atg tcc ctg gat gcc tgg ctg gac agc cac cac agg gag ctg cag gca      690
Met Ser Leu Asp Ala Trp Leu Asp Ser His His Arg Glu Leu Gln Ala
181                 186                 191                 196

ggc aca cca ctc agc ctg ttt ggg gac acc tat gag acc cag gtg atc      738
Gly Thr Pro Leu Ser Leu Phe Gly Asp Thr Tyr Glu Thr Gln Val Ile
197                 202                 207                 212

gcc tat ggg caa ggc agc agc gaa ggc ctg aga cag aat gtg gac gtg      786
Ala Tyr Gly Gln Gly Ser Ser Glu Gly Leu Arg Gln Asn Val Asp Val
213                 218                 223                 228

tgg ctg tgg cag ctg gag ggc tcc tcg gtg gtg aca atg ggg gga cgg      834
Trp Leu Trp Gln Leu Glu Gly Ser Ser Val Val Thr Met Gly Gly Arg
229                 234                 239                 244

cgc ctg agc ctg gcc cct gat gac agc ctc ctg gtg cta gct ggg acc      882
Arg Leu Ser Leu Ala Pro Asp Asp Ser Leu Leu Val Leu Ala Gly Thr
245                 250                 255                 260

tcg tat gcc tgg gag cga aca caa ggc tct gtg gcc ctg tct gtg acc      930
Ser Tyr Ala Trp Glu Arg Thr Gln Gly Ser Val Ala Leu Ser Val Thr
261                 266                 271                 276

cag gac cct gcc tgc aag aag ccc ctg ggg tga ccctcttg ccatggcctg      981
```

```
Gln Asp Pro Ala Cys Lys Lys Pro Leu Gly  *
277                 282                 287

aagcagccac aggtgtgcca agcaccctcg agtgccatcc ctgccaaaca actctcccag   1041

cccccactac ctctctgtgt actgccgctg tgtcccccac agacctgcac attgttgtca   1101

cccaccctcc tgcccttctc agcccagatg ccatgcccct gggcgggcag cagctcccca   1161

tcttctctgg cagactcagc ccactgcctt gccagtcttg ccaggtggtc tacccccggc   1221

cccgctcctg cccattcctc tgtccctgca gactcagtgc agcacttcca caccaagaag   1281

gccctcaata aaggcttcct gaggaacgca aaaaaaaaa                          1320
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<210> 34
<211> 4176
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1508)..(3430)

<400> 34

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ggaactcagc accgcgcagg actcggcgtg agcctcggcg ccggaggtac tgcatttgca    120

ccgatgctgc ccacggcgct cggacgcggg gcccacgccg ctgattatcc ggcgtccaac    180

ttctctccca cacaccggga tcgctgactg gtcccaatgg atgtggtgtg aaggaagcgc    240

acgcgtcctc cgtggaacac gccggccgtc ggcgttaaac ttgtaggaca aaccgccggg    300

agacggcgag ggcggcccga tgccaccagg gaaaacagac ccaaccaggc ctggcatccg    360

cacagacccg ggggaggcgg aagtgggtcc cggggaggcg gaagcgggtc gcgggttccg    420

gcggaggggg aagtgggttc cggggaggcg gaagcgggtc ttggggaggc ggaagtgggt    480

cccggggagg cggaagcggg tcttggggag gcggaagcgg gttccgggga gacagaagcg    540

ggttccgggg aggcggaagc gggtcccggg gaggcggaat cgggttccgg ggaggcggaa    600

gcgggtcctg gggaggcaga agcgggtctt ggggaggcgg aagtgggttc cggggaggca    660

gacgcatgtt ccgggggacg gggaagcagg ttccggggag gcggaagcgg gtcctgggga    720

ggcggattcg ggttccgggg aggtggaagc gggtcctggg gaggcggaag cgggttccgg    780

gggacgggga agtgggttcc agggaggcgg acgcgggttc cggggaggcg gaagccggtc    840

ttggggaggc ggaagtgggt tccgggggag ggggaagcgg gttccgggga ggcggaagcg    900
```

```
ggtcttgggg aggcggaagt gggttccggg gaggcggaag cgggtcccgg ggaggcggag    960

gcgggttccg gggaggcgga agcgggtcct ggggaggcgg aagcgggtct tggggaggcg   1020

gaagagggtt ccggggaggc ggaagcgggt cctggggagg cagaagccgg ttgtactgcg   1080

caggccgagc gcgccggtag tggcgtgcgg gagtggctga tcattttccc agacgccgta   1140

atgactgcag ctgtaggaca gctgctctct cagaagacgg gggactatgc acggcgctgt   1200

caccctgca ggtgacttca cacggtttag tgacgccgtg ggaacccgga ccccagcgcc   1260

tccgggtggg ggcagccgcc ggccgccggc cggggatggg ggtccggggt ggcgggagag   1320

caggaaggat ggggagggga cacctggctc gcggggtccg ggggtcccgg aggagagggt   1380

gggggagggg aggccgccgc gaacgggctc ccgggggggg tgggggggac tcacccgcac   1440

gacgtaggag accccgggcc ccaggaccct ggcgtcgggg tgtagccagc cgtgcgcggg   1500

tttgtgg  atg aag ctg ccc ttc cgg atc cac tcg gcg gcg gcg gcg gcg      1549
         Met Lys Leu Pro Phe Arg Ile His Ser Ala Ala Ala Ala Ala
           1               5                  10

tcc ccg gac ccc gcc gcc ccc cgc ccg ccc cgc gac ccc cgc gac ccc      1597
Ser Pro Asp Pro Ala Ala Pro Arg Pro Pro Arg Asp Pro Arg Asp Pro
 15                  20                  25                  30

gcg ccc cga cag cgg ctg agc gcg ggc agg gga cag ggc gcg gcg cag      1645
Ala Pro Arg Gln Arg Leu Ser Ala Gly Arg Gly Gln Gly Ala Ala Gln
 31                  36                  41                  46

cgg ggc tcg cag gcg ccc agg acg gcg gcc gcc agc gcc ggg acg ccc      1693
Arg Gly Ser Gln Ala Pro Arg Thr Ala Ala Ala Ser Ala Gly Thr Pro
 47                  52                  57                  62

ccc ggg ccc gcc ggc tcg ggt tgg ggg tcc gcg ccc ccc gag gcc cca      1741
Pro Gly Pro Ala Gly Ser Gly Trp Gly Ser Ala Pro Pro Glu Ala Pro
 63                  68                  73                  78

gcc gcc cgc gcc gcc gcc ggg ccg cgg ccc agg aag ccg ccc ggg gcc      1789
Ala Ala Arg Ala Ala Ala Gly Pro Arg Pro Arg Lys Pro Pro Gly Ala
 79                  84                  89                  94

gcg aac ttc cac tgc ggc att cgg ggc agc aac gcg cag aag gtg gtg      1837
Ala Asn Phe His Cys Gly Ile Arg Gly Ser Asn Ala Gln Lys Val Val
 95                 100                 105                 110

ggc gcc tcg ggc tcg ggg ggc gcg ggc ccc caa ccc gat ccg gcg ggc      1885
Gly Ala Ser Gly Ser Gly Gly Ala Gly Pro Gln Pro Asp Pro Ala Gly
111                 116                 121                 126

ccg ggg ggc gtc ccg gcg ctg gcg gcc gcc gtc ctg ggc gcc tgc gag      1933
Pro Gly Gly Val Pro Ala Leu Ala Ala Ala Val Leu Gly Ala Cys Glu
127                 132                 137                 142
```

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ccc cgc tgc gcc gcg ccc tgt ccc ctg ccc gcg ctc agc cgc tgt cgg     1981
Pro Arg Cys Ala Ala Pro Cys Pro Leu Pro Ala Leu Ser Arg Cys Arg
143                 148                 153                 158

ggc gcg ggg tcg cgg ggg tcg cgg ggc ggg cgg ggg gcg gcg ggg tcc     2029
Gly Ala Gly Ser Arg Gly Ser Arg Gly Gly Arg Gly Ala Ala Gly Ser
159                 164                 169                 174

ggg gac gcc gcc gcc gcc gcc gag tgg atc cgg aag ggc agc ttc atc     2077
Gly Asp Ala Ala Ala Ala Ala Glu Trp Ile Arg Lys Gly Ser Phe Ile
175                 180                 185                 190

cac aaa ccc gcg cac ggc tgg cta cac ccc gac gcc agg gtc ctg ggg     2125
His Lys Pro Ala His Gly Trp Leu His Pro Asp Ala Arg Val Leu Gly
191                 196                 201                 206

ccc ggg gtc tcc tac gtc gtg cgg tac atg ggc tgc atc gag gtt ctc     2173
Pro Gly Val Ser Tyr Val Val Arg Tyr Met Gly Cys Ile Glu Val Leu
207                 212                 217                 222

cgc tct atg cgc tcc ctg gac ttt aac acg cgc acg cag gtg acc agg     2221
Arg Ser Met Arg Ser Leu Asp Phe Asn Thr Arg Thr Gln Val Thr Arg
223                 228                 233                 238

gaa gcc atc aac cgg ctc cat gag gcc gtg cct ggc gtc cgg gga tcc     2269
Glu Ala Ile Asn Arg Leu His Glu Ala Val Pro Gly Val Arg Gly Ser
239                 244                 249                 254

tgg aag aaa aag gcc ccc aac aag gcc ctg gcg tcc gtc ctg ggc aag     2317
Trp Lys Lys Lys Ala Pro Asn Lys Ala Leu Ala Ser Val Leu Gly Lys
255                 260                 265                 270

agc aac ctt cgc ttt gcc ggc atg agc atc tcc atc cac atc tcc act     2365
Ser Asn Leu Arg Phe Ala Gly Met Ser Ile Ser Ile His Ile Ser Thr
271                 276                 281                 286

gat ggc ctc agc ctc tcc gtg cct gcc acg cgc cag gtc atc gcc aac     2413
Asp Gly Leu Ser Leu Ser Val Pro Ala Thr Arg Gln Val Ile Ala Asn
287                 292                 297                 302

cac cac atg ccg tcc atc tcc ttc gcg tca ggc gga gac acg gac atg     2461
His His Met Pro Ser Ile Ser Phe Ala Ser Gly Gly Asp Thr Asp Met
303                 308                 313                 318

acg gat tac gtg gcc tac gtc gcc aag gac ccc atc aac cag aga gcc     2509
Thr Asp Tyr Val Ala Tyr Val Ala Lys Asp Pro Ile Asn Gln Arg Ala
319                 324                 329                 334

tgc cac atc ctg gag tgc tgt gag ggc ctg gca cag agc atc atc agc     2557
Cys His Ile Leu Glu Cys Cys Glu Gly Leu Ala Gln Ser Ile Ile Ser
335                 340                 345                 350

acc gtg ggc caa gct ttc gag ctg cgc ttc aag cag tac ctg cac agc     2605
Thr Val Gly Gln Ala Phe Glu Leu Arg Phe Lys Gln Tyr Leu His Ser
351                 356                 361                 366

ccg ccc aag gtg gcg ctg ccc cca gaa agg ctg gca ggg ccg gag gag     2653
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09509203.1 : 09509203

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Pro Pro Lys Val Ala Leu Pro Pro Glu Arg Leu Ala Gly Pro Glu Glu
367                 372                 377                 382

tcg gcc tgg ggg gac gag gag gac tct ttg gag cac aat tac tac aac     2701
Ser Ala Trp Gly Asp Glu Glu Asp Ser Leu Glu His Asn Tyr Tyr Asn
383                 388                 393                 398

agc atc ccg ggg aag gag ccg ccg ctg ggc ggg cta gtg gac tcc agg     2749
Ser Ile Pro Gly Lys Glu Pro Pro Leu Gly Gly Leu Val Asp Ser Arg
399                 404                 409                 414

ctg gcc ctg aca cag ccc tgc gcc ctc acg gcc ctc gac cag ggc cca     2797
Leu Ala Leu Thr Gln Pro Cys Ala Leu Thr Ala Leu Asp Gln Gly Pro
415                 420                 425                 430

tct cct tct cta aga gat gcc tgc agc ctg cca tgg gac gtg ggg tcc     2845
Ser Pro Ser Leu Arg Asp Ala Cys Ser Leu Pro Trp Asp Val Gly Ser
431                 436                 441                 446

acc ggt aca gct cca ccg ggg gac ggc tac gtg cag gcg gac gcc cgg     2893
Thr Gly Thr Ala Pro Pro Gly Asp Gly Tyr Val Gln Ala Asp Ala Arg
447                 452                 457                 462

ggc ccc ccg gac cac gag gag cac ctg tat gtc aac acc cag ggt ctg     2941
Gly Pro Pro Asp His Glu Glu His Leu Tyr Val Asn Thr Gln Gly Leu
463                 468                 473                 478

gac gcc ccc gag ccg gag gac agc ccc aaa aag gat ctg ttt gac atg     2989
Asp Ala Pro Glu Pro Glu Asp Ser Pro Lys Lys Asp Leu Phe Asp Met
479                 484                 489                 494

cga ccc ttt gag gat gcc ctg aag ttg cat gag tgc tca gtg gcg gca     3037
Arg Pro Phe Glu Asp Ala Leu Lys Leu His Glu Cys Ser Val Ala Ala
495                 500                 505                 510

ggc gtg aca gca gcc cct ctt ccc ttg gag gac cag tgg ccc agc ccc     3085
Gly Val Thr Ala Ala Pro Leu Pro Leu Glu Asp Gln Trp Pro Ser Pro
511                 516                 521                 526

cct acc cgc cgg gcc cct gtg gcc ccc acg gag gaa cag ctg cgt cag     3133
Pro Thr Arg Arg Ala Pro Val Ala Pro Thr Glu Glu Gln Leu Arg Gln
527                 532                 537                 542

gag ccc tgg tac cac ggc cgg atg agc cgc cgg gcg gca gag agg atg     3181
Glu Pro Trp Tyr His Gly Arg Met Ser Arg Arg Ala Ala Glu Arg Met
543                 548                 553                 558

ctt cga gct gac ggg gac ttc ctt gtg cga gac agc gtc acc aac ccc     3229
Leu Arg Ala Asp Gly Asp Phe Leu Val Arg Asp Ser Val Thr Asn Pro
559                 564                 569                 574

ggg cag tat gtc ctc acc ggc atg cac gcc ggg cag ccc aag cac ctg     3277
Gly Gln Tyr Val Leu Thr Gly Met His Ala Gly Gln Pro Lys His Leu
575                 580                 585                 590

ctg ctc gtg gac ccc gag ggc gtg gta cgg acg aag gac gtg ctg ttt     3325
Leu Leu Val Asp Pro Glu Gly Val Val Arg Thr Lys Asp Val Leu Phe
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591                 596                 601                 606

gag agc atc agc cac ctg atc gac cac cac ctg cag aac ggg cag ccc     3373
Glu Ser Ile Ser His Leu Ile Asp His His Leu Gln Asn Gly Gln Pro
607                 612                 617                 622

atc gtg gcc gcc gag agt gag ctg cac ctg cgt ggc gtg gtc tca cgg     3421
Ile Val Ala Ala Glu Ser Glu Leu His Leu Arg Gly Val Val Ser Arg
623                 628                 633                 638

gag ccc tga gccaggt gaccgttctc agccctggct cctgcctgtt ctcagccccg     3477
Glu Pro  *
639

gctcctgcct gtcatggcct tggggctctc agccctcctc ctggatcctg gtcaggccga   3537

accaccgctg cctctccttc ctccgcatga gcctctggca tggtccttcc tccagctggc   3597

cccgggctgg gcagagcctc ctcctgccgg ggcccctgcc cacccctcc tttgcctgga   3657

gtgagggtgt tcataccaaa gacggaacca tttcgccttt aaagaaaata tatccagaag   3717

cagccgctgc ctcggagccc tggcccgtgg gtccccctct cgcctggctg gttcggtcta   3777

acgccccgga gagtcagagc tcccaggacc ctggggagga ggcggattcc gggcctggct   3837

gggcttcctc ttcccacctg aggactgggt gcacagttgt ctttgagggg ggacgcttaa   3897

ggtgctttgg ggttctcagg ccaggataca tgctggcgct gaagtgcagg cagccttgag   3957

gtcacctggg atctcggggt agccaggctg ctccaagaca gtggatatcg aggcagtcgt   4017

gaggccccta ctccacctgg gagcagggga aggacgtggt tgcctggcct gggctgcgcc   4077

cagcagcttc cccccaatcc tgccctccca gctgtcgacc cagatgggat gttcggatcg   4137

gtttgtaatt aaacctggga atggccacaa gaaaaaaaa                          4176
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Oligo Primer Pair No. 5

<210> 35
<211> 2722
<212> DNA
<213> Homo sapiens

<220>
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<222> (68)..(1021)

<400> 35

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tgctggg  atg act atg gag acc caa atg tct cag aat gta tgt ccc aga     109
         Met Thr Met Glu Thr Gln Met Ser Gln Asn Val Cys Pro Arg
           1               5                  10
```

```
aac ctg tgg ctg ctt caa cca ttg aca gtt ttg ctg ctg ctg gct tct      157
Asn Leu Trp Leu Leu Gln Pro Leu Thr Val Leu Leu Leu Leu Ala Ser
 15                  20                  25                  30

gca gac agt caa gct gca gct ccc cca aag gct gtg ctg aaa ctt gag      205
Ala Asp Ser Gln Ala Ala Ala Pro Pro Lys Ala Val Leu Lys Leu Glu
 31                  36                  41                  46

ccc ccg tgg atc aac gtg ctc cag gag gac tct gtg act ctg aca tgc      253
Pro Pro Trp Ile Asn Val Leu Gln Glu Asp Ser Val Thr Leu Thr Cys
 47                  52                  57                  62

cag ggg gct cgc agc cct gag agc gac tcc att cag tgg ttc cac aat      301
Gln Gly Ala Arg Ser Pro Glu Ser Asp Ser Ile Gln Trp Phe His Asn
 63                  68                  73                  78

ggg aat ctc att ccc acc cac acg cag ccc agc tac agg ttc aag gcc      349
Gly Asn Leu Ile Pro Thr His Thr Gln Pro Ser Tyr Arg Phe Lys Ala
 79                  84                  89                  94

aac aac aat gac agc ggg gag tac acg tgc cag act ggc cag acc agc      397
Asn Asn Asn Asp Ser Gly Glu Tyr Thr Cys Gln Thr Gly Gln Thr Ser
 95                 100                 105                 110

ctc agc gac cct gtg cat ctg act gtg ctt tcc gaa tgg ctg gtg ctc      445
Leu Ser Asp Pro Val His Leu Thr Val Leu Ser Glu Trp Leu Val Leu
111                 116                 121                 126

cag acc cct cac ctg gag ttc cag gag gga gaa acc atc atg ctg agg      493
Gln Thr Pro His Leu Glu Phe Gln Glu Gly Glu Thr Ile Met Leu Arg
127                 132                 137                 142

tgc cac agc tgg aag gac aag cct ctg gtc aag gtc aca ttc ttc cag      541
Cys His Ser Trp Lys Asp Lys Pro Leu Val Lys Val Thr Phe Phe Gln
143                 148                 153                 158

aat gga aaa tcc cag aaa ttc tcc cat ttg gat ccc acc ttc tcc atc      589
Asn Gly Lys Ser Gln Lys Phe Ser His Leu Asp Pro Thr Phe Ser Ile
159                 164                 169                 174

cca caa gca aac cac agt cac agt ggt gat tac cac tgc aca gga aac      637
Pro Gln Ala Asn His Ser His Ser Gly Asp Tyr His Cys Thr Gly Asn
175                 180                 185                 190

ata ggc tac acg ctg ttc tca tcc aag cct gtg acc atc act gtc caa      685
Ile Gly Tyr Thr Leu Phe Ser Ser Lys Pro Val Thr Ile Thr Val Gln
191                 196                 201                 206

gtg ccc agc atg ggc agc tct tca cca atg ggg atc att gtg gct gtg      733
Val Pro Ser Met Gly Ser Ser Ser Pro Met Gly Ile Ile Val Ala Val
207                 212                 217                 222

gtc att gcg act gct gta gca gcc att gtt gct gct gta gtg gcc ttg      781
Val Ile Ala Thr Ala Val Ala Ala Ile Val Ala Ala Val Val Ala Leu
223                 228                 233                 238

atc tac tgc agg aaa aag cgg att tca gcc aat tcc act gat cct gtg      829
```

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Ile Tyr Cys Arg Lys Lys Arg Ile Ser Ala Asn Ser Thr Asp Pro Val
239                 244                 249                 254

aag gct gcc caa ttt gag cca cct gga cgt caa atg att gcc atc aga      877
Lys Ala Ala Gln Phe Glu Pro Pro Gly Arg Gln Met Ile Ala Ile Arg
255                 260                 265                 270

aag aga caa ctt gaa gaa acc aac aat gac tat gaa aca gct gac ggc      925
Lys Arg Gln Leu Glu Glu Thr Asn Asn Asp Tyr Glu Thr Ala Asp Gly
271                 276                 281                 286

ggc tac atg act ctg aac ccc agg gca cct act gac gat gat aaa aac      973
Gly Tyr Met Thr Leu Asn Pro Arg Ala Pro Thr Asp Asp Asp Lys Asn
287                 292                 297                 302

atc tac ctg act ctt cct ccc aac gac cat gtc aac agt aat aac taa     1021
Ile Tyr Leu Thr Leu Pro Pro Asn Asp His Val Asn Ser Asn Asn  *
303                 308                 313                 318

agagtaacgt tatgccatgt ggtcatactc tcagcttgct gagtggatga caaaaagagg   1081

ggaattgtta aaggaaaatt taaatggaga ctggaaaaat cctgagcaaa caaaaccacc   1141

tggcccttag aaatagcttt aactttgctt aaactacaaa cacaagcaaa acttcacggg   1201

gtcatactac atacaagcat aagcaaaact taacttggat catttctggt aaatgcttat   1261

gttagaaata agacaacccc agccaatcac aagcagccta ctaacatata attaggtgac   1321

tagggacttt ctaagaagat acctaccccc aaaaaacaat tatgtaattg aaaaccaacc   1381

gattgccttt attttgcttc cacattttcc caataaatac ttgcctgtga cattttgcca   1441

ctggaacact aaacttcatg aattgcgcct caggattttt cctttaacat ctttttttt   1501

ttttgacaga gtctcaatct gttacccggg ctgggagtgc agtggtgcta tcttgggctc   1561

actggcaaac ccgcctccca gggttttaag gcgatttctt catggcctca gcctcccagt   1621

aggctgggga ttagagggca tgtgccatca tacccagcta atttttgtat tttttatttt   1681

ttttttttag tagagacagg gtttcgcaat gttggccagg ccgatctcga acttctggcc   1741

tctagcgatc tgcccgcctc ggcctcccaa agtgctggga tgaccagcat cagccccaat   1801

gtccagcctc tttaacatct tctttcctat gccctctctg tggatcccta ctgctggttt   1861

ctgccttctc catgctgaga acaaaatcac ctattcactg cttatgcagt cggaagctcc   1921

agaagaacaa agagcccaat taccagaacc acattaagtc tccattgttt tgccttggga   1981

tttgagaaga gaattagaga ggtgaggatc tggtatttcc tggactaaat tccccttggg   2041

gaagacgaag ggatgctgca gttccaaaag agaaggactc ttccagagtc atctacctga   2101

gtcccaaagc tccctgtcct gaaagccaca gacaatatgg tcccaaatga ctgactgcac   2161
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cttctgtgcc tcagccgttc ttgacatcaa gaatcttctg ttccacatcc acacagccaa   2221

tacaattagt caaaccactg ttattaacag atgtagcaac atgagaaacg cttatgttac   2281

aggttacatg agagcaatca tgtaagtcta tatgacttca gaaatgttaa aatagactaa   2341

cctctaacaa caaattaaaa gtgattgttt caaggtgatg caattattga tgacctattt   2401

tatttttcta taatgatcat atattacctt tgtaataaaa cattataacc aaaacattct   2461

gtttaccttt tcagggctgt attgattggg gtgtagactg aactatccgg ggtctgtttc   2521

ttttcggtga tgaaagtctt gagaaggtag taatggataa gatgtgaggg agaggagaga   2581

gggagatttg gagtgtaggg tgagtgcccc tcttcttaga actgaatact cttcttctaa   2641

tgaacttgta ttcttgtttc catgtcttct tccctttcct tctatagcaa ataaagcatt   2701

cactttgttt tggaaaaaaa a                                            2722
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<210> 36
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<400> 36

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tgctggg  atg act atg gag acc caa atg tct cag aat gta tgt ccc aga     109
         Met Thr Met Glu Thr Gln Met Ser Gln Asn Val Cys Pro Arg
           1               5                  10

aac ctg tgg ctg ctt caa cca ttg aca gtt ttg ctg ctg ctg gct tct      157
Asn Leu Trp Leu Leu Gln Pro Leu Thr Val Leu Leu Leu Leu Ala Ser
 15                  20                  25                  30

gca gac agt caa gct gca gct ccc cca aag gct gtg ctg aaa ctt gag      205
Ala Asp Ser Gln Ala Ala Ala Pro Pro Lys Ala Val Leu Lys Leu Glu
 31                  36                  41                  46

ccc ccg tgg atc aac gtg ctc cag gag gac tct gtg act ctg aca tgc      253
Pro Pro Trp Ile Asn Val Leu Gln Glu Asp Ser Val Thr Leu Thr Cys
 47                  52                  57                  62

cag ggg gct cgc agc cct gag agc gac tcc att cag tgg ttc cac aat      301
Gln Gly Ala Arg Ser Pro Glu Ser Asp Ser Ile Gln Trp Phe His Asn
 63                  68                  73                  78

ggg aat ctc att ccc acc cac acg cag ccc agc tac agg ttc aag gcc      349
Gly Asn Leu Ile Pro Thr His Thr Gln Pro Ser Tyr Arg Phe Lys Ala
```

```
 79                  84                  89                  94

aac aac aat gac agc ggg gag tac acg tgc cag act ggc cag acc agc      397
Asn Asn Asn Asp Ser Gly Glu Tyr Thr Cys Gln Thr Gly Gln Thr Ser
 95                 100                 105                 110

ctc agc gac cct gtg cat ctg act gtg ctt tcc gaa tgg ctg gtg ctc      445
Leu Ser Asp Pro Val His Leu Thr Val Leu Ser Glu Trp Leu Val Leu
111                 116                 121                 126

cag acc cct cac ctg gag ttc cag gag gga gaa acc atc atg ctg agg      493
Gln Thr Pro His Leu Glu Phe Gln Glu Gly Glu Thr Ile Met Leu Arg
127                 132                 137                 142

tgc cac agc tgg aag gac aag cct ctg gtc aag gtc aca ttc ttc cag      541
Cys His Ser Trp Lys Asp Lys Pro Leu Val Lys Val Thr Phe Phe Gln
143                 148                 153                 158

aat gga aaa tcc cag aaa ttc tcc cat ttg gat ccc acc ttc tcc atc      589
Asn Gly Lys Ser Gln Lys Phe Ser His Leu Asp Pro Thr Phe Ser Ile
159                 164                 169                 174

cca caa gca aac cac agt cac agt ggt gat tac cac tgc aca gga aac      637
Pro Gln Ala Asn His Ser His Ser Gly Asp Tyr His Cys Thr Gly Asn
175                 180                 185                 190

ata ggc tac acg ctg ttc tca tcc aag cct gtg acc atc act gtc caa      685
Ile Gly Tyr Thr Leu Phe Ser Ser Lys Pro Val Thr Ile Thr Val Gln
191                 196                 201                 206

gcc aat tcc act gat cct gtg aag gct gcc caa ttt gag cca cct gga      733
Ala Asn Ser Thr Asp Pro Val Lys Ala Ala Gln Phe Glu Pro Pro Gly
207                 212                 217                 222

cgt caa atg att gcc atc aga aag aga caa ctt gaa gaa acc aac aat      781
Arg Gln Met Ile Ala Ile Arg Lys Arg Gln Leu Glu Glu Thr Asn Asn
223                 228                 233                 238

gac tat gaa aca gct gac ggc ggc tac atg act ctg aac ccc agg gca      829
Asp Tyr Glu Thr Ala Asp Gly Gly Tyr Met Thr Leu Asn Pro Arg Ala
239                 244                 249                 254

cct act gac gat gat aaa aac atc tac ctg act ctt cct ccc aac gac      877
Pro Thr Asp Asp Asp Lys Asn Ile Tyr Leu Thr Leu Pro Pro Asn Asp
255                 260                 265                 270

cat gtc aac agt aat aac taa ag agtaacgtta tgccatgtgg tcatactctc      930
His Val Asn Ser Asn Asn  *
271                 276

agcttgctga gtggatgaca aaaagagggg aattgttaaa ggaaaattta aatggagact    990

ggaaaaatcc tgagcaaaca aaaccacctg gcccttagaa atagctttaa ctttgcttaa   1050

actacaaaca caagcaaaac ttcacggggt catactacat acaagcataa gcaaaactta   1110

acttggatca tttctggtaa atgcttatgt tagaaataag acaaccccag ccaatcacaa   1170
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gcagcctact aacatataat taggtgacta gggactttct aagaagatac ctacccccaa 1230

aaaacaatta tgtaattgaa aaccaaccga ttgcctttat tttgcttcca cattttccca 1290

ataaatactt gcctgtgaca ttttgccact ggaacactaa acttcatgaa ttgcgcctca 1350

ggatttttcc tttaacatct ttttttttt ttgacagagt ctcaatctgt tacccgggct 1410

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tgctgggatg accagcatca gccccaatgt ccagcctctt taacatcttc tttcctatgc 1710

cctctctgtg gatccctact gctggtttct gccttctcca tgctgagaac aaaatcacct 1770

attcactgct tatgcagtcg gaagctccag aagaacaaag agcccaatta ccagaaccac 1830

attaagtctc cattgttttg ccttgggatt tgagaagaga attagagagg tgaggatctg 1890

gtatttcctg gactaaattc cccttgggga agacgaaggg atgctgcagt tccaaaagag 1950

aaggactctt ccagagtcat ctacctgagt cccaaagctc cctgtcctga aagccacaga 2010

caatatggtc ccaaatgact gactgcacct tctgtgcctc agccgttctt gacatcaaga 2070

atcttctgtt ccacatccac acagccaata caattagtca aaccactgtt attaacagat 2130

gtagcaacat gagaaacgct tatgttacag gttacatgag agcaatcatg taagtctata 2190

tgacttcaga aatgttaaaa tagactaacc tctaacaaca aattaaaagt gattgtttca 2250

aggtgatgca attattgatg acctatttta tttttctata atgatcatat attacctttg 2310

taataaaaca ttataaccaa aacattctgt ttacctttc agggctgtat tgattggggt 2370

gtagactgaa ctatccgggg tctgtttctt ttcggtgatg aaagtcttga gaaggtagta 2430

atggataaga tgtgagggag aggagagagg gagatttgga gtgtagggtg agtgcccctc 2490

ttcttagaac tgaatactct tcttctaatg aacttgtatt cttgtttcca tgtcttcttc 2550

cctttccttc tatagcaaat aaagcattca ctttgttttg gaaaaaaaa 2599

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<213> Homo sapiens

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<222> (267)..(3308)

<400> 37

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tccggacgct ggagaagctc acagcatctg tggccggtgg tgcagctaac ttttttggtg    180

acattgaaag agatttaggt ccaagagata cgagcagggg aattaggggt gggaatttgg    240

gggacagagg ctgttcttca gcggaa atg gcc tat gcc tcc tgg cag agg tgg     293
                            Met Ala Tyr Ala Ser Trp Gln Arg Trp
                              1               5

tcc cca gtg gaa tgg gcc cgg tgg atg tgg aca gcg gtg acc agc agt      341
Ser Pro Val Glu Trp Ala Arg Trp Met Trp Thr Ala Val Thr Ser Ser
 10                  15                  20                  25

ggg gac tcc agt ctg ctg gtg ctt cag gga gac tct gga aaa agg agt      389
Gly Asp Ser Ser Leu Leu Val Leu Gln Gly Asp Ser Gly Lys Arg Ser
 26                  31                  36                  41

tcc gat tct gaa gag gca ttt gag acc ccg gag tca acg acc cct gtc      437
Ser Asp Ser Glu Glu Ala Phe Glu Thr Pro Glu Ser Thr Thr Pro Val
 42                  47                  52                  57

aaa gct ccg cca gct cca ccc cca cca ccc ccc gaa gtc atc cca gaa      485
Lys Ala Pro Pro Ala Pro Pro Pro Pro Pro Pro Glu Val Ile Pro Glu
 58                  63                  68                  73

ccc gag gtc agc aca cag cca ccc ccg gaa gaa cca gga tgt ggt tct      533
Pro Glu Val Ser Thr Gln Pro Pro Pro Glu Glu Pro Gly Cys Gly Ser
 74                  79                  84                  89

gag aca gtc cct gtc cct gat ggc cca cgg agc gac tcg gtg gaa gga      581
Glu Thr Val Pro Val Pro Asp Gly Pro Arg Ser Asp Ser Val Glu Gly
 90                  95                 100                 105

agt ccc ttc cgt ccc ccg tca cac tcc ttc tct gcc gtc ttc gat gaa      629
Ser Pro Phe Arg Pro Pro Ser His Ser Phe Ser Ala Val Phe Asp Glu
106                 111                 116                 121

gac aag ccg ata gcc agc agt ggg act tac aac ttg gac ttt gac aac      677
Asp Lys Pro Ile Ala Ser Ser Gly Thr Tyr Asn Leu Asp Phe Asp Asn
122                 127                 132                 137

att gag ctt gtg gat acc ttt cag acc ttg gag cct cgt gcc tca gac      725
Ile Glu Leu Val Asp Thr Phe Gln Thr Leu Glu Pro Arg Ala Ser Asp
138                 143                 148                 153

gct aag aat cag gag ggc aaa gtg aac aca cgg agg aag tcc acg gat      773
Ala Lys Asn Gln Glu Gly Lys Val Asn Thr Arg Arg Lys Ser Thr Asp
154                 159                 164                 169
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tcc gtc ccc atc tct aag tct aca ctg tcc cgg tcg ctc agc ctg caa      821
Ser Val Pro Ile Ser Lys Ser Thr Leu Ser Arg Ser Leu Ser Leu Gln
170                 175                 180                 185

gcc agt gac ttt gat ggt gct tct tcc tca ggc aat ccc gag gcc gtg      869
Ala Ser Asp Phe Asp Gly Ala Ser Ser Ser Gly Asn Pro Glu Ala Val
186                 191                 196                 201

gcc ctt gcc cca gat gca tat agc acg ggt tcc agc agt gct tct agt      917
Ala Leu Ala Pro Asp Ala Tyr Ser Thr Gly Ser Ser Ser Ala Ser Ser
202                 207                 212                 217

acc ctt aag cga act aaa aaa ccg agg ccg cct tcc tta aaa aag aaa      965
Thr Leu Lys Arg Thr Lys Lys Pro Arg Pro Pro Ser Leu Lys Lys Lys
218                 223                 228                 233

cag acc acc aag aaa ccc aca gag acc ccc cca gtg aag gag acg caa     1013
Gln Thr Thr Lys Lys Pro Thr Glu Thr Pro Pro Val Lys Glu Thr Gln
234                 239                 244                 249

cag gag cca gat gaa gag agc ctt gtc ccc agt ggg gag aat cta gca     1061
Gln Glu Pro Asp Glu Glu Ser Leu Val Pro Ser Gly Glu Asn Leu Ala
250                 255                 260                 265

tct gag acg aaa acg gaa tct gcc aag acg gaa ggt cct agc cca gcc     1109
Ser Glu Thr Lys Thr Glu Ser Ala Lys Thr Glu Gly Pro Ser Pro Ala
266                 271                 276                 281

tta ttg gag gag acg ccc ctt gag ccc gct gtg ggg ccc aaa gct gcc     1157
Leu Leu Glu Glu Thr Pro Leu Glu Pro Ala Val Gly Pro Lys Ala Ala
282                 287                 292                 297

tgc cct ctg gac tca gag agt gca gaa ggg gtt gtc ccc ccg gct tct     1205
Cys Pro Leu Asp Ser Glu Ser Ala Glu Gly Val Val Pro Pro Ala Ser
298                 303                 308                 313

gga ggt ggc aga gtg cag aac tca ccc cct gtc ggg agg aaa acg ctg     1253
Gly Gly Gly Arg Val Gln Asn Ser Pro Pro Val Gly Arg Lys Thr Leu
314                 319                 324                 329

cct ctt acc acg gcc ccg gag gca ggg gag gta acc cca tcg gat agc     1301
Pro Leu Thr Thr Ala Pro Glu Ala Gly Glu Val Thr Pro Ser Asp Ser
330                 335                 340                 345

ggg ggg caa gag gac tct cca gcc aaa ggg ctc tcc gta agg ctg gag     1349
Gly Gly Gln Glu Asp Ser Pro Ala Lys Gly Leu Ser Val Arg Leu Glu
346                 351                 356                 361

ttt gac tat tct gag gac aag agt agt tgg gac aac cag cag gaa aac     1397
Phe Asp Tyr Ser Glu Asp Lys Ser Ser Trp Asp Asn Gln Gln Glu Asn
362                 367                 372                 377

ccc cct cct acc aaa aag ata ggc aaa aag cca gtt gcc aaa atg ccc     1445
Pro Pro Pro Thr Lys Lys Ile Gly Lys Lys Pro Val Ala Lys Met Pro
378                 383                 388                 393

ctg agg agg cca aag atg aaa aag aca ccc gag aaa ctt gac aac act     1493
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Leu Arg Arg Pro Lys Met Lys Lys Thr Pro Glu Lys Leu Asp Asn Thr
394                 399                 404                 409

cct gcc tca cct ccc aga tcc cct gct gaa ccc aat gac atc ccc att     1541
Pro Ala Ser Pro Pro Arg Ser Pro Ala Glu Pro Asn Asp Ile Pro Ile
410                 415                 420                 425

gct aaa ggt act tac acc ttt gat att gac aag tgg gat gac ccc aat     1589
Ala Lys Gly Thr Tyr Thr Phe Asp Ile Asp Lys Trp Asp Asp Pro Asn
426                 431                 436                 441

ttt aac cct ttt tct tcc acc tca aaa atg cag gag tct ccc aaa ctg     1637
Phe Asn Pro Phe Ser Ser Thr Ser Lys Met Gln Glu Ser Pro Lys Leu
442                 447                 452                 457

ccc caa caa tca tac aac ttt gac cca gac acc tgt gat gag tcc gtt     1685
Pro Gln Gln Ser Tyr Asn Phe Asp Pro Asp Thr Cys Asp Glu Ser Val
458                 463                 468                 473

gac ccc ttt aag aca tcc tct aag acc ccc agc tca cct tct aaa tcc     1733
Asp Pro Phe Lys Thr Ser Ser Lys Thr Pro Ser Ser Pro Ser Lys Ser
474                 479                 484                 489

cca gcc tcc ttt gag atc cca gcc agt gct atg gaa gcc aat gga gtg     1781
Pro Ala Ser Phe Glu Ile Pro Ala Ser Ala Met Glu Ala Asn Gly Val
490                 495                 500                 505

gac ggg gat ggg cta aac aag ccc gcc aag aag aag aag acg ccc cta     1829
Asp Gly Asp Gly Leu Asn Lys Pro Ala Lys Lys Lys Lys Thr Pro Leu
506                 511                 516                 521

aag act gac aca ttt agg gtg aaa aag tcg cca aaa cgg tct cct ctc     1877
Lys Thr Asp Thr Phe Arg Val Lys Lys Ser Pro Lys Arg Ser Pro Leu
522                 527                 532                 537

tct gat cca cct tcc cag gac ccc acc cca gct gct aca cca gaa aca     1925
Ser Asp Pro Pro Ser Gln Asp Pro Thr Pro Ala Ala Thr Pro Glu Thr
538                 543                 548                 553

cca cca gtg atc tct gcg gtg gtc cac gcc aca gat gag gaa aag ctg     1973
Pro Pro Val Ile Ser Ala Val Val His Ala Thr Asp Glu Glu Lys Leu
554                 559                 564                 569

gcg gtc acc aac cag aag tgg acg tgc atg aca gtg gac cta gag gct     2021
Ala Val Thr Asn Gln Lys Trp Thr Cys Met Thr Val Asp Leu Glu Ala
570                 575                 580                 585

gac aaa cag gac tac ccg cag ccc tcg gac ctg tcc acc ttt gta aac     2069
Asp Lys Gln Asp Tyr Pro Gln Pro Ser Asp Leu Ser Thr Phe Val Asn
586                 591                 596                 601

gag acc aaa ttc agt tca ccc act gag gag ttg gat tac aga aac tcc     2117
Glu Thr Lys Phe Ser Ser Pro Thr Glu Glu Leu Asp Tyr Arg Asn Ser
602                 607                 612                 617

tat gaa att gaa tat atg gag aaa att ggc tcc tcc tta cct cag gac     2165
Tyr Glu Ile Glu Tyr Met Glu Lys Ile Gly Ser Ser Leu Pro Gln Asp
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618                 623                 628                 633

gac gat gcc ccg aag aag cag gcc ttg tac ctt atg ttt gac act tct     2213
Asp Asp Ala Pro Lys Lys Gln Ala Leu Tyr Leu Met Phe Asp Thr Ser
634                 639                 644                 649

cag gag agc cct gtc aag tca tct ccc gtc cgc atg tca gag tcc ccg     2261
Gln Glu Ser Pro Val Lys Ser Ser Pro Val Arg Met Ser Glu Ser Pro
650                 655                 660                 665

acg ccg tgt tca ggg tca agt ttt gaa gag act gaa gcc ctt gtg aac     2309
Thr Pro Cys Ser Gly Ser Ser Phe Glu Glu Thr Glu Ala Leu Val Asn
666                 671                 676                 681

act gct gcg aaa aac cag cat cct gtc cca cga gga ctg gcc cct aac     2357
Thr Ala Ala Lys Asn Gln His Pro Val Pro Arg Gly Leu Ala Pro Asn
682                 687                 692                 697

caa gag tca cac ttg cag gtg cca gag aaa tcc tcc cag aag gag ctg     2405
Gln Glu Ser His Leu Gln Val Pro Glu Lys Ser Ser Gln Lys Glu Leu
698                 703                 708                 713

gag gcc atg ggc ttg ggc acc cct tca gaa gcg att gaa att aca gct     2453
Glu Ala Met Gly Leu Gly Thr Pro Ser Glu Ala Ile Glu Ile Thr Ala
714                 719                 724                 729

ccc gag ggc tcc ttt gcc tct gct gac gcc ctc ctc agc agg cta gct     2501
Pro Glu Gly Ser Phe Ala Ser Ala Asp Ala Leu Leu Ser Arg Leu Ala
730                 735                 740                 745

cac ccc gtc tct ctc tgt ggt gca ctt gac tat ctg gag ccc gac tta     2549
His Pro Val Ser Leu Cys Gly Ala Leu Asp Tyr Leu Glu Pro Asp Leu
746                 751                 756                 761

gca gaa aag aac ccc cca cta ttc gct cag aaa ctc cag aga gag gct     2597
Ala Glu Lys Asn Pro Pro Leu Phe Ala Gln Lys Leu Gln Arg Glu Ala
762                 767                 772                 777

gct cac cca aca gac gtc tcc atc tcc aaa aca gcc ttg tac tcc cgc     2645
Ala His Pro Thr Asp Val Ser Ile Ser Lys Thr Ala Leu Tyr Ser Arg
778                 783                 788                 793

atc ggg acc gct gag gtg gag aaa cct gca ggc ctt ctg ttc cag cag     2693
Ile Gly Thr Ala Glu Val Glu Lys Pro Ala Gly Leu Leu Phe Gln Gln
794                 799                 804                 809

ccc gac ctg gac tct gcc ctc cag atc gcc aga gca gag atc ata acc     2741
Pro Asp Leu Asp Ser Ala Leu Gln Ile Ala Arg Ala Glu Ile Ile Thr
810                 815                 820                 825

aag gag aga gag gtc tca gaa tgg aaa gat aaa tat gaa gaa agc agg     2789
Lys Glu Arg Glu Val Ser Glu Trp Lys Asp Lys Tyr Glu Glu Ser Arg
826                 831                 836                 841

cgg gaa gtg atg gaa atg agg aaa ata gtg gcc gag tat gag aag acc     2837
Arg Glu Val Met Glu Met Arg Lys Ile Val Ala Glu Tyr Glu Lys Thr
842                 847                 852                 857
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atc gct cag atg ata gag gac gaa cag aga gag aag tca gtc tcc cac     2885
Ile Ala Gln Met Ile Glu Asp Glu Gln Arg Glu Lys Ser Val Ser His
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cag acg gtg cag cag ctg gtt ctg gag aag gag caa gcc ctg gcc gac     2933
Gln Thr Val Gln Gln Leu Val Leu Glu Lys Glu Gln Ala Leu Ala Asp
874                 879                 884                 889

ctg aac tcc gtg gag aag tct ctg gcc gac ctc ttc aga aga tat gag     2981
Leu Asn Ser Val Glu Lys Ser Leu Ala Asp Leu Phe Arg Arg Tyr Glu
890                 895                 900                 905

aag atg aag gag gtc cta gaa ggc ttc cgc aag aat gaa gag gtg ttg     3029
Lys Met Lys Glu Val Leu Glu Gly Phe Arg Lys Asn Glu Glu Val Leu
906                 911                 916                 921

aag aga tgt gcg cag gag tac ctg tcc cgg gtg aag aag gag gag cag     3077
Lys Arg Cys Ala Gln Glu Tyr Leu Ser Arg Val Lys Lys Glu Glu Gln
922                 927                 932                 937

agg tac cag gcc ctg aag gtg cac gcg gag gag aaa ctg gac agg gcc     3125
Arg Tyr Gln Ala Leu Lys Val His Ala Glu Glu Lys Leu Asp Arg Ala
938                 943                 948                 953

aat gct gag att gct cag gtt cga ggc aag gcc cag cag gag caa gcc     3173
Asn Ala Glu Ile Ala Gln Val Arg Gly Lys Ala Gln Gln Glu Gln Ala
954                 959                 964                 969

gcc cac cag gcc agc ctg cgg aag gag cag ctg cga gtg gac gcc ctg     3221
Ala His Gln Ala Ser Leu Arg Lys Glu Gln Leu Arg Val Asp Ala Leu
970                 975                 980                 985

gaa agg acg ctg gag cag aag aat aaa gaa ata gaa gaa ctc acc aag     3269
Glu Arg Thr Leu Glu Gln Lys Asn Lys Glu Ile Glu Glu Leu Thr Lys
986                 991                 996                1001

att tgt gac gaa ctg att gcc aaa atg ggg aaa agc taa ctctgaaccg      3318
Ile Cys Asp Glu Leu Ile Ala Lys Met Gly Lys Ser  *
1002                1007                1012

aatgttttgg acttaactgt tgagtgcaat atgaccgtcg gcacactgct gttcctccag   3378

ttccatggac aggttctgtt ttcacttttt cgtatgcact actgtatttc ctttctaaat   3438

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ccttaaggag tgtaaacttg atctgcattt gctgatttgt ttttaaaaaa acaagaaatg   3738

catgtttcaa ataaaattct ctattgtaaa taaaattttt tctttggatc ttggcaataa   3798
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Met Ala Tyr Ala Ser Trp Gln Arg Trp
1 5

tcc cca gtg gaa tgg gcc cgg tgg atg tgg aca gcg gtg acc agc agt 341
Ser Pro Val Glu Trp Ala Arg Trp Met Trp Thr Ala Val Thr Ser Ser
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ggg gac tcc agt ctg ctg gtg ctt cag gga gac tct gga aaa agg agt 389
Gly Asp Ser Ser Leu Leu Val Leu Gln Gly Asp Ser Gly Lys Arg Ser
26 31 36 41

tcc gat tct gaa gag gca ttt gag acc ccg gag tca acg acc cct gtc 437
Ser Asp Ser Glu Glu Ala Phe Glu Thr Pro Glu Ser Thr Thr Pro Val
42 47 52 57

aaa gct ccg cca gct cca ccc cca cca ccc ccc gaa gtc atc cca gaa 485
Lys Ala Pro Pro Ala Pro Pro Pro Pro Pro Pro Glu Val Ile Pro Glu
58 63 68 73

ccc gag gtc agc aca cag cca ccc ccg gaa gaa cca gga tgt ggt tct 533
Pro Glu Val Ser Thr Gln Pro Pro Pro Glu Glu Pro Gly Cys Gly Ser
74 79 84 89

gag aca gtc cct gtc cct gat ggc cca cgg agc gac tcg gtg gaa gga 581
Glu Thr Val Pro Val Pro Asp Gly Pro Arg Ser Asp Ser Val Glu Gly
90 95 100 105

agt ccc ttc cgt ccc ccg tca cac tcc ttc tct gcc gtc ttc gat gaa 629
Ser Pro Phe Arg Pro Pro Ser His Ser Phe Ser Ala Val Phe Asp Glu

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106                 111                 116                 121

gac aag ccg ata gcc agc agt ggg act tac aac ttg gac ttt gac aac      677
Asp Lys Pro Ile Ala Ser Ser Gly Thr Tyr Asn Leu Asp Phe Asp Asn
122                 127                 132                 137

att gag ctt gtg gat acc ttt cag acc ttg gag cct cgt gcc tca gac      725
Ile Glu Leu Val Asp Thr Phe Gln Thr Leu Glu Pro Arg Ala Ser Asp
138                 143                 148                 153

gct aag aat cag gag ggc aaa gtg aac aca cgg agg aag tcc acg gat      773
Ala Lys Asn Gln Glu Gly Lys Val Asn Thr Arg Arg Lys Ser Thr Asp
154                 159                 164                 169

tcc gtc ccc atc tct aag tct aca ctg tcc cgg tcg ctc agc ctg caa      821
Ser Val Pro Ile Ser Lys Ser Thr Leu Ser Arg Ser Leu Ser Leu Gln
170                 175                 180                 185

gcc agt gac ttt gat ggt gct tct tcc tca ggc aat ccc gag gcc gtg      869
Ala Ser Asp Phe Asp Gly Ala Ser Ser Ser Gly Asn Pro Glu Ala Val
186                 191                 196                 201

gcc ctt gcc cca gat gca tat agc acg ggt tcc agc agt gct tct agt      917
Ala Leu Ala Pro Asp Ala Tyr Ser Thr Gly Ser Ser Ser Ala Ser Ser
202                 207                 212                 217

acc ctt aag cga act aaa aaa ccg agg ccg cct tcc tta aaa aag aaa      965
Thr Leu Lys Arg Thr Lys Lys Pro Arg Pro Pro Ser Leu Lys Lys Lys
218                 223                 228                 233

cag acc acc aag aaa ccc aca gag acc ccc cca gtg aag gag acg caa     1013
Gln Thr Thr Lys Lys Pro Thr Glu Thr Pro Pro Val Lys Glu Thr Gln
234                 239                 244                 249

cag gag cca gat gaa gag agc ctt gtc ccc agt ggg gag aat cta gca     1061
Gln Glu Pro Asp Glu Glu Ser Leu Val Pro Ser Gly Glu Asn Leu Ala
250                 255                 260                 265

tct gag acg aaa acg gaa tct gcc aag acg gaa ggt cct agc cca gcc     1109
Ser Glu Thr Lys Thr Glu Ser Ala Lys Thr Glu Gly Pro Ser Pro Ala
266                 271                 276                 281

tta ttg gag gag acg ccc ctt gag ccc gct gtg ggg ccc aaa gct gcc     1157
Leu Leu Glu Glu Thr Pro Leu Glu Pro Ala Val Gly Pro Lys Ala Ala
282                 287                 292                 297

tgc cct ctg gac tca gag agt gca gaa ggg gtt gtc ccc ccg gct tct     1205
Cys Pro Leu Asp Ser Glu Ser Ala Glu Gly Val Val Pro Pro Ala Ser
298                 303                 308                 313

gga ggt ggc aga gtg cag aac tca ccc cct gtc ggg agg aaa acg ctg     1253
Gly Gly Gly Arg Val Gln Asn Ser Pro Pro Val Gly Arg Lys Thr Leu
314                 319                 324                 329

cct ctt acc acg gcc ccg gag gca ggg gag gta acc cca tcg gat agc     1301
Pro Leu Thr Thr Ala Pro Glu Ala Gly Glu Val Thr Pro Ser Asp Ser
330                 335                 340                 345
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346                 351                 356                 361

ttt gac tat tct gag gac aag agt agt tgg gac aac cag cag gaa aac     1397
Phe Asp Tyr Ser Glu Asp Lys Ser Ser Trp Asp Asn Gln Gln Glu Asn
362                 367                 372                 377

ccc cct cct acc aaa aag ata ggc aaa aag cca gtt gcc aaa atg ccc     1445
Pro Pro Pro Thr Lys Lys Ile Gly Lys Lys Pro Val Ala Lys Met Pro
378                 383                 388                 393

ctg agg agg cca aag atg aaa aag aca ccc gag aaa ctt gac aac act     1493
Leu Arg Arg Pro Lys Met Lys Lys Thr Pro Glu Lys Leu Asp Asn Thr
394                 399                 404                 409

cct gcc tca cct ccc aga tcc cct gct gaa ccc aat gac atc ccc att     1541
Pro Ala Ser Pro Pro Arg Ser Pro Ala Glu Pro Asn Asp Ile Pro Ile
410                 415                 420                 425

gct aaa ggt act tac acc ttt gat att gac aag tgg gat gac ccc aat     1589
Ala Lys Gly Thr Tyr Thr Phe Asp Ile Asp Lys Trp Asp Asp Pro Asn
426                 431                 436                 441

ttt aac cct ttt tct tcc acc tca aaa atg cag gag tct ccc aaa ctg     1637
Phe Asn Pro Phe Ser Ser Thr Ser Lys Met Gln Glu Ser Pro Lys Leu
442                 447                 452                 457

ccc caa caa tca tac aac ttt gac cca gac acc tgt gat gag tcc gtt     1685
Pro Gln Gln Ser Tyr Asn Phe Asp Pro Asp Thr Cys Asp Glu Ser Val
458                 463                 468                 473

gac ccc ttt aag aca tcc tct aag acc ccc agc tca cct tct aaa tcc     1733
Asp Pro Phe Lys Thr Ser Ser Lys Thr Pro Ser Ser Pro Ser Lys Ser
474                 479                 484                 489

cca gcc tcc ttt gag atc cca gcc agt gct atg gaa gcc aat gga gtg     1781
Pro Ala Ser Phe Glu Ile Pro Ala Ser Ala Met Glu Ala Asn Gly Val
490                 495                 500                 505

gac ggg gat ggg cta aac aag ccc gcc aag aag aag aag acg ccc cta     1829
Asp Gly Asp Gly Leu Asn Lys Pro Ala Lys Lys Lys Lys Thr Pro Leu
506                 511                 516                 521

aag act gac aca ttt agg gtg aaa aag tcg cca aaa cgg tct cct ctc     1877
Lys Thr Asp Thr Phe Arg Val Lys Lys Ser Pro Lys Arg Ser Pro Leu
522                 527                 532                 537

tct gat cca cct tcc cag gac ccc acc cca gct gct aca cca gaa aca     1925
Ser Asp Pro Pro Ser Gln Asp Pro Thr Pro Ala Ala Thr Pro Glu Thr
538                 543                 548                 553

cca cca gtg atc tct gcg gtg gtc cac gcc aca gat gag gaa aag ctg     1973
Pro Pro Val Ile Ser Ala Val Val His Ala Thr Asp Glu Glu Lys Leu
554                 559                 564                 569
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gcg gtc acc aac cag aag tgg acg tgc atg aca gtg gac cta gag gct     2021
Ala Val Thr Asn Gln Lys Trp Thr Cys Met Thr Val Asp Leu Glu Ala
570                 575                 580                 585

gac aaa cag gac tac ccg cag ccc tcg gac ctg tcc acc ttt gta aac     2069
Asp Lys Gln Asp Tyr Pro Gln Pro Ser Asp Leu Ser Thr Phe Val Asn
586                 591                 596                 601

gag acc aaa ttc agt tca ccc act gag gag ttg gat tac aga aac tcc     2117
Glu Thr Lys Phe Ser Ser Pro Thr Glu Glu Leu Asp Tyr Arg Asn Ser
602                 607                 612                 617

tat gaa att gaa tat atg gag aaa att ggc tcc tcc tta cct cag gac     2165
Tyr Glu Ile Glu Tyr Met Glu Lys Ile Gly Ser Ser Leu Pro Gln Asp
618                 623                 628                 633

gac gat gcc ccg aag aag cag gcc ttg tac ctt atg ttt gac act tct     2213
Asp Asp Ala Pro Lys Lys Gln Ala Leu Tyr Leu Met Phe Asp Thr Ser
634                 639                 644                 649

cag gag agc cct gtc aag tca tct ccc gtc cgc atg tca gag tcc ccg     2261
Gln Glu Ser Pro Val Lys Ser Ser Pro Val Arg Met Ser Glu Ser Pro
650                 655                 660                 665

acg ccg tgt tca ggg tca agt ttt gaa gag act gaa gcc ctt gtg aac     2309
Thr Pro Cys Ser Gly Ser Ser Phe Glu Glu Thr Glu Ala Leu Val Asn
666                 671                 676                 681

act gct gcg aaa aac cag cat cct gtc cca cga gga ctg gcc cct aac     2357
Thr Ala Ala Lys Asn Gln His Pro Val Pro Arg Gly Leu Ala Pro Asn
682                 687                 692                 697

caa gag tca cac ttg cag gtg cca gag aaa tcc tcc cag aag gag ctg     2405
Gln Glu Ser His Leu Gln Val Pro Glu Lys Ser Ser Gln Lys Glu Leu
698                 703                 708                 713

gag gcc atg ggc ttg ggc acc cct tca gaa gcg att gaa att aga gag     2453
Glu Ala Met Gly Leu Gly Thr Pro Ser Glu Ala Ile Glu Ile Arg Glu
714                 719                 724                 729

gct gct cac cca aca gac gtc tcc atc tcc aaa aca gcc ttg tac tcc     2501
Ala Ala His Pro Thr Asp Val Ser Ile Ser Lys Thr Ala Leu Tyr Ser
730                 735                 740                 745

cgc atc ggg acc gct gag gtg gag aaa cct gca ggc ctt ctg ttc cag     2549
Arg Ile Gly Thr Ala Glu Val Glu Lys Pro Ala Gly Leu Leu Phe Gln
746                 751                 756                 761

cag ccc gac ctg gac tct gcc ctc cag atc gcc aga gca gag atc ata     2597
Gln Pro Asp Leu Asp Ser Ala Leu Gln Ile Ala Arg Ala Glu Ile Ile
762                 767                 772                 777

acc aag gag aga gag gtc tca gaa tgg aaa gat aaa tat gaa gaa agc     2645
Thr Lys Glu Arg Glu Val Ser Glu Trp Lys Asp Lys Tyr Glu Glu Ser
778                 783                 788                 793

agg cgg gaa gtg atg gaa atg agg aaa ata gtg gcc gag tat gag aag     2693
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Arg Arg Glu Val Met Glu Met Arg Lys Ile Val Ala Glu Tyr Glu Lys
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Thr Ile Ala Gln Met Ile Glu Asp Glu Gln Arg Glu Lys Ser Val Ser
810                 815                 820                 825

cac cag acg gtg cag cag ctg gtt ctg gag aag gag caa gcc ctg gcc     2789
His Gln Thr Val Gln Gln Leu Val Leu Glu Lys Glu Gln Ala Leu Ala
826                 831                 836                 841

gac ctg aac tcc gtg gag aag tct ctg gcc gac ctc ttc aga aga tat     2837
Asp Leu Asn Ser Val Glu Lys Ser Leu Ala Asp Leu Phe Arg Arg Tyr
842                 847                 852                 857

gag aag atg aag gag gtc cta gaa ggc ttc cgc aag aat gaa gag gtg     2885
Glu Lys Met Lys Glu Val Leu Glu Gly Phe Arg Lys Asn Glu Glu Val
858                 863                 868                 873

ttg aag aga tgt gcg cag gag tac ctg tcc cgg gtg aag aag gag gag     2933
Leu Lys Arg Cys Ala Gln Glu Tyr Leu Ser Arg Val Lys Lys Glu Glu
874                 879                 884                 889

cag agg tac cag gcc ctg aag gtg cac gcg gag gag aaa ctg gac agg     2981
Gln Arg Tyr Gln Ala Leu Lys Val His Ala Glu Glu Lys Leu Asp Arg
890                 895                 900                 905

gcc aat gct gag att gct cag gtt cga ggc aag gcc cag cag gag caa     3029
Ala Asn Ala Glu Ile Ala Gln Val Arg Gly Lys Ala Gln Gln Glu Gln
906                 911                 916                 921

gcc gcc cac cag gcc agc ctg cgg aag gag cag ctg cga gtg gac gcc     3077
Ala Ala His Gln Ala Ser Leu Arg Lys Glu Gln Leu Arg Val Asp Ala
922                 927                 932                 937

ctg gaa agg acg ctg gag cag aag aat aaa gaa ata gaa gaa ctc acc     3125
Leu Glu Arg Thr Leu Glu Gln Lys Asn Lys Glu Ile Glu Glu Leu Thr
938                 943                 948                 953

aag att tgt gac gaa ctg att gcc aaa atg ggg aaa agc taa ctctgaa     3174
Lys Ile Cys Asp Glu Leu Ile Ala Lys Met Gly Lys Ser  *
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 26                  31                  36                  41

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Ser Asp Ser Glu Glu Ala Phe Glu Thr Pro Glu Ser Thr Thr Pro Val
 42                  47                  52                  57

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Lys Ala Pro Pro Ala Pro Pro Pro Pro Pro Pro Glu Val Ile Pro Glu
 58                  63                  68                  73

ccc gag gtc agc aca cag cca ccc ccg gaa gaa cca gga tgt ggt tct      533
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 74                  79                  84                  89

gag aca gtc cct gtc cct gat ggc cca cgg agc gac tcg gtg gaa gga      581
Glu Thr Val Pro Val Pro Asp Gly Pro Arg Ser Asp Ser Val Glu Gly
 90                  95                 100                 105
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106                 111                 116                 121

gac aag ccg ata gcc agc agt ggg act tac aac ttg gac ttt gac aac      677
Asp Lys Pro Ile Ala Ser Ser Gly Thr Tyr Asn Leu Asp Phe Asp Asn
122                 127                 132                 137

att gag ctt gtg gat acc ttt cag acc ttg gag cct cgt gcc tca gac      725
Ile Glu Leu Val Asp Thr Phe Gln Thr Leu Glu Pro Arg Ala Ser Asp
138                 143                 148                 153

gct aag aat cag gag ggc aaa gtg aac aca cgg agg aag tcc acg gat      773
Ala Lys Asn Gln Glu Gly Lys Val Asn Thr Arg Arg Lys Ser Thr Asp
154                 159                 164                 169

tcc gtc ccc atc tct aag tct aca ctg tcc cgg tcg ctc agc ctg caa      821
Ser Val Pro Ile Ser Lys Ser Thr Leu Ser Arg Ser Leu Ser Leu Gln
170                 175                 180                 185

gcc agt gac ttt gat ggt gct tct tcc tca ggc aat ccc gag gcc gtg      869
Ala Ser Asp Phe Asp Gly Ala Ser Ser Ser Gly Asn Pro Glu Ala Val
186                 191                 196                 201

gcc ctt gcc cca gat gca tat agc acg ggt tcc agc agt gct tct agt      917
Ala Leu Ala Pro Asp Ala Tyr Ser Thr Gly Ser Ser Ser Ala Ser Ser
202                 207                 212                 217

acc ctt aag cga act aaa aaa ccg agg ccg cct tcc tta aaa aag aaa      965
Thr Leu Lys Arg Thr Lys Lys Pro Arg Pro Pro Ser Leu Lys Lys Lys
218                 223                 228                 233

cag acc acc aag aaa ccc aca gag acc ccc cca gtg aag gag acg caa     1013
Gln Thr Thr Lys Lys Pro Thr Glu Thr Pro Pro Val Lys Glu Thr Gln
234                 239                 244                 249

cag gag cca gat gaa gag agc ctt gtc ccc agt ggg gag aat cta gca     1061
Gln Glu Pro Asp Glu Glu Ser Leu Val Pro Ser Gly Glu Asn Leu Ala
250                 255                 260                 265

tct gag acg aaa acg gaa tct gcc aag acg gaa ggt cct agc cca gcc     1109
Ser Glu Thr Lys Thr Glu Ser Ala Lys Thr Glu Gly Pro Ser Pro Ala
266                 271                 276                 281

tta ttg gag gag acg ccc ctt gag ccc gct gtg ggg ccc aaa gct gcc     1157
Leu Leu Glu Glu Thr Pro Leu Glu Pro Ala Val Gly Pro Lys Ala Ala
282                 287                 292                 297

tgc cct ctg gac tca gag agt gca gaa ggg gtt gtc ccc ccg gct tct     1205
Cys Pro Leu Asp Ser Glu Ser Ala Glu Gly Val Val Pro Pro Ala Ser
298                 303                 308                 313

gga ggt ggc aga gtg cag aac tca ccc cct gtc ggg agg aaa acg ctg     1253
Gly Gly Gly Arg Val Gln Asn Ser Pro Pro Val Gly Arg Lys Thr Leu
314                 319                 324                 329

cct ctt acc acg gcc ccg gag gca ggg gag gta acc cca tcg gat agc     1301
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Pro Leu Thr Thr Ala Pro Glu Ala Gly Glu Val Thr Pro Ser Asp Ser
330                 335                 340                 345

ggg ggg caa gag gac tct cca gcc aaa ggg ctc tcc gta agg ctg gag     1349
Gly Gly Gln Glu Asp Ser Pro Ala Lys Gly Leu Ser Val Arg Leu Glu
346                 351                 356                 361

ttt gac tat tct gag gac aag agt agt tgg gac aac cag cag gaa aac     1397
Phe Asp Tyr Ser Glu Asp Lys Ser Ser Trp Asp Asn Gln Gln Glu Asn
362                 367                 372                 377

ccc cct cct acc aaa aag ata ggc aaa aag cca gtt gcc aaa atg ccc     1445
Pro Pro Pro Thr Lys Lys Ile Gly Lys Lys Pro Val Ala Lys Met Pro
378                 383                 388                 393

ctg agg agg cca aag atg aaa aag aca ccc gag aaa ctt gac aac act     1493
Leu Arg Arg Pro Lys Met Lys Lys Thr Pro Glu Lys Leu Asp Asn Thr
394                 399                 404                 409

cct gcc tca cct ccc aga tcc cct gct gaa ccc aat gac atc ccc att     1541
Pro Ala Ser Pro Pro Arg Ser Pro Ala Glu Pro Asn Asp Ile Pro Ile
410                 415                 420                 425

gct aaa ggt act tac acc ttt gat att gac aag tgg gat gac ccc aat     1589
Ala Lys Gly Thr Tyr Thr Phe Asp Ile Asp Lys Trp Asp Asp Pro Asn
426                 431                 436                 441

ttt aac cct ttt tct tcc acc tca aaa atg cag gag tct ccc aaa ctg     1637
Phe Asn Pro Phe Ser Ser Thr Ser Lys Met Gln Glu Ser Pro Lys Leu
442                 447                 452                 457

ccc caa caa tca tac aac ttt gac cca gac acc tgt gat gag tcc gtt     1685
Pro Gln Gln Ser Tyr Asn Phe Asp Pro Asp Thr Cys Asp Glu Ser Val
458                 463                 468                 473

gac ccc ttt aag aca tcc tct aag acc ccc agc tca cct tct aaa tcc     1733
Asp Pro Phe Lys Thr Ser Ser Lys Thr Pro Ser Ser Pro Ser Lys Ser
474                 479                 484                 489

cca gcc tcc ttt gag atc cca gcc agt gct atg gaa gcc aat gga gtg     1781
Pro Ala Ser Phe Glu Ile Pro Ala Ser Ala Met Glu Ala Asn Gly Val
490                 495                 500                 505

gac ggg gat ggg cta aac aag ccc gcc aag aag aag aag acg ccc cta     1829
Asp Gly Asp Gly Leu Asn Lys Pro Ala Lys Lys Lys Lys Thr Pro Leu
506                 511                 516                 521

aag acg atg gtt gaa gat gtg atg tct gtg tgt tct ctg ttt gac aca     1877
Lys Thr Met Val Glu Asp Val Met Ser Val Cys Ser Leu Phe Asp Thr
522                 527                 532                 537

ttt agg gtg aaa aag tcg cca aaa cgg tct cct ctc tct gat cca cct     1925
Phe Arg Val Lys Lys Ser Pro Lys Arg Ser Pro Leu Ser Asp Pro Pro
538                 543                 548                 553

tcc cag gac ccc acc cca gct gct aca cca gaa aca cca cca gtg atc     1973
Ser Gln Asp Pro Thr Pro Ala Ala Thr Pro Glu Thr Pro Pro Val Ile
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554                 559                 564                 569

tct gcg gtg gtc cac gcc aca gat gag gaa aag ctg gcg gtc acc aac     2021
Ser Ala Val Val His Ala Thr Asp Glu Glu Lys Leu Ala Val Thr Asn
570                 575                 580                 585

cag aag tgg acg tgc atg aca gtg gac cta gag gct gac aaa cag gac     2069
Gln Lys Trp Thr Cys Met Thr Val Asp Leu Glu Ala Asp Lys Gln Asp
586                 591                 596                 601

tac ccg cag ccc tcg gac ctg tcc acc ttt gta aac gag acc aaa ttc     2117
Tyr Pro Gln Pro Ser Asp Leu Ser Thr Phe Val Asn Glu Thr Lys Phe
602                 607                 612                 617

agt tca ccc act gag gag ttg gat tac aga aac tcc tat gaa att gaa     2165
Ser Ser Pro Thr Glu Glu Leu Asp Tyr Arg Asn Ser Tyr Glu Ile Glu
618                 623                 628                 633

tat atg gag aaa att ggc tcc tcc tta cct cag gac gac gat gcc ccg     2213
Tyr Met Glu Lys Ile Gly Ser Ser Leu Pro Gln Asp Asp Asp Ala Pro
634                 639                 644                 649

aag aag cag gcc ttg tac ctt atg ttt gac act tct cag gag agc cct     2261
Lys Lys Gln Ala Leu Tyr Leu Met Phe Asp Thr Ser Gln Glu Ser Pro
650                 655                 660                 665

gtc aag tca tct ccc gtc cgc atg tca gag tcc ccg acg ccg tgt tca     2309
Val Lys Ser Ser Pro Val Arg Met Ser Glu Ser Pro Thr Pro Cys Ser
666                 671                 676                 681

ggg tca agt ttt gaa gag act gaa gcc ctt gtg aac act gct gcg aaa     2357
Gly Ser Ser Phe Glu Glu Thr Glu Ala Leu Val Asn Thr Ala Ala Lys
682                 687                 692                 697

aac cag cat cct gtc cca cga gga ctg gcc cct aac caa gag tca cac     2405
Asn Gln His Pro Val Pro Arg Gly Leu Ala Pro Asn Gln Glu Ser His
698                 703                 708                 713

ttg cag gtg cca gag aaa tcc tcc cag aag gag ctg gag gcc atg ggc     2453
Leu Gln Val Pro Glu Lys Ser Ser Gln Lys Glu Leu Glu Ala Met Gly
714                 719                 724                 729

ttg ggc acc cct tca gaa gcg att gaa att aca gct ccc gag ggc tcc     2501
Leu Gly Thr Pro Ser Glu Ala Ile Glu Ile Thr Ala Pro Glu Gly Ser
730                 735                 740                 745

ttt gcc tct gct gac gcc ctc ctc agc agg cta gct cac ccc gtc tct     2549
Phe Ala Ser Ala Asp Ala Leu Leu Ser Arg Leu Ala His Pro Val Ser
746                 751                 756                 761

ctc tgt ggt gca ctt gac tat ctg gag ccc gac tta gca gaa aag aac     2597
Leu Cys Gly Ala Leu Asp Tyr Leu Glu Pro Asp Leu Ala Glu Lys Asn
762                 767                 772                 777

ccc cca cta ttc gct cag aaa ctc cag aga gag gct gct cac cca aca     2645
Pro Pro Leu Phe Ala Gln Lys Leu Gln Arg Glu Ala Ala His Pro Thr
778                 783                 788                 793
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gac gtc tcc atc tcc aaa aca gcc ttg tac tcc cgc atc ggg acc gct     2693
Asp Val Ser Ile Ser Lys Thr Ala Leu Tyr Ser Arg Ile Gly Thr Ala
794                 799                 804                 809

gag gtg gag aaa cct gca ggc ctt ctg ttc cag cag ccc gac ctg gac     2741
Glu Val Glu Lys Pro Ala Gly Leu Leu Phe Gln Gln Pro Asp Leu Asp
810                 815                 820                 825

tct gcc ctc cag atc gcc aga gca gag atc ata acc aag gag aga gag     2789
Ser Ala Leu Gln Ile Ala Arg Ala Glu Ile Ile Thr Lys Glu Arg Glu
826                 831                 836                 841

gtc tca gaa tgg aaa gat aaa tat gaa gaa agc agg cgg gaa gtg atg     2837
Val Ser Glu Trp Lys Asp Lys Tyr Glu Glu Ser Arg Arg Glu Val Met
842                 847                 852                 857

gaa atg agg aaa ata gtg gcc gag tat gag aag acc atc gct cag atg     2885
Glu Met Arg Lys Ile Val Ala Glu Tyr Glu Lys Thr Ile Ala Gln Met
858                 863                 868                 873

ata gag gac gaa cag aga gag aag tca gtc tcc cac cag acg gtg cag     2933
Ile Glu Asp Glu Gln Arg Glu Lys Ser Val Ser His Gln Thr Val Gln
874                 879                 884                 889

cag ctg gtt ctg gag aag gag caa gcc ctg gcc gac ctg aac tcc gtg     2981
Gln Leu Val Leu Glu Lys Glu Gln Ala Leu Ala Asp Leu Asn Ser Val
890                 895                 900                 905

gag aag tct ctg gcc gac ctc ttc aga aga tat gag aag atg aag gag     3029
Glu Lys Ser Leu Ala Asp Leu Phe Arg Arg Tyr Glu Lys Met Lys Glu
906                 911                 916                 921

gtc cta gaa ggc ttc cgc aag aat gaa gag gtg ttg aag aga tgt gcg     3077
Val Leu Glu Gly Phe Arg Lys Asn Glu Glu Val Leu Lys Arg Cys Ala
922                 927                 932                 937

cag gag tac ctg tcc cgg gtg aag aag gag gag cag agg tac cag gcc     3125
Gln Glu Tyr Leu Ser Arg Val Lys Lys Glu Glu Gln Arg Tyr Gln Ala
938                 943                 948                 953

ctg aag gtg cac gcg gag gag aaa ctg gac agg gcc aat gct gag att     3173
Leu Lys Val His Ala Glu Glu Lys Leu Asp Arg Ala Asn Ala Glu Ile
954                 959                 964                 969

gct cag gtt cga ggc aag gcc cag cag gag caa gcc gcc cac cag gcc     3221
Ala Gln Val Arg Gly Lys Ala Gln Gln Glu Gln Ala Ala His Gln Ala
970                 975                 980                 985

agc ctg cgg aag gag cag ctg cga gtg gac gcc ctg gaa agg acg ctg     3269
Ser Leu Arg Lys Glu Gln Leu Arg Val Asp Ala Leu Glu Arg Thr Leu
986                 991                 996                1001

gag cag aag aat aaa gaa ata gaa gaa ctc acc aag att tgt gac gaa     3317
Glu Gln Lys Asn Lys Glu Ile Glu Glu Leu Thr Lys Ile Cys Asp Glu
1002                1007                1012                1017
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ctg att gcc aaa atg ggg aaa agc taa ctctg aaccgaatgt tttggactta     3369
Leu Ile Ala Lys Met Gly Lys Ser  *
1018                1023

actgttgagt gcaatatgac cgtcggcaca ctgctgttcc tccagttcca tggacaggtt   3429

ctgttttcac tttttcgtat gcactactgt atttcctttc taaataaaat tgatttgatt   3489

gtatgcagta ctaaggagac tatcagaatt tcttgctatt ggtttgcatt ttcctagtat   3549

aattcatagc aagttgacct cagagttcct gtatcaggga gattgtctga ttctctaata   3609

aaagacacat tgctgacctt ggccttgccc tttgtacaca agttccccag ggtgagcagc   3669

ttttggattt aatatgaaca tgtacagcgt gcatagggac tcttgcctta aggagtgtaa   3729

acttgatctg catttgctga tttgttttta aaaaaacaag aaatgcatgt ttcaaataaa   3789

attctctatt gtaaataaaa ttttttcttt ggatcttggc aataagtgtg cctcgaattt   3849

attttctggg aagggttgag tcttttctca cctttgtcaa ataccagatt tggcttcgtg   3909

ctcttctctg tctgggctca tttctttgtc catagactta aataatattt cctttgttat   3969

cgtggctgca tttgtaggat gaagctaatg ag                                 4001
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<400> 40

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aaaaaagaga tctctcgagg atccgaattc gcggccgcgt cgaccgcagt gctgctcgcg    120

ggtctggcta gtcaggcgaa gtttgcaga  atg gaa tct aat ttt aat caa gag      173
                                    Met Glu Ser Asn Phe Asn Gln Glu
                                      1               5

gga gta cct cga cca tct tat gtt ttt agt gct gac cca att gca agg      221
Gly Val Pro Arg Pro Ser Tyr Val Phe Ser Ala Asp Pro Ile Ala Arg
  9                  14                  19                  24

cct tca gaa ata aat ttc gat ggc att aag ctt gat ctg tct cat gaa      269
Pro Ser Glu Ile Asn Phe Asp Gly Ile Lys Leu Asp Leu Ser His Glu
 25                  30                  35                  40

ttt tcc tta gtt gct cca aat act gag gca aac agt ttc gaa tct aaa      317
Phe Ser Leu Val Ala Pro Asn Thr Glu Ala Asn Ser Phe Glu Ser Lys
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 41                  46                  51                  56

gat tat ctc cag gtt tgt ctt cga ata aga cca ttt aca cag tca gaa      365
Asp Tyr Leu Gln Val Cys Leu Arg Ile Arg Pro Phe Thr Gln Ser Glu
 57                  62                  67                  72

aaa gaa ctt gag tct gag ggc tgt gtg cat att ctg gat tca cag act      413
Lys Glu Leu Glu Ser Glu Gly Cys Val His Ile Leu Asp Ser Gln Thr
 73                  78                  83                  88

gtt gtg ctg aaa gag cct caa tgc atc ctt ggt cgg tta agt gaa aaa      461
Val Val Leu Lys Glu Pro Gln Cys Ile Leu Gly Arg Leu Ser Glu Lys
 89                  94                  99                 104

agc tca ggg cag atg gca cag aaa ttc agt ttt tcc aag gtt ttt ggc      509
Ser Ser Gly Gln Met Ala Gln Lys Phe Ser Phe Ser Lys Val Phe Gly
105                 110                 115                 120

cca gca act aca cag aag gaa ttc ttt cag ggt tgc att atg caa cca      557
Pro Ala Thr Thr Gln Lys Glu Phe Phe Gln Gly Cys Ile Met Gln Pro
121                 126                 131                 136

gta aaa gac ctc ttg aaa gga cag agt cgt ctg att ttt act tac ggg      605
Val Lys Asp Leu Leu Lys Gly Gln Ser Arg Leu Ile Phe Thr Tyr Gly
137                 142                 147                 152

cta acc aat tca gga aaa aca tat aca ttt caa ggg aca gaa gaa aat      653
Leu Thr Asn Ser Gly Lys Thr Tyr Thr Phe Gln Gly Thr Glu Glu Asn
153                 158                 163                 168

att ggc att ctg cct cga act ttg aat gta tta ttt gat agt ctt caa      701
Ile Gly Ile Leu Pro Arg Thr Leu Asn Val Leu Phe Asp Ser Leu Gln
169                 174                 179                 184

gaa aga ctg tat aca aag atg aac ctt aaa cca cat aga tcc aga gaa      749
Glu Arg Leu Tyr Thr Lys Met Asn Leu Lys Pro His Arg Ser Arg Glu
185                 190                 195                 200

tac tta agg tta tca tca gaa caa gag aaa gaa gaa att gct agc aaa      797
Tyr Leu Arg Leu Ser Ser Glu Gln Glu Lys Glu Glu Ile Ala Ser Lys
201                 206                 211                 216

agt gca ttg ctt cgg caa att aaa gag gtt act gtg cat aat gat agt      845
Ser Ala Leu Leu Arg Gln Ile Lys Glu Val Thr Val His Asn Asp Ser
217                 222                 227                 232

gat gat act ctt tat gga agt tta act aac tct ttg aat atc tca gag      893
Asp Asp Thr Leu Tyr Gly Ser Leu Thr Asn Ser Leu Asn Ile Ser Glu
233                 238                 243                 248

ttt gaa gaa tcc ata aaa gat tat gaa caa gcc aac ttg aat atg gct      941
Phe Glu Glu Ser Ile Lys Asp Tyr Glu Gln Ala Asn Leu Asn Met Ala
249                 254                 259                 264

aat agt ata aaa ttt tct gtg tgg gtt tct ttc ttt gaa att tac aat      989
Asn Ser Ile Lys Phe Ser Val Trp Val Ser Phe Phe Glu Ile Tyr Asn
265                 270                 275                 280
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gaa tat att tat gac tta ttt gtt cct gta tca tct aaa ttc caa aag     1037
Glu Tyr Ile Tyr Asp Leu Phe Val Pro Val Ser Ser Lys Phe Gln Lys
281                 286                 291                 296

aga aag atg ctg cgc ctt tcc caa gac gta aag ggc tat tct ttt ata     1085
Arg Lys Met Leu Arg Leu Ser Gln Asp Val Lys Gly Tyr Ser Phe Ile
297                 302                 307                 312

aaa gat cta caa tgg att caa gta tct gat tcc aaa gaa gcc tat aga     1133
Lys Asp Leu Gln Trp Ile Gln Val Ser Asp Ser Lys Glu Ala Tyr Arg
313                 318                 323                 328

ctt tta aaa cta gga ata aag cac cag agt gtt gcc ttc aca aaa ttg     1181
Leu Leu Lys Leu Gly Ile Lys His Gln Ser Val Ala Phe Thr Lys Leu
329                 334                 339                 344

aat aat gct tcc agt aga agt cac agc ata ttc act gtt aaa ata tta     1229
Asn Asn Ala Ser Ser Arg Ser His Ser Ile Phe Thr Val Lys Ile Leu
345                 350                 355                 360

cag att gaa gat tct gaa atg tct cgt gta att cga gtc agt gaa tta     1277
Gln Ile Glu Asp Ser Glu Met Ser Arg Val Ile Arg Val Ser Glu Leu
361                 366                 371                 376

tct tta tgt gat ctt gct ggt tca gaa cga act atg aag aca cag aat     1325
Ser Leu Cys Asp Leu Ala Gly Ser Glu Arg Thr Met Lys Thr Gln Asn
377                 382                 387                 392

gaa ggt gaa agg tta aga gag act ggg aat atc aac act tct tta ttg     1373
Glu Gly Glu Arg Leu Arg Glu Thr Gly Asn Ile Asn Thr Ser Leu Leu
393                 398                 403                 408

act ctg gga aag tgt att aac gtc ttg aag aat agt gaa aag tca aag     1421
Thr Leu Gly Lys Cys Ile Asn Val Leu Lys Asn Ser Glu Lys Ser Lys
409                 414                 419                 424

ttt caa cag cat gtg cct ttc cgg gaa agt aaa ctg act cac tat ttt     1469
Phe Gln Gln His Val Pro Phe Arg Glu Ser Lys Leu Thr His Tyr Phe
425                 430                 435                 440

caa agt ttt ttt aat ggt aaa ggg aaa att tgt atg att gtc aat atc     1517
Gln Ser Phe Phe Asn Gly Lys Gly Lys Ile Cys Met Ile Val Asn Ile
441                 446                 451                 456

agc caa tgt tat tta gcc tat gat gaa aca ctc aat gta ttg aag ttc     1565
Ser Gln Cys Tyr Leu Ala Tyr Asp Glu Thr Leu Asn Val Leu Lys Phe
457                 462                 467                 472

tcc gcc att gca caa aaa gtt tgt gtc cca gac act tta aat tcc tct     1613
Ser Ala Ile Ala Gln Lys Val Cys Val Pro Asp Thr Leu Asn Ser Ser
473                 478                 483                 488

caa gag aaa tta ttt gga cct gtc aaa tct tct caa gat gta tca cta     1661
Gln Glu Lys Leu Phe Gly Pro Val Lys Ser Ser Gln Asp Val Ser Leu
489                 494                 499                 504
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gac agt aat tca aac agt aaa ata tta aat gta aaa aga gcc acc att     1709
Asp Ser Asn Ser Asn Ser Lys Ile Leu Asn Val Lys Arg Ala Thr Ile
505                 510                 515                 520

tca tgg gaa aat agt cta gaa gat ttg atg gaa gac gag gat ttg gtt     1757
Ser Trp Glu Asn Ser Leu Glu Asp Leu Met Glu Asp Glu Asp Leu Val
521                 526                 531                 536

gag gag cta gaa aac gct gaa gaa act caa aat gtg gaa act aaa ctt     1805
Glu Glu Leu Glu Asn Ala Glu Glu Thr Gln Asn Val Glu Thr Lys Leu
537                 542                 547                 552

ctt gat gaa gat cta gat aaa aca tta gag gaa aat aag gct ttc att     1853
Leu Asp Glu Asp Leu Asp Lys Thr Leu Glu Glu Asn Lys Ala Phe Ile
553                 558                 563                 568

agc cac gag gag aaa aga aaa ctg ttg gac tta ata gaa gac ttg aaa     1901
Ser His Glu Glu Lys Arg Lys Leu Leu Asp Leu Ile Glu Asp Leu Lys
569                 574                 579                 584

aaa aaa ctg ata aat gaa aaa aag gaa aaa tta acc ttg gaa ttt aaa     1949
Lys Lys Leu Ile Asn Glu Lys Lys Glu Lys Leu Thr Leu Glu Phe Lys
585                 590                 595                 600

att cga gaa gaa gtt aca cag gag ttt act cag tat tgg gct caa cgg     1997
Ile Arg Glu Glu Val Thr Gln Glu Phe Thr Gln Tyr Trp Ala Gln Arg
601                 606                 611                 616

gaa gct gac ttt aag gag act ctg ctt caa gaa cga gag ata tta gaa     2045
Glu Ala Asp Phe Lys Glu Thr Leu Leu Gln Glu Arg Glu Ile Leu Glu
617                 622                 627                 632

gaa aat gct gaa cgt cgt ttg gct atc ttc aag gat ttg gtt ggt aaa     2093
Glu Asn Ala Glu Arg Arg Leu Ala Ile Phe Lys Asp Leu Val Gly Lys
633                 638                 643                 648

tgt gac act cga gaa gaa gca gcg aaa gac att tgt gcc aca aaa gtt     2141
Cys Asp Thr Arg Glu Glu Ala Ala Lys Asp Ile Cys Ala Thr Lys Val
649                 654                 659                 664

gaa act gaa gaa gct act gct tgt tta gaa cta aag ttt aat caa att     2189
Glu Thr Glu Glu Ala Thr Ala Cys Leu Glu Leu Lys Phe Asn Gln Ile
665                 670                 675                 680

aaa gct gaa tta gct aaa acc aaa gga gaa tta atc aaa acc aaa gaa     2237
Lys Ala Glu Leu Ala Lys Thr Lys Gly Glu Leu Ile Lys Thr Lys Glu
681                 686                 691                 696

gag tta aaa aag aga gaa aat gaa tca gat tca ttg att caa gag ctt     2285
Glu Leu Lys Lys Arg Glu Asn Glu Ser Asp Ser Leu Ile Gln Glu Leu
697                 702                 707                 712

gag aca tct aat aag aaa ata att aca cag aat caa aga att aaa gaa     2333
Glu Thr Ser Asn Lys Lys Ile Ile Thr Gln Asn Gln Arg Ile Lys Glu
713                 718                 723                 728

ttg ata aat ata att gat caa aaa gaa gat act atc aac gaa ttt cag     2381
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Leu Ile Asn Ile Ile Asp Gln Lys Glu Asp Thr Ile Asn Glu Phe Gln
729                 734                 739                 744

aac cta aag tct cat atg gaa aac aca ttt aaa tgc aat gac aag gct     2429
Asn Leu Lys Ser His Met Glu Asn Thr Phe Lys Cys Asn Asp Lys Ala
745                 750                 755                 760

gat aca tct tct tta ata ata aac aat aaa ttg att tgt aat gaa aca     2477
Asp Thr Ser Ser Leu Ile Ile Asn Asn Lys Leu Ile Cys Asn Glu Thr
761                 766                 771                 776

gtt gaa gta cct aag gac agc aaa tct aaa atc tgt tca gaa aga aaa     2525
Val Glu Val Pro Lys Asp Ser Lys Ser Lys Ile Cys Ser Glu Arg Lys
777                 782                 787                 792

aga gta aat gaa aat gaa ctt cag caa gat gaa cca cca gca aag aaa     2573
Arg Val Asn Glu Asn Glu Leu Gln Gln Asp Glu Pro Pro Ala Lys Lys
793                 798                 803                 808

ggg tct atc cat gtt agt tca gct atc act gaa gac caa aag aaa agt     2621
Gly Ser Ile His Val Ser Ser Ala Ile Thr Glu Asp Gln Lys Lys Ser
809                 814                 819                 824

gaa gaa gtg cga ccg aac att gca gaa att gaa gac atc aga gtt tta     2669
Glu Glu Val Arg Pro Asn Ile Ala Glu Ile Glu Asp Ile Arg Val Leu
825                 830                 835                 840

caa gaa aat aat gaa gga ctg aga gca ttt tta ctc act att gag aat     2717
Gln Glu Asn Asn Glu Gly Leu Arg Ala Phe Leu Leu Thr Ile Glu Asn
841                 846                 851                 856

gaa ctt aaa aat gaa aag gaa gaa aaa gca gaa tta aat aaa cag att     2765
Glu Leu Lys Asn Glu Lys Glu Glu Lys Ala Glu Leu Asn Lys Gln Ile
857                 862                 867                 872

gtt cat ttt cag cag gaa ctt tct ctt tct gaa aaa aag aat tta act     2813
Val His Phe Gln Gln Glu Leu Ser Leu Ser Glu Lys Lys Asn Leu Thr
873                 878                 883                 888

tta agt aaa gag gtc caa caa att cag tca aat tat gat att gca att     2861
Leu Ser Lys Glu Val Gln Gln Ile Gln Ser Asn Tyr Asp Ile Ala Ile
889                 894                 899                 904

gct gaa tta cat gtg cag aaa agt aaa aat caa gaa cag gag gaa aag     2909
Ala Glu Leu His Val Gln Lys Ser Lys Asn Gln Glu Gln Glu Glu Lys
905                 910                 915                 920

atc atg aaa ttg tca aat gag ata gaa act gct aca aga agc att aca     2957
Ile Met Lys Leu Ser Asn Glu Ile Glu Thr Ala Thr Arg Ser Ile Thr
921                 926                 931                 936

aat aat gtt tca caa ata aaa tta atg cac acg aaa ata gac gaa cta     3005
Asn Asn Val Ser Gln Ile Lys Leu Met His Thr Lys Ile Asp Glu Leu
937                 942                 947                 952

cgt act ctt gat tca gtt tct cag att tca aac ata gat ttg ctc aat     3053
Arg Thr Leu Asp Ser Val Ser Gln Ile Ser Asn Ile Asp Leu Leu Asn
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 953                 958                 963                 968

 ctc agg gat ctg tca aat ggt tct gag gag gat aat ttg cca aat aca     3101
 Leu Arg Asp Leu Ser Asn Gly Ser Glu Glu Asp Asn Leu Pro Asn Thr
 969                 974                 979                 984

 cag tta gac ctt tta ggt aat gat tat ttg gta agt aag caa gtt aaa     3149
 Gln Leu Asp Leu Leu Gly Asn Asp Tyr Leu Val Ser Lys Gln Val Lys
 985                 990                 995                1000

 gaa tat cga att caa gaa ccc aat agg gaa aat tct ttc cac tct agt     3197
 Glu Tyr Arg Ile Gln Glu Pro Asn Arg Glu Asn Ser Phe His Ser Ser
1001                1006                1011                1016

 att gaa gct att tgg gaa gaa tgt aaa gag att gtg aag gcc tct tcc     3245
 Ile Glu Ala Ile Trp Glu Glu Cys Lys Glu Ile Val Lys Ala Ser Ser
1017                1022                1027                1032

 aaa aaa agt cat cag att gag gaa ctg gaa caa caa att gaa aaa ttg     3293
 Lys Lys Ser His Gln Ile Glu Glu Leu Glu Gln Gln Ile Glu Lys Leu
1033                1038                1043                1048

 cag gca gaa gta aaa ggc tat aag gat gaa aac aat aga cta aag gag     3341
 Gln Ala Glu Val Lys Gly Tyr Lys Asp Glu Asn Asn Arg Leu Lys Glu
1049                1054                1059                1064

 aag gag cat aaa aac caa gat gac cta cta aaa gaa aaa gaa act ctt     3389
 Lys Glu His Lys Asn Gln Asp Asp Leu Leu Lys Glu Lys Glu Thr Leu
1065                1070                1075                1080

 ata cag cag ctg aaa gaa gaa ttg caa gaa aaa aat gtt act ctt gat     3437
 Ile Gln Gln Leu Lys Glu Glu Leu Gln Glu Lys Asn Val Thr Leu Asp
1081                1086                1091                1096

 gtt caa ata cag cat gta gtt gaa gga aag aga gcg ctt tca gaa ctt     3485
 Val Gln Ile Gln His Val Val Glu Gly Lys Arg Ala Leu Ser Glu Leu
1097                1102                1107                1112

 aca caa ggt gtt act tgc tat aag gca aaa ata aag gaa ctt gaa aca     3533
 Thr Gln Gly Val Thr Cys Tyr Lys Ala Lys Ile Lys Glu Leu Glu Thr
1113                1118                1123                1128

 att tta gag act cag aaa gtt gaa cgt agt cat tca gcc aag tta gaa     3581
 Ile Leu Glu Thr Gln Lys Val Glu Arg Ser His Ser Ala Lys Leu Glu
1129                1134                1139                1144

 caa gac att ttg gaa aag gaa tct atc atc tta aag cta gaa aga aat     3629
 Gln Asp Ile Leu Glu Lys Glu Ser Ile Ile Leu Lys Leu Glu Arg Asn
1145                1150                1155                1160

 ttg aag gaa ttt caa gaa cat ctt cag gat tct gtc aaa aac acc aaa     3677
 Leu Lys Glu Phe Gln Glu His Leu Gln Asp Ser Val Lys Asn Thr Lys
1161                1166                1171                1176

 gat tta aat gta aag gaa ctc aag ctg aaa gaa gaa atc aca cag tta     3725
 Asp Leu Asn Val Lys Glu Leu Lys Leu Lys Glu Glu Ile Thr Gln Leu
1177                1182                1187                1192
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 aca aat aat ttg caa gat atg aaa cat tta ctt caa tta aaa gaa gaa     3773
 Thr Asn Asn Leu Gln Asp Met Lys His Leu Leu Gln Leu Lys Glu Glu
1193                1198                1203                1208

 gaa gaa gaa acc aac agg caa gaa aca gaa aaa ttg aaa gag gaa ctc     3821
 Glu Glu Glu Thr Asn Arg Gln Glu Thr Glu Lys Leu Lys Glu Glu Leu
1209                1214                1219                1224

 tct gca agc tct gct cgt acc cag aat ctg aaa gca gat ctt cag agg     3869
 Ser Ala Ser Ser Ala Arg Thr Gln Asn Leu Lys Ala Asp Leu Gln Arg
1225                1230                1235                1240

 aag gaa gaa gat tat gct gac ctg aaa gag aaa ctg act gat gcc aaa     3917
 Lys Glu Glu Asp Tyr Ala Asp Leu Lys Glu Lys Leu Thr Asp Ala Lys
1241                1246                1251                1256

 aag cag att aag caa gta cag aaa gag gta tct gta atg cgt gat gag     3965
 Lys Gln Ile Lys Gln Val Gln Lys Glu Val Ser Val Met Arg Asp Glu
1257                1262                1267                1272

 gat aaa tta ctg agg att aaa att aat gaa ctg gag aaa aag aaa aac     4013
 Asp Lys Leu Leu Arg Ile Lys Ile Asn Glu Leu Glu Lys Lys Lys Asn
1273                1278                1283                1288

 cag tgt tct cag gaa tta gat atg aag cag cga acc att cag caa ctc     4061
 Gln Cys Ser Gln Glu Leu Asp Met Lys Gln Arg Thr Ile Gln Gln Leu
1289                1294                1299                1304

 aag gag cag tta aat aat cag aaa gtg gaa gaa gct ata caa cag tat     4109
 Lys Glu Gln Leu Asn Asn Gln Lys Val Glu Glu Ala Ile Gln Gln Tyr
1305                1310                1315                1320

 gag aga gca tgc aaa gat cta aat gtt aaa gag aaa ata att gaa gac     4157
 Glu Arg Ala Cys Lys Asp Leu Asn Val Lys Glu Lys Ile Ile Glu Asp
1321                1326                1331                1336

 atg cga atg aca cta gaa gaa cag gaa caa act cag gta gaa cag gat     4205
 Met Arg Met Thr Leu Glu Glu Gln Glu Gln Thr Gln Val Glu Gln Asp
1337                1342                1347                1352

 caa gtg ctt gag gct aaa tta gag gaa gtt gaa agg ctg gcc aca gaa     4253
 Gln Val Leu Glu Ala Lys Leu Glu Glu Val Glu Arg Leu Ala Thr Glu
1353                1358                1363                1368

 ttg gaa aaa tgg aag gaa aaa tgc aat gat ttg gaa acc aaa aac aat     4301
 Leu Glu Lys Trp Lys Glu Lys Cys Asn Asp Leu Glu Thr Lys Asn Asn
1369                1374                1379                1384

 caa agg tca aat aaa gaa cat gag aac aac aca gat gtg ctt gga aag     4349
 Gln Arg Ser Asn Lys Glu His Glu Asn Asn Thr Asp Val Leu Gly Lys
1385                1390                1395                1400

 ctc act aat ctt caa gat gag tta cag gag tct gaa cag aaa tat aat     4397
 Leu Thr Asn Leu Gln Asp Glu Leu Gln Glu Ser Glu Gln Lys Tyr Asn
1401                1406                1411                1416
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 gct gat aga aag aaa tgg tta gaa gaa aaa atg atg ctt atc act caa     4445
 Ala Asp Arg Lys Lys Trp Leu Glu Glu Lys Met Met Leu Ile Thr Gln
1417                1422                1427                1432

 gcg aaa gaa gca gag aat ata cga aat aaa gag atg aaa aaa tat gct     4493
 Ala Lys Glu Ala Glu Asn Ile Arg Asn Lys Glu Met Lys Lys Tyr Ala
1433                1438                1443                1448

 gag gac agg gag cgt ttt ttt aag caa cag aat gaa atg gaa ata ctg     4541
 Glu Asp Arg Glu Arg Phe Phe Lys Gln Gln Asn Glu Met Glu Ile Leu
1449                1454                1459                1464

 aca gcc cag ctg aca gag aaa gat agt gac ctt caa aag tgg cga gaa     4589
 Thr Ala Gln Leu Thr Glu Lys Asp Ser Asp Leu Gln Lys Trp Arg Glu
1465                1470                1475                1480

 gaa cga gat caa ctg gtt gca gct tta gaa ata cag cta aaa gca ctg     4637
 Glu Arg Asp Gln Leu Val Ala Ala Leu Glu Ile Gln Leu Lys Ala Leu
1481                1486                1491                1496

 ata tcc agt aat gta cag aaa gat aat gaa att gaa caa cta aaa agg     4685
 Ile Ser Ser Asn Val Gln Lys Asp Asn Glu Ile Glu Gln Leu Lys Arg
1497                1502                1507                1512

 atc ata tca gag act tct aaa ata gaa aca caa atc atg gat atc aag     4733
 Ile Ile Ser Glu Thr Ser Lys Ile Glu Thr Gln Ile Met Asp Ile Lys
1513                1518                1523                1528

 ccc aaa cgt att agt tca gca gat cct gac aaa ctt caa act gaa cct     4781
 Pro Lys Arg Ile Ser Ser Ala Asp Pro Asp Lys Leu Gln Thr Glu Pro
1529                1534                1539                1544

 cta tcg aca agt ttt gaa att tcc aga aat aaa ata gag gat gga tct     4829
 Leu Ser Thr Ser Phe Glu Ile Ser Arg Asn Lys Ile Glu Asp Gly Ser
1545                1550                1555                1560

 gta gtc ctt gac tct tgt gaa gtg tca aca gaa aat gat caa agc act     4877
 Val Val Leu Asp Ser Cys Glu Val Ser Thr Glu Asn Asp Gln Ser Thr
1561                1566                1571                1576

 cga ttt cca aaa cct gag tta gag att caa ttt aca cct tta cag cca     4925
 Arg Phe Pro Lys Pro Glu Leu Glu Ile Gln Phe Thr Pro Leu Gln Pro
1577                1582                1587                1592

 aac aaa atg gca gtg aaa cac cct ggt tgt acc aca cca gtg aca gtt     4973
 Asn Lys Met Ala Val Lys His Pro Gly Cys Thr Thr Pro Val Thr Val
1593                1598                1603                1608

 aag att ccc aag gct cgg aag agg aag agt aat gaa atg gag gag gac     5021
 Lys Ile Pro Lys Ala Arg Lys Arg Lys Ser Asn Glu Met Glu Glu Asp
1609                1614                1619                1624

 ttg gtg aaa tgt gaa aat aag aag aat gct aca ccc aga act aat ttg     5069
 Leu Val Lys Cys Glu Asn Lys Lys Asn Ala Thr Pro Arg Thr Asn Leu
1625                1630                1635                1640

 aaa ttt cct att tca gat gat aga aat tct tct gtc aaa aag gaa caa     5117
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 Lys Phe Pro Ile Ser Asp Asp Arg Asn Ser Ser Val Lys Lys Glu Gln
1641                1646                1651                1656

 aag gtt gcc ata cgt cca tca tct aag aaa aca tat tct tta cgg agt     5165
 Lys Val Ala Ile Arg Pro Ser Ser Lys Lys Thr Tyr Ser Leu Arg Ser
1657                1662                1667                1672

 cag gca tcc ata att ggt gta aac ctg gcc act aag aaa aaa gaa gga     5213
 Gln Ala Ser Ile Ile Gly Val Asn Leu Ala Thr Lys Lys Lys Glu Gly
1673                1678                1683                1688

 aca cta cag aaa ttt gga gac ttc tta caa cat tct ccc tca att ctt     5261
 Thr Leu Gln Lys Phe Gly Asp Phe Leu Gln His Ser Pro Ser Ile Leu
1689                1694                1699                1704

 caa tca aaa gca aag aag ata att gaa aca atg agc tct tca aag ctc     5309
 Gln Ser Lys Ala Lys Lys Ile Ile Glu Thr Met Ser Ser Ser Lys Leu
1705                1710                1715                1720

 tca aat gta gaa gca agt aaa gaa aat gtg tct caa cca aaa cga gcc     5357
 Ser Asn Val Glu Ala Ser Lys Glu Asn Val Ser Gln Pro Lys Arg Ala
1721                1726                1731                1736

 aaa cgg aaa tta tac aca agt gaa att tca tct cct att gat ata tca     5405
 Lys Arg Lys Leu Tyr Thr Ser Glu Ile Ser Ser Pro Ile Asp Ile Ser
1737                1742                1747                1752

 ggc caa gtg att tta atg gac cag aaa atg aag gag agt gat cac cag     5453
 Gly Gln Val Ile Leu Met Asp Gln Lys Met Lys Glu Ser Asp His Gln
1753                1758                1763                1768

 att atc aaa cga cga ctt cga aca aaa aca gcc aaa taa atcacttatg      5502
 Ile Ile Lys Arg Arg Leu Arg Thr Lys Thr Ala Lys  *
1769                1774                1779

 gaaatgttta atataaattt tatagtcata gtcattggaa cttgcatcct gtattgtaaa   5562

 tataaatgta tatattatgc attaaatcac tctgcatata gattgctgtt ttatacatag   5622

 tataatttta attcaataaa tgagtcaaaa tttgtatatt tttataaggc ttttttataa   5682

 tagcttcttt caaactgtat ttccctatta tctcagacat tggatcagtg aagatcctag   5742

 gaaagaggct gttattctca tttattttgc tatacaggat gtaataggtc aggtatttgg   5802

 tttacttata tttaacaatg tcttatgaat ttttttttact ttatctgtta tacaactgat   5862

 tttacatatc tgtttggatt atagctagga tttggagaat aagtgtgtac agatcacaaa   5922

 acatgtatat acattattta gaaaagatct caagtcttta attagaatgt ctcacttatt   5982

 ttgtaaacat tttgtgggta catagtacat gtatatattt acggggtatg tgagatgttt   6042

 tgacacaggc atgcaatgtg aaatacgtgt atcatggaga atgaggtatc catcccctca   6102

 agcatttttc ctttgaatta cagataatcc aattacattc tttagatcat ttaaaaatat   6162
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Docket No. 5656.0050-00

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acaagtaagt tattattgat tatagtcact ctattgtgct atcagatagt agatcattct   6222

ttttatctta tttgtttttg tacccattaa ccatccccac ctccccctgc aaccgtcagt   6282

acccttacca gccactggta accattcttc tactctgtat gcccatgagg tcaattgatt   6342

ttatttttag atcccataaa taaatgagaa catgcaaaaa aaaa                    6386
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<213> Homo sapiens

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<222> (100)..(561)

<400> 41

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gggagcagca agcccacggg tagcagctga ggccccaga   atg gcc aag ttt ctt     114
                                             Met Ala Lys Phe Leu
                                               1

tcc caa gac caa att aat gag tac aag gaa tgc ttc tcc ctg tat gac      162
Ser Gln Asp Gln Ile Asn Glu Tyr Lys Glu Cys Phe Ser Leu Tyr Asp
  6                  11                  16                  21

aag cag cag agg ggg aag ata aaa gcc acc gac ctc atg gtg gcc atg      210
Lys Gln Gln Arg Gly Lys Ile Lys Ala Thr Asp Leu Met Val Ala Met
 22                  27                  32                  37

agg tgc ctg ggg gcc agc ccg acg cca ggg gag gtg cag cgg cac ctg      258
Arg Cys Leu Gly Ala Ser Pro Thr Pro Gly Glu Val Gln Arg His Leu
 38                  43                  48                  53

cag acc cac ggg ata gac gga aat gga gag ctg gat ttc tcc act ttt      306
Gln Thr His Gly Ile Asp Gly Asn Gly Glu Leu Asp Phe Ser Thr Phe
 54                  59                  64                  69

ctg acc att atg cac atg caa ata aaa caa gaa gac cca aag aaa gaa      354
Leu Thr Ile Met His Met Gln Ile Lys Gln Glu Asp Pro Lys Lys Glu
 70                  75                  80                  85

att ctt cta gcc atg ttg atg gtg gac aag gag aag aaa ggt tac gtc      402
Ile Leu Leu Ala Met Leu Met Val Asp Lys Glu Lys Lys Gly Tyr Val
 86                  91                  96                 101

atg gcg tcc gac ctg cgg tca aaa ctc acg agt ctg ggg gag aag ctc      450
Met Ala Ser Asp Leu Arg Ser Lys Leu Thr Ser Leu Gly Glu Lys Leu
102                 107                 112                 117

acc cac aag gaa gtg gat gat ctc ttc agg gaa gca gat atc gaa ccc      498
Thr His Lys Glu Val Asp Asp Leu Phe Arg Glu Ala Asp Ile Glu Pro
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118                 123                 128                 133

aat ggc aaa gtg aag tat gat gaa ttt atc cac aag atc acc ctt cct      546
Asn Gly Lys Val Lys Tyr Asp Glu Phe Ile His Lys Ile Thr Leu Pro
134                 139                 144                 149

gga cgg gac tat tga aggaggagaa tgggagagcc tcccctgggc ctgaaaactt      601
Gly Arg Asp Tyr  *
150

ggagcaatta attttttta aaaagtgttc ttttcacttg ggagagatgg caaacacagt    661

ggcaagacaa cattacccaa ctatagaaga gaggctaact agcaacaata atagatgatt    721

tcagccatgg tatgagtaga tctttaataa aagatttgta ttgattttat taaaaaaaaa    781

aa                                                                  783
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<210> 42
<211> 1166
<212> DNA
<213> Homo sapiens

<220>
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<222> (256)..(924)

<400> 42

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agaagacaga ctgaaggagc ttgcgacttt tccgcctcgg caaccggacc cagcagcaag    180

caggacgggc ggcgctctgc tactggtccc gttaagccag agtagcccaa gccctgaagt    240

cactgctcat ccgga atg gaa atc ccg ccg acc aac tac cca gcc tcc agg      291
                Met Glu Ile Pro Pro Thr Asn Tyr Pro Ala Ser Arg
                  1               5                  10

gcg gcc ttg gtg gca cag aac tac atc aac tac cag cag ggg acc ccg      339
Ala Ala Leu Val Ala Gln Asn Tyr Ile Asn Tyr Gln Gln Gly Thr Pro
 13                  18                  23                  28

cac agg gtg ttt gag gtg cag aag gtc aaa caa gcc agc atg gag gat      387
His Arg Val Phe Glu Val Gln Lys Val Lys Gln Ala Ser Met Glu Asp
 29                  34                  39                  44

att cca gga aga gga cat aag tat cac ctt aaa ttt gct gtt gaa gaa      435
Ile Pro Gly Arg Gly His Lys Tyr His Leu Lys Phe Ala Val Glu Glu
 45                  50                  55                  60

att ata caa aaa caa gtt aag gtg aac tgc aca gct gaa gta ctt tac      483
Ile Ile Gln Lys Gln Val Lys Val Asn Cys Thr Ala Glu Val Leu Tyr
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 61                  66                  71                  76

cct tca acg gga caa gaa act gca cca gaa gtc aac ttc aca ttt gaa      531
Pro Ser Thr Gly Gln Glu Thr Ala Pro Glu Val Asn Phe Thr Phe Glu
 77                  82                  87                  92

gga gaa act gga aag aat cca gat gaa gaa gac aac aca ttt tat caa      579
Gly Glu Thr Gly Lys Asn Pro Asp Glu Glu Asp Asn Thr Phe Tyr Gln
 93                  98                 103                 108

aga ctt aag tcc atg aag gaa ccg cta gaa gca caa aat att cca gac      627
Arg Leu Lys Ser Met Lys Glu Pro Leu Glu Ala Gln Asn Ile Pro Asp
109                 114                 119                 124

aat ttt gga aat gta tct cca gaa atg acg ctc gtt cta cat tta gcc      675
Asn Phe Gly Asn Val Ser Pro Glu Met Thr Leu Val Leu His Leu Ala
125                 130                 135                 140

tgg gtt gcc tgt ggt tat ata ata tgg caa aat tct act gaa gac aca      723
Trp Val Ala Cys Gly Tyr Ile Ile Trp Gln Asn Ser Thr Glu Asp Thr
141                 146                 151                 156

tgg tat aaa atg gta aaa att caa act gtc aag caa gtg caa aga aat      771
Trp Tyr Lys Met Val Lys Ile Gln Thr Val Lys Gln Val Gln Arg Asn
157                 162                 167                 172

gat gac ttt att gaa tta gac tac acc att cta ctt cat aat ata gca      819
Asp Asp Phe Ile Glu Leu Asp Tyr Thr Ile Leu Leu His Asn Ile Ala
173                 178                 183                 188

tct cag gag att att ccc tgg caa atg caa gtt ctc tgg cat cca caa      867
Ser Gln Glu Ile Ile Pro Trp Gln Met Gln Val Leu Trp His Pro Gln
189                 194                 199                 204

tac ggc act aaa gta aaa cat aat agc cgt ctg cca aag gaa gta caa      915
Tyr Gly Thr Lys Val Lys His Asn Ser Arg Leu Pro Lys Glu Val Gln
205                 210                 215                 220

ctg gaa taa acaaaaa ccctaacact ggaagtgtaa acatgtctat tgatgtgtat      971
Leu Glu  *
221

gccaatttca ctggcatcta gcttatgagg ccaaataatc ccaaagtgtc actttatata   1031

aatgtcttga ttacagtata gaactttata gagtccataa tacaaagtat cactacataa   1091

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<400> 43
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ggagc atg ggc tct cag gct gct gct gag tgg agg aac tgg gcc tcc 167
Met Gly Ser Gln Ala Ala Ala Glu Trp Arg Asn Trp Ala Ser
1 5 10

tgg gag ggg tcc tcc agc ctc tct gga tgc tcc atg ggg tgc ttc aag 215
Trp Glu Gly Ser Ser Ser Leu Ser Gly Cys Ser Met Gly Cys Phe Lys
15 20 25 30

gat gac cgc atc gtc ttc tgg act tgg atg ttc tcc acc tac ttc atg 263
Asp Asp Arg Ile Val Phe Trp Thr Trp Met Phe Ser Thr Tyr Phe Met
31 36 41 46

gag aaa tgg gct ccc cgg cag gac gac atg ctt ttc tat gtg cgc cgg 311
Glu Lys Trp Ala Pro Arg Gln Asp Asp Met Leu Phe Tyr Val Arg Arg
47 52 57 62

aag ctg gcg tac tcc ggc agc gaa agc ggt gca gac ggg agg aag gca 359
Lys Leu Ala Tyr Ser Gly Ser Glu Ser Gly Ala Asp Gly Arg Lys Ala
63 68 73 78

gct gag cct gag gtg gag gtg gag gtg tac cgg cgg gac tcc aag aag 407
Ala Glu Pro Glu Val Glu Val Glu Val Tyr Arg Arg Asp Ser Lys Lys
79 84 89 94

ctg cca ggc ctg gga gac cct gac atc gac tgg gag gag agc gtc tgc 455
Leu Pro Gly Leu Gly Asp Pro Asp Ile Asp Trp Glu Glu Ser Val Cys
95 100 105 110

ctg aat ctc atc ctg cag aag ctg gac tac atg gtg acc tgt gcg gtg 503
Leu Asn Leu Ile Leu Gln Lys Leu Asp Tyr Met Val Thr Cys Ala Val
111 116 121 126

tgc aca cgt gct gac ggc ggg gac att cac atc cat aag aag aaa tct 551
Cys Thr Arg Ala Asp Gly Gly Asp Ile His Ile His Lys Lys Lys Ser
127 132 137 142

cag caa gtg ttc gcg tcc ccc agt aaa cac ccc atg gac agc aag ggg 599
Gln Gln Val Phe Ala Ser Pro Ser Lys His Pro Met Asp Ser Lys Gly
143 148 153 158

gag gag tcc aag atc agc tac ccc aac atc ttc ttc atg att gac agc 647
Glu Glu Ser Lys Ile Ser Tyr Pro Asn Ile Phe Phe Met Ile Asp Ser
159 164 169 174

ttc gag gag gtg ttc agc gac atg acc gta ggg gaa gga gag atg gtc 695
Phe Glu Glu Val Phe Ser Asp Met Thr Val Gly Glu Gly Glu Met Val
175 180 185 190

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tgt gtg gag ctg gtg gct agt gac aaa acc aac acg ttc cag ggg gtc      743
Cys Val Glu Leu Val Ala Ser Asp Lys Thr Asn Thr Phe Gln Gly Val
191                 196                 201                 206

atc ttt cag ggc tcc atc cgc tac gag gcg ctc aag aag gtg tat gac      791
Ile Phe Gln Gly Ser Ile Arg Tyr Glu Ala Leu Lys Lys Val Tyr Asp
207                 212                 217                 222

aac cgg gtg agc gtg gcc gcc cgc atg gca cag aag atg tcg ttt ggc      839
Asn Arg Val Ser Val Ala Ala Arg Met Ala Gln Lys Met Ser Phe Gly
223                 228                 233                 238

ttc tac aag tac agc aac atg gag ttt gtg cgc atg aag ggc ccc cag      887
Phe Tyr Lys Tyr Ser Asn Met Glu Phe Val Arg Met Lys Gly Pro Gln
239                 244                 249                 254

ggc aag ggc cac gcc gag atg gcg gtc agc cga gtg tct aca ggt gac      935
Gly Lys Gly His Ala Glu Met Ala Val Ser Arg Val Ser Thr Gly Asp
255                 260                 265                 270

aca tcc ccc tgt ggg act gaa gag gac tcc agc cca gct tcg ccc atg      983
Thr Ser Pro Cys Gly Thr Glu Glu Asp Ser Ser Pro Ala Ser Pro Met
271                 276                 281                 286

cac gag cgg gtg acc tcc ttc agc aca ccc ccc acc cca gaa cgg aac     1031
His Glu Arg Val Thr Ser Phe Ser Thr Pro Pro Thr Pro Glu Arg Asn
287                 292                 297                 302

aac cgg cct gcc ttc ttc tcc cca tcc ctc aag agg aag gtg ccc cgg     1079
Asn Arg Pro Ala Phe Phe Ser Pro Ser Leu Lys Arg Lys Val Pro Arg
303                 308                 313                 318

aac cgg atc gct gag atg aag aag tcg cac tcg gcc aac gac agc gag     1127
Asn Arg Ile Ala Glu Met Lys Lys Ser His Ser Ala Asn Asp Ser Glu
319                 324                 329                 334

gag ttc ttc cgg gag gac gac ggt gga gcc gat ctg cac aat gca acc     1175
Glu Phe Phe Arg Glu Asp Asp Gly Gly Ala Asp Leu His Asn Ala Thr
335                 340                 345                 350

aac ctg cgg tct cgg tcc ctg tcg ggc aca gga cgg tcc ctg gtc ggg     1223
Asn Leu Arg Ser Arg Ser Leu Ser Gly Thr Gly Arg Ser Leu Val Gly
351                 356                 361                 366

tcc tgg ctg aag ctg aac aga gca gat gga aac ttc ctt ctc tat gca     1271
Ser Trp Leu Lys Leu Asn Arg Ala Asp Gly Asn Phe Leu Leu Tyr Ala
367                 372                 377                 382

cac tta acc tac gtc acg ttg ccg ctg cat cgg att tta aca gac atc     1319
His Leu Thr Tyr Val Thr Leu Pro Leu His Arg Ile Leu Thr Asp Ile
383                 388                 393                 398

ctg gaa gtt cgg cag aag ccc atc ctg atg acc tag ccgc gtgcggagcc     1369
Leu Glu Val Arg Gln Lys Pro Ile Leu Met Thr  *
399                 404                 409
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aaaaatttca gaaaaattgt ctcaatttga ctagaatatc aatgaaccag gaaaactgaa    240

gcaccttccc taaagaaaac ttgggtatac aattactcca cagacagagc tgagggtttt    300

ttacccaaat cagtcactgg attttgctgc ctgatacgtg aatcttcttg gaatttttct    360

catgtggatc taaggggaat gctttatt   atg gct gct gtt gtc caa cag aac     412
                                 Met Ala Ala Val Val Gln Gln Asn
                                   1               5

gac cta gta ttt gaa ttt gct agt aac gtc atg gag gat gaa cga cag      460
Asp Leu Val Phe Glu Phe Ala Ser Asn Val Met Glu Asp Glu Arg Gln
  9                  14                  19                  24

ctt ggt gat cca gct att ttt cct gcc gta att gtg gaa cat gtt cct      508
Leu Gly Asp Pro Ala Ile Phe Pro Ala Val Ile Val Glu His Val Pro
 25                  30                  35                  40

ggt gct gat att ctc aat agt tat gcc ggt cta gcc tgt gtg gaa gag      556
Gly Ala Asp Ile Leu Asn Ser Tyr Ala Gly Leu Ala Cys Val Glu Glu
 41                  46                  51                  56

ccc agt gac atg att act gag agt tca ctg gat gtt gct gaa gaa gaa      604
Pro Ser Asp Met Ile Thr Glu Ser Ser Leu Asp Val Ala Glu Glu Glu
 57                  62                  67                  72

atc ata gac gat gat gat gat gac atc acc ctt aca gtt gaa gct tct      652
Ile Ile Asp Asp Asp Asp Asp Asp Ile Thr Leu Thr Val Glu Ala Ser
 73                  78                  83                  88

tgt cat gac ggg gat gaa aca att gaa act att gag gct gct gag gca      700
Cys His Asp Gly Asp Glu Thr Ile Glu Thr Ile Glu Ala Ala Glu Ala
 89                  94                  99                 104

ctc ctc aat atg gat tcc cct ggc cct atg ctg gat gaa aaa cga ata      748
Leu Leu Asn Met Asp Ser Pro Gly Pro Met Leu Asp Glu Lys Arg Ile
105                 110                 115                 120

aat aat aat ata ttt agt tca cct gaa gat gac atg gtt gtt gcc cca      796
Asn Asn Asn Ile Phe Ser Ser Pro Glu Asp Asp Met Val Val Ala Pro
121                 126                 131                 136

gtc acc cat gtg tcc gtc aca tta gat ggg att cct gaa gtg atg gaa      844
Val Thr His Val Ser Val Thr Leu Asp Gly Ile Pro Glu Val Met Glu
137                 142                 147                 152

aca cag cag gtg caa gaa aaa tat gca gac tca ccg gga gcc tca tca      892
Thr Gln Gln Val Gln Glu Lys Tyr Ala Asp Ser Pro Gly Ala Ser Ser
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153                 158                 163                 168

cca gaa cag cct aag agg aaa aaa gga aga aaa act aaa cca cca cga      940
Pro Glu Gln Pro Lys Arg Lys Lys Gly Arg Lys Thr Lys Pro Pro Arg
169                 174                 179                 184

cca gat tcc cca gcc act acg cca aat ata tct gtg aag aag aaa aac      988
Pro Asp Ser Pro Ala Thr Thr Pro Asn Ile Ser Val Lys Lys Lys Asn
185                 190                 195                 200

aaa gat gga aag gga aac aca att tat ctt tgg gag ttt tta ctg gca     1036
Lys Asp Gly Lys Gly Asn Thr Ile Tyr Leu Trp Glu Phe Leu Leu Ala
201                 206                 211                 216

ctg ctc cag gac aag gct act tgt cct aaa tac atc aag tgg acc cag     1084
Leu Leu Gln Asp Lys Ala Thr Cys Pro Lys Tyr Ile Lys Trp Thr Gln
217                 222                 227                 232

cga gag aaa ggc att ttt aaa ttg gtg gat tct aaa gca gtg tcc agg     1132
Arg Glu Lys Gly Ile Phe Lys Leu Val Asp Ser Lys Ala Val Ser Arg
233                 238                 243                 248

ttg tgg ggg aag cac aaa aac aaa cct gat atg aat tat gag acc atg     1180
Leu Trp Gly Lys His Lys Asn Lys Pro Asp Met Asn Tyr Glu Thr Met
249                 254                 259                 264

gga aga gca ctc agg tac tat tac caa agg ggt att ctg gca aaa gtg     1228
Gly Arg Ala Leu Arg Tyr Tyr Tyr Gln Arg Gly Ile Leu Ala Lys Val
265                 270                 275                 280

gaa ggt cag cgc ttg gtg tat cag ttt aaa gaa atg cca aaa gat ctt     1276
Glu Gly Gln Arg Leu Val Tyr Gln Phe Lys Glu Met Pro Lys Asp Leu
281                 286                 291                 296

ata tat ata aat gat gag gat cca agt tcc agc ata gag tct tca gat     1324
Ile Tyr Ile Asn Asp Glu Asp Pro Ser Ser Ser Ile Glu Ser Ser Asp
297                 302                 307                 312

cca tcg cta tct tca tca gcc act tca aat agg aat caa acc agc cgg     1372
Pro Ser Leu Ser Ser Ser Ala Thr Ser Asn Arg Asn Gln Thr Ser Arg
313                 318                 323                 328

tcg aga gta tct tca agt cca ggg gta aaa gga gga gcc act tca gtt     1420
Ser Arg Val Ser Ser Ser Pro Gly Val Lys Gly Gly Ala Thr Ser Val
329                 334                 339                 344

cta aaa cca ggg aat tct aaa gct gca aaa ccc aaa gat cct gtg gaa     1468
Leu Lys Pro Gly Asn Ser Lys Ala Ala Lys Pro Lys Asp Pro Val Glu
345                 350                 355                 360

gtt gca caa cca tca gaa gtt ttg agg aca gtg cag ccc acg cag tct     1516
Val Ala Gln Pro Ser Glu Val Leu Arg Thr Val Gln Pro Thr Gln Ser
361                 366                 371                 376

cca tat cct acc cag ctc ttc cgg act gtt cat gta gta cag cca gta     1564
Pro Tyr Pro Thr Gln Leu Phe Arg Thr Val His Val Val Gln Pro Val
377                 382                 387                 392
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cag gct gtc cca gag gga gaa gca gct aga acc agt acc atg cag gat     1612
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393                 398                 403                 408

gaa aca tta aat tct tcc gtt cag agt att agg act ata cag gct cca     1660
Glu Thr Leu Asn Ser Ser Val Gln Ser Ile Arg Thr Ile Gln Ala Pro
409                 414                 419                 424

acc caa gtt cca gtg gtt gtg tct cct agg aat cag cag ttg cat aca     1708
Thr Gln Val Pro Val Val Val Ser Pro Arg Asn Gln Gln Leu His Thr
425                 430                 435                 440

gta aca ctc caa aca gtg cca ctc aca aca gtt ata gcc agc aca gat     1756
Val Thr Leu Gln Thr Val Pro Leu Thr Thr Val Ile Ala Ser Thr Asp
441                 446                 451                 456

cca tca gca ggt act gga tct cag aag ttt att tta caa gcc att cca     1804
Pro Ser Ala Gly Thr Gly Ser Gln Lys Phe Ile Leu Gln Ala Ile Pro
457                 462                 467                 472

tca tca cag ccc atg aca gta ctg aaa gaa aat gtc atg ctg cag tca     1852
Ser Ser Gln Pro Met Thr Val Leu Lys Glu Asn Val Met Leu Gln Ser
473                 478                 483                 488

caa aag gcg ggc tct cct cct tca att gtc ttg ggc cct gcc cag gtt     1900
Gln Lys Ala Gly Ser Pro Pro Ser Ile Val Leu Gly Pro Ala Gln Val
489                 494                 499                 504

cag cag gtc ctt act agc aat gtt cag acc att tgc aat gga acc gtc     1948
Gln Gln Val Leu Thr Ser Asn Val Gln Thr Ile Cys Asn Gly Thr Val
505                 510                 515                 520

agt gtg gct tcc tct cca tcc ttc agt gct act gca cct gtg gtg acc     1996
Ser Val Ala Ser Ser Pro Ser Phe Ser Ala Thr Ala Pro Val Val Thr
521                 526                 531                 536

ttt tct cct cgc agt tca cag ctg gtt gct cac cca cct ggc act gta     2044
Phe Ser Pro Arg Ser Ser Gln Leu Val Ala His Pro Pro Gly Thr Val
537                 542                 547                 552

atc act tca gtt atc aaa act caa gaa aca aaa act ctt aca cag gaa     2092
Ile Thr Ser Val Ile Lys Thr Gln Glu Thr Lys Thr Leu Thr Gln Glu
553                 558                 563                 568

gta gag aaa aag gaa tct gaa gat cat ttg aaa gag aac act gag aaa     2140
Val Glu Lys Lys Glu Ser Glu Asp His Leu Lys Glu Asn Thr Glu Lys
569                 574                 579                 584

acg gag cag cag cca cag cct tat gtg atg gta gtg tcc agt tcc aat     2188
Thr Glu Gln Gln Pro Gln Pro Tyr Val Met Val Val Ser Ser Ser Asn
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gga ttt act tct cag gta gct atg aaa caa aac gaa ctg ctg gaa ccc     2236
Gly Phe Thr Ser Gln Val Ala Met Lys Gln Asn Glu Leu Leu Glu Pro
601                 606                 611                 616
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aac tct ttt tag tta atataccaaa gcttatgaat aattgtttgt taattgaaca 2291
Asn Ser Phe *
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catgtggatc taaggggaat gctttatt   atg gct gct gtt gtc caa cag aac     412
                                 Met Ala Ala Val Val Gln Gln Asn
                                   1               5

gac cta gta ttt gaa ttt gct agt aac gtc atg gag gat gaa cga cag      460
Asp Leu Val Phe Glu Phe Ala Ser Asn Val Met Glu Asp Glu Arg Gln
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ctt ggt gat cca gct att ttt cct gcc gta att gtg gaa cat gtt cct      508
Leu Gly Asp Pro Ala Ile Phe Pro Ala Val Ile Val Glu His Val Pro
 25                  30                  35                  40

ggt gct gat att ctc aat agt tat gcc ggt cta gcc tgt gtg gaa gag      556
Gly Ala Asp Ile Leu Asn Ser Tyr Ala Gly Leu Ala Cys Val Glu Glu
 41                  46                  51                  56

ccc agt gac atg att act gag agt tca ctg gat gtt gct gaa gaa gaa      604
Pro Ser Asp Met Ile Thr Glu Ser Ser Leu Asp Val Ala Glu Glu Glu
 57                  62                  67                  72

atc ata gac gat gat gat gat gac atc acc ctt aca gtt gaa gct tct      652
Ile Ile Asp Asp Asp Asp Asp Asp Ile Thr Leu Thr Val Glu Ala Ser
 73                  78                  83                  88

tgt cat gac ggg gat gaa aca att gaa act att gag gct gct gag gca      700
Cys His Asp Gly Asp Glu Thr Ile Glu Thr Ile Glu Ala Ala Glu Ala
 89                  94                  99                 104

ctc ctc aat atg gat tcc cct ggc cct atg ctg gat gaa aaa cga ata      748
Leu Leu Asn Met Asp Ser Pro Gly Pro Met Leu Asp Glu Lys Arg Ile
105                 110                 115                 120

aat ggg att cct gaa gtg atg gaa aca cag cag gtg caa gaa aaa tat      796
Asn Gly Ile Pro Glu Val Met Glu Thr Gln Gln Val Gln Glu Lys Tyr
121                 126                 131                 136

gca gac tca ccg gga gcc tca tca cca gaa cag cct aag agg aaa aaa      844
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137                 142                 147                 152
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169                 174                 179                 184

tat ctt tgg gag ttt tta ctg gca ctg ctc cag gac aag gct act tgt      988
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185                 190                 195                 200

cct aaa tac atc aag tgg acc cag cga gag aaa ggc att ttt aaa ttg     1036
Pro Lys Tyr Ile Lys Trp Thr Gln Arg Glu Lys Gly Ile Phe Lys Leu
201                 206                 211                 216

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Val Asp Ser Lys Ala Val Ser Arg Leu Trp Gly Lys His Lys Asn Lys
217                 222                 227                 232

cct gat atg aat tat gag acc atg gga aga gca ctc agg tac tat tac     1132
Pro Asp Met Asn Tyr Glu Thr Met Gly Arg Ala Leu Arg Tyr Tyr Tyr
233                 238                 243                 248

caa agg ggt att ctg gca aaa gtg gaa ggt cag cgc ttg gtg tat cag     1180
Gln Arg Gly Ile Leu Ala Lys Val Glu Gly Gln Arg Leu Val Tyr Gln
249                 254                 259                 264

ttt aaa gaa atg cca aaa gat ctt ata tat ata aat gat gag gat cca     1228
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265                 270                 275                 280

agt tcc agc ata gag tct tca gat cca tcg cta tct tca tca gcc act     1276
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281                 286                 291                 296

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297                 302                 307                 312

gta aaa gga gga gcc act tca gtt cta aaa cca ggg aat tct aaa gct     1372
Val Lys Gly Gly Ala Thr Ser Val Leu Lys Pro Gly Asn Ser Lys Ala
313                 318                 323                 328

gca aaa ccc aaa gat cct gtg gaa gtt gca caa cca tca gaa gtt ttg     1420
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329                 334                 339                 344

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Arg Thr Val Gln Pro Thr Gln Ser Pro Tyr Pro Thr Gln Leu Phe Arg
345                 350                 355                 360

act gtt cat gta gta cag cca gta cag gct gtc cca gag gga gaa gca     1516
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Ser Ile Arg Thr Ile Gln Ala Pro Thr Gln Val Pro Val Val Val Ser
393                 398                 403                 408

cct agg aat cag cag ttg cat aca gta aca ctc caa aca gtg cca ctc     1660
Pro Arg Asn Gln Gln Leu His Thr Val Thr Leu Gln Thr Val Pro Leu
409                 414                 419                 424

aca aca gtt ata gcc agc aca gat cca tca gca ggt act gga tct cag     1708
Thr Thr Val Ile Ala Ser Thr Asp Pro Ser Ala Gly Thr Gly Ser Gln
425                 430                 435                 440

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Lys Phe Ile Leu Gln Ala Ile Pro Ser Ser Gln Pro Met Thr Val Leu
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aaa gaa aat gtc atg ctg cag tca caa aag gcg ggc tct cct cct tca     1804
Lys Glu Asn Val Met Leu Gln Ser Gln Lys Ala Gly Ser Pro Pro Ser
457                 462                 467                 472

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Ile Val Leu Gly Pro Ala Gln Val Gln Gln Val Leu Thr Ser Asn Val
473                 478                 483                 488

cag acc att tgc aat gga acc gtc agt gtg gct tcc tct cca tcc ttc     1900
Gln Thr Ile Cys Asn Gly Thr Val Ser Val Ala Ser Ser Pro Ser Phe
489                 494                 499                 504

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Ser Ala Thr Ala Pro Val Val Thr Phe Ser Pro Arg Ser Ser Gln Leu
505                 510                 515                 520

gtt gct cac cca cct ggc act gta atc act tca gtt atc aaa act caa     1996
Val Ala His Pro Pro Gly Thr Val Ile Thr Ser Val Ile Lys Thr Gln
521                 526                 531                 536

gaa aca aaa act ctt aca cag gaa gta gag aaa aag gaa tct gaa gat     2044
Glu Thr Lys Thr Leu Thr Gln Glu Val Glu Lys Lys Glu Ser Glu Asp
537                 542                 547                 552

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553                 558                 563                 568

gtg atg gta gtg tcc agt tcc aat gga ttt act tct cag gta gct atg     2140
Val Met Val Val Ser Ser Ser Asn Gly Phe Thr Ser Gln Val Ala Met
569                 574                 579                 584

aaa caa aac gaa ctg ctg gaa ccc aac tct ttt tag ttaa tataccaaag     2190
Lys Gln Asn Glu Leu Leu Glu Pro Asn Ser Phe  *
585                 590                 595

cttatgaata attgtttgtt aattgaacat tttcaattat atgcagactg actgattcta   2250
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ctgattcttt tgtaaataca gaacttaaat agaaggcaac aggaaattta tataggaact 2550

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gactagacta gatgatcacc actttctctt ctagttctaa ttttttaat tctaatacct 2910

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atgctatgtt ttcatattac agagtgaatt tgtatttaaa caaaaattta aattttggaa 3510

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ttcaaaacag ctacaacggg aaaaagagag ttttgtccca cagtcagcag gccactagtt    180

tattaacttc cagtcacctt gatttttgct aaa atg aag act ctg cag tct aca     234
                                    Met Lys Thr Leu Gln Ser Thr
                                      1               5

ctt ctc ctg tta ctg ctt gtg cct ctg ata aag cca gca cca cca acc      282
Leu Leu Leu Leu Leu Leu Val Pro Leu Ile Lys Pro Ala Pro Pro Thr
  8                  13                  18                  23

cag cag gac tca cgc att atc tat gat tat gga aca gat aat ttt gaa      330
Gln Gln Asp Ser Arg Ile Ile Tyr Asp Tyr Gly Thr Asp Asn Phe Glu
 24                  29                  34                  39

gaa tcc ata ttt agc caa gat tat gag gat aaa tac ctg gat gga aaa      378
Glu Ser Ile Phe Ser Gln Asp Tyr Glu Asp Lys Tyr Leu Asp Gly Lys
 40                  45                  50                  55

aat att aag gaa aaa gaa act gtg ata ata ccc aat gag aaa agt ctt      426
Asn Ile Lys Glu Lys Glu Thr Val Ile Ile Pro Asn Glu Lys Ser Leu
 56                  61                  66                  71

caa tta caa aaa gat gag gca ata aca cca tta cct ccc aag aaa gaa      474
Gln Leu Gln Lys Asp Glu Ala Ile Thr Pro Leu Pro Pro Lys Lys Glu
 72                  77                  82                  87

aat gat gaa atg ccc acg tgt ctg ctg tgt gtt tgt tta agt ggc tct      522
Asn Asp Glu Met Pro Thr Cys Leu Leu Cys Val Cys Leu Ser Gly Ser
 88                  93                  98                 103

gta tac tgt gaa gaa gtt gac att gat gct gta cca ccc tta cca aag      570
Val Tyr Cys Glu Glu Val Asp Ile Asp Ala Val Pro Pro Leu Pro Lys
104                 109                 114                 119

gaa tca gcc tat ctt tac gca cga ttc aac aaa att aaa aag ctg act      618
Glu Ser Ala Tyr Leu Tyr Ala Arg Phe Asn Lys Ile Lys Lys Leu Thr
120                 125                 130                 135

gcc aaa gat ttt gca gac ata cct aac tta aga aga ctc gat ttt aca      666
Ala Lys Asp Phe Ala Asp Ile Pro Asn Leu Arg Arg Leu Asp Phe Thr
136                 141                 146                 151

gga aat ttg ata gaa gat ata gaa gat ggt act ttt tca aaa ctt tct      714
Gly Asn Leu Ile Glu Asp Ile Glu Asp Gly Thr Phe Ser Lys Leu Ser
152                 157                 162                 167

ctg tta gaa gaa ctt tca ctt gct gaa aat caa cta cta aaa ctt cca      762
Leu Leu Glu Glu Leu Ser Leu Ala Glu Asn Gln Leu Leu Lys Leu Pro
168                 173                 178                 183
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gtt ctt cct ccc aag ctc act tta ttt aat gca aaa tac aac aaa atc      810
Val Leu Pro Pro Lys Leu Thr Leu Phe Asn Ala Lys Tyr Asn Lys Ile
184                 189                 194                 199

aag agt agg gga atc aaa gca aat gca ttc aaa aaa ctg aat aac ctc      858
Lys Ser Arg Gly Ile Lys Ala Asn Ala Phe Lys Lys Leu Asn Asn Leu
200                 205                 210                 215

acc ttc ctc tac ttg gac cat aat gcc ctg gaa tcc gtg cct ctt aat      906
Thr Phe Leu Tyr Leu Asp His Asn Ala Leu Glu Ser Val Pro Leu Asn
216                 221                 226                 231

tta cca gaa agt cta cgt gta att cat ctt cag ttc aac aac ata gct      954
Leu Pro Glu Ser Leu Arg Val Ile His Leu Gln Phe Asn Asn Ile Ala
232                 237                 242                 247

tca att aca gat gac aca ttc tgc aag gct aat gac acc agt tac atc     1002
Ser Ile Thr Asp Asp Thr Phe Cys Lys Ala Asn Asp Thr Ser Tyr Ile
248                 253                 258                 263

cgg gac cgc att gaa gag ata cgc ctg gag ggc aat cca atc gtc ctg     1050
Arg Asp Arg Ile Glu Glu Ile Arg Leu Glu Gly Asn Pro Ile Val Leu
264                 269                 274                 279

gga aag cat cca aac agt ttt att tgc tta aaa aga tta ccg ata ggg     1098
Gly Lys His Pro Asn Ser Phe Ile Cys Leu Lys Arg Leu Pro Ile Gly
280                 285                 290                 295

tca tac ttt taa cct ctattggtac aacatataaa tgaaagtaca cctacactaa     1153
Ser Tyr Phe  *
296

tagtctgtct caacaatgag taaaggaact taagtattgg tttaatatta accttgtatc   1213

tcattttgaa ggaatttaat attttaagca aggatgttca aaatcttaca tataataagt   1273

aaaaagtaag actgaatgtc tacgttcgaa acaaagtaat atgaaaatat ttaaacagca   1333

ttacaaaatc ctagtttata ctagactacc atttaaaaat catgttttta tataaatgcc   1393

caaatttgag atgcattatt cctattacta atgatgtaag tacgaggata aatccaagaa   1453

actttcaact ctttgccttt cctggccttt actggatccc aaaagcattt aaggtacatg   1513

ttccaaaaac tttgaaaagc taaatgtttc ccatgatcgc tcattcttct tttatgattc   1573

atacgttatt ccttataaag taagaacttt gttttcctcc tatcaaggca gctattttat   1633

taaatttttc acttagtctg agaaatagca gatagtctca tatttaggaa aactttccaa   1693

ataaaataaa tgttattctc tgataaagag ctaatacaga aatgttcaag ttattttact   1753

ttctggtaat gtcttcagta aaatattttc tttatctaaa tattaacatt ctaagtctac   1813

caaaaaaagt tttaaactca agcaggccaa aaccaatatg cttataagaa ataatgaaaa   1873

gttcatccat ttctgataaa gttctctatg gcaaagtctt tcaaatacga gataactgca   1933
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aaatattttc cttttatact acagaaatga gaatctcatc aataaattag ttcaagcata 1993

agatgaaaac agaatattct gtggtgccag tgcacactac cttcccaccc atacacatcc 2053

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ctcatgataa actgacatgg ctaactgcaa gaattaaatc ttctatctga gagtaataat 2173

ttatgatgac tcagtggtgc cagagtaaag tttctaaaat aacattcctc tcacttgtac 2233

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aagttgacct caagataaca tttttcatta aagcatctga gatctaagaa cacaattatt 2533

attctaacaa tgattattag ctcattcact tattttgata actaatgatc acagctatta 2593

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Met Asp Pro Gln Asn Gln His Gly
1 5

agt ggc agt tcg tta gtt gtt atc cag cag cct tct ttg gat agc cgt 160
Ser Gly Ser Ser Leu Val Val Ile Gln Gln Pro Ser Leu Asp Ser Arg
9 14 19 24

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ccg aga tta gac tat gag aga gag att cag cct act gct att ttg tcc      208
Pro Arg Leu Asp Tyr Glu Arg Glu Ile Gln Pro Thr Ala Ile Leu Ser
 25                  30                  35                  40

tta gac cag atc aag gcc ata aga ggc agc aat gaa tac aca gaa ggg      256
Leu Asp Gln Ile Lys Ala Ile Arg Gly Ser Asn Glu Tyr Thr Glu Gly
 41                  46                  51                  56

cct tcg gtg gtg aaa aga cct gct cct cgg aca gca cca aga caa gaa      304
Pro Ser Val Val Lys Arg Pro Ala Pro Arg Thr Ala Pro Arg Gln Glu
 57                  62                  67                  72

aag cat gaa agg act cat gaa atc ata cca att aat gtg aat aat aac      352
Lys His Glu Arg Thr His Glu Ile Ile Pro Ile Asn Val Asn Asn Asn
 73                  78                  83                  88

tac gag cac aga cac aca agc cac ctg gga cat gca gta ctc cca agt      400
Tyr Glu His Arg His Thr Ser His Leu Gly His Ala Val Leu Pro Ser
 89                  94                  99                 104

aat gcc agg ggc ccc att ttg agc aga tca acc agc act gga agt gca      448
Asn Ala Arg Gly Pro Ile Leu Ser Arg Ser Thr Ser Thr Gly Ser Ala
105                 110                 115                 120

gcc agc tct ggg agc aac agc agt gcc tct tct gaa cag gga ctg tta      496
Ala Ser Ser Gly Ser Asn Ser Ser Ala Ser Ser Glu Gln Gly Leu Leu
121                 126                 131                 136

gga agg tca cca cca acc aga cca gtc cct ggt cat agg tct gaa agg      544
Gly Arg Ser Pro Pro Thr Arg Pro Val Pro Gly His Arg Ser Glu Arg
137                 142                 147                 152

gca atc cgg acc cag ccc aag caa ctg att gtg gat gac ttg aag ggt      592
Ala Ile Arg Thr Gln Pro Lys Gln Leu Ile Val Asp Asp Leu Lys Gly
153                 158                 163                 168

tcc ttg aaa gag gac ctg aca cag cac aag ttc att tgt gaa cag tgt      640
Ser Leu Lys Glu Asp Leu Thr Gln His Lys Phe Ile Cys Glu Gln Cys
169                 174                 179                 184

ggg aag tgc aag tgt gga gaa tgc act gct ccc agg acc cta cca tcc      688
Gly Lys Cys Lys Cys Gly Glu Cys Thr Ala Pro Arg Thr Leu Pro Ser
185                 190                 195                 200

tgt ttg gcc tgt aac cgg cag tgc ctt tgc tct gct gag agc atg gtg      736
Cys Leu Ala Cys Asn Arg Gln Cys Leu Cys Ser Ala Glu Ser Met Val
201                 206                 211                 216

gaa tat gga acc tgc atg tgc tta gtc aag ggc atc ttc tac cac tgc      784
Glu Tyr Gly Thr Cys Met Cys Leu Val Lys Gly Ile Phe Tyr His Cys
217                 222                 227                 232

tcc aat gac gac gaa ggg gat tcc tat tca gat aat cct tgc tcc tgt      832
Ser Asn Asp Asp Glu Gly Asp Ser Tyr Ser Asp Asn Pro Cys Ser Cys
233                 238                 243                 248

tca caa tca cac tgc tgc tct aga tac ctg tgt atg gga gcc atg tct      880
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Ser Gln Ser His Cys Cys Ser Arg Tyr Leu Cys Met Gly Ala Met Ser
249                 254                 259                 264

tta ttt tta cct tgc tta ctc tgt tat cct cct gct aaa gga tgc ctg      928
Leu Phe Leu Pro Cys Leu Leu Cys Tyr Pro Pro Ala Lys Gly Cys Leu
265                 270                 275                 280

aag ctg tgc agg agg tgt tat gac tgg atc cat cgc cca ggg tgc aga      976
Lys Leu Cys Arg Arg Cys Tyr Asp Trp Ile His Arg Pro Gly Cys Arg
281                 286                 291                 296

tgt aag aac tcc aac act gtc tat tgt aag ctg gag agc tgc ccc tcc     1024
Cys Lys Asn Ser Asn Thr Val Tyr Cys Lys Leu Glu Ser Cys Pro Ser
297                 302                 307                 312

cgg ggt cag ggt aaa cca tca tga tttttggagg tgggttgtac ctcctgaact    1078
Arg Gly Gln Gly Lys Pro Ser  *
313                 318

tctagctttc aagttgtggc tgtttttttgt ttttgttttt gtttttgttt tctttagaat   1138

ttttccctgt ttcccacctt ctcttcccct gttgccaagg tctaactcat ggatttttct   1198

ctttcctcat ggatgatctt cagcaagagt ggactgggaa gctgcacctg gctcccactt   1258

tcaacaagag cctctgccat ccacttgagg gtattgagag ccagtgggct tttgtgtagc   1318

ctttttgttc tgcaagcaac tttctaaagt tgtgtacatg aacatacacc cacatccaga   1378

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aaaagcaact gtttaattgc ttaaataagc tatgtattaa atctgtctcc agttagggct   1498

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ctatttttaa gacaaaagtc tgttaaactt ttttattgta aagaatattt attatgcgaa   2098

tctctattat tttatggtat ttattgcaaa agactgttga aatgtactca tgtttgaata   2158

taacaaaata tcaatactta acggaaaata aggtgacacg aagaaagtac atatgttaac   2218
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Docket No. 5760.5.0

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tataatgcag aaaatatatt aattaatgaa aaaaaaaaaa aaaaaaagtc gacgcggccg   2278

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gctaagacgc caggaccccc cggaagccta gaa atg gga cca ttg aca ttt atg     174
                                      Met Gly Pro Leu Thr Phe Met
                                        1               5

gat gtg gcc ata gaa ttc tgt ctg gag gag tgg caa tgc ctg gac att      222
Asp Val Ala Ile Glu Phe Cys Leu Glu Glu Trp Gln Cys Leu Asp Ile
  8                  13                  18                  23

gca cag cag aat tta tat agg aat gtg atg tta gag aac tac aga aac      270
Ala Gln Gln Asn Leu Tyr Arg Asn Val Met Leu Glu Asn Tyr Arg Asn
 24                  29                  34                  39

ctg gtc ttc ctg ggt att gct gtc tct aag cca gac ctg atc acc tgt      318
Leu Val Phe Leu Gly Ile Ala Val Ser Lys Pro Asp Leu Ile Thr Cys
 40                  45                  50                  55

ctg gag caa gaa aaa gag cct tgg gag cct atg agg aga cat gaa atg      366
Leu Glu Gln Glu Lys Glu Pro Trp Glu Pro Met Arg Arg His Glu Met
 56                  61                  66                  71

gta gcc aaa ccc cca gtt atg tgt tct cat ttt acc caa gac ttt tgg      414
Val Ala Lys Pro Pro Val Met Cys Ser His Phe Thr Gln Asp Phe Trp
 72                  77                  82                  87

cca gag cag cat ata aaa gat cct ttc caa aaa gcg aca ctg aga aga      462
Pro Glu Gln His Ile Lys Asp Pro Phe Gln Lys Ala Thr Leu Arg Arg
 88                  93                  98                 103

tat aaa aac tgt gaa cat aaa aat gta cat tta aaa aaa gac cat aaa      510
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Tyr Lys Asn Cys Glu His Lys Asn Val His Leu Lys Lys Asp His Lys
104                 109                 114                 119

agt gtg gat gag tgt aag gtg cac aga gga ggt tat aat gga ttt aac      558
Ser Val Asp Glu Cys Lys Val His Arg Gly Gly Tyr Asn Gly Phe Asn
120                 125                 130                 135

caa tgt ttg cca gct acc cag agc aaa ata ttt cta ttt gat aaa tgt      606
Gln Cys Leu Pro Ala Thr Gln Ser Lys Ile Phe Leu Phe Asp Lys Cys
136                 141                 146                 151

gtg aaa gcc ttt cat aaa ttt tca aat tca aac aga cat aag ata agc      654
Val Lys Ala Phe His Lys Phe Ser Asn Ser Asn Arg His Lys Ile Ser
152                 157                 162                 167

cat act gaa aaa aaa ctt ttc aaa tgc aaa gaa tgt ggc aaa tca ttt      702
His Thr Glu Lys Lys Leu Phe Lys Cys Lys Glu Cys Gly Lys Ser Phe
168                 173                 178                 183

tgc atg ctt cca cat cta gct caa cat aaa ata att cat acc aga gtg      750
Cys Met Leu Pro His Leu Ala Gln His Lys Ile Ile His Thr Arg Val
184                 189                 194                 199

aat ttc tgc aaa tgt gaa aaa tgt gga aaa gct ttt aac tgc cct tca      798
Asn Phe Cys Lys Cys Glu Lys Cys Gly Lys Ala Phe Asn Cys Pro Ser
200                 205                 210                 215

atc atc act aaa cat aag aga att aat act gga gag aaa ccc tac aca      846
Ile Ile Thr Lys His Lys Arg Ile Asn Thr Gly Glu Lys Pro Tyr Thr
216                 221                 226                 231

tgt gaa gaa tgt ggc aaa gtc ttt aat tgg tcc tca cgc ctt act aca      894
Cys Glu Glu Cys Gly Lys Val Phe Asn Trp Ser Ser Arg Leu Thr Thr
232                 237                 242                 247

cat aaa aaa aat tat act aga tac aaa ctc tac aaa tgt gaa gaa tgt      942
His Lys Lys Asn Tyr Thr Arg Tyr Lys Leu Tyr Lys Cys Glu Glu Cys
248                 253                 258                 263

ggc aaa gct ttt aac aag tcc tca atc ctt act acc cat aag ata att      990
Gly Lys Ala Phe Asn Lys Ser Ser Ile Leu Thr Thr His Lys Ile Ile
264                 269                 274                 279

cgc act gga gag aaa ttc tac aaa tgt aaa gaa tgt gcc aaa gct ttt     1038
Arg Thr Gly Glu Lys Phe Tyr Lys Cys Lys Glu Cys Ala Lys Ala Phe
280                 285                 290                 295

aac caa tcc tca aac ctt act gaa cat aag aaa att cat cct gga gag     1086
Asn Gln Ser Ser Asn Leu Thr Glu His Lys Lys Ile His Pro Gly Glu
296                 301                 306                 311

aaa cct tac aaa tgt gaa gaa tgt ggc aaa gcc ttt aac tgg ccc tca     1134
Lys Pro Tyr Lys Cys Glu Glu Cys Gly Lys Ala Phe Asn Trp Pro Ser
312                 317                 322                 327

act ctt act aaa cat aag aga att cat act gga gag aaa ccc tac aca     1182
Thr Leu Thr Lys His Lys Arg Ile His Thr Gly Glu Lys Pro Tyr Thr
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Document 5 of 6 - 20050176060

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328                 333                 338                 343

tgt gaa gaa tgt ggc aaa gct ttt aac cag ttc tca aac ctt act aca     1230
Cys Glu Glu Cys Gly Lys Ala Phe Asn Gln Phe Ser Asn Leu Thr Thr
344                 349                 354                 359

cat aag aga atc cat act gca gag aaa ttc tat aaa tgt aca gaa tgt     1278
His Lys Arg Ile His Thr Ala Glu Lys Phe Tyr Lys Cys Thr Glu Cys
360                 365                 370                 375

ggt gaa gct ttt agc cgg tcc tca aac ctt act aaa cat aag aaa att     1326
Gly Glu Ala Phe Ser Arg Ser Ser Asn Leu Thr Lys His Lys Lys Ile
376                 381                 386                 391

cat act gaa aag aaa ccc tac aaa tgt gaa gaa tgt ggc aaa gct ttt     1374
His Thr Glu Lys Lys Pro Tyr Lys Cys Glu Glu Cys Gly Lys Ala Phe
392                 397                 402                 407

aag tgg tcc tca aag ctt act gaa cat aag tta act cat act gga gag     1422
Lys Trp Ser Ser Lys Leu Thr Glu His Lys Leu Thr His Thr Gly Glu
408                 413                 418                 423

aaa ccc tac aaa tgt gaa gaa tgt ggc aaa gcc ttt aac tgg ccc tca     1470
Lys Pro Tyr Lys Cys Glu Glu Cys Gly Lys Ala Phe Asn Trp Pro Ser
424                 429                 434                 439

acc ctt act aaa cat aac aga att cat act gga gag aaa ccc tac aaa     1518
Thr Leu Thr Lys His Asn Arg Ile His Thr Gly Glu Lys Pro Tyr Lys
440                 445                 450                 455

tgt gaa gta tgt ggc aaa gct ttt aac cag ttc tca aac ctt act aca     1566
Cys Glu Val Cys Gly Lys Ala Phe Asn Gln Phe Ser Asn Leu Thr Thr
456                 461                 466                 471

cat aag aga att cat act gca gaa aaa ccg tac aaa tgt gaa gaa tgt     1614
His Lys Arg Ile His Thr Ala Glu Lys Pro Tyr Lys Cys Glu Glu Cys
472                 477                 482                 487

ggc aaa gct ttt agc cgg tcc tca aac ctt act aaa cat aag aaa att     1662
Gly Lys Ala Phe Ser Arg Ser Ser Asn Leu Thr Lys His Lys Lys Ile
488                 493                 498                 503

cac att gaa aag aaa ccc tac aaa tgt gaa gaa tgt ggc aaa gct ttt     1710
His Ile Glu Lys Lys Pro Tyr Lys Cys Glu Glu Cys Gly Lys Ala Phe
504                 509                 514                 519

aag tgg tcc tca aag ctt act gaa cat aag ata act cat act gga gag     1758
Lys Trp Ser Ser Lys Leu Thr Glu His Lys Ile Thr His Thr Gly Glu
520                 525                 530                 535

aaa ccc tac aaa tgt gaa gaa tgt ggc aaa gct ttt aac cat ttc tca     1806
Lys Pro Tyr Lys Cys Glu Glu Cys Gly Lys Ala Phe Asn His Phe Ser
536                 541                 546                 551

atc ctt acc aaa cat aag agg att cat act gga gag aaa ccc tac aag     1854
Ile Leu Thr Lys His Lys Arg Ile His Thr Gly Glu Lys Pro Tyr Lys
552                 557                 562                 567
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tgt gaa gaa tgt ggc aaa gct ttt acc caa tcc tca aac ctt act aca     1902
Cys Glu Glu Cys Gly Lys Ala Phe Thr Gln Ser Ser Asn Leu Thr Thr
568                 573                 578                 583

cat aag aaa att cat act gga gag aaa ttc tac aaa tgt gaa gaa tgt     1950
His Lys Lys Ile His Thr Gly Glu Lys Phe Tyr Lys Cys Glu Glu Cys
584                 589                 594                 599

ggc aaa gct ttt acc caa tct tca aac ctt act aca cat aaa aaa att     1998
Gly Lys Ala Phe Thr Gln Ser Ser Asn Leu Thr Thr His Lys Lys Ile
600                 605                 610                 615

cat act gga gga aaa ccc tac aaa tgt gaa gaa tgt ggc aaa gct ttt     2046
His Thr Gly Gly Lys Pro Tyr Lys Cys Glu Glu Cys Gly Lys Ala Phe
616                 621                 626                 631

aac cag ttc tca act ctt act aaa cat aag ata att cac act gag gag     2094
Asn Gln Phe Ser Thr Leu Thr Lys His Lys Ile Ile His Thr Glu Glu
632                 637                 642                 647

aaa ccc tac aaa tgt gaa gaa tgt ggc aaa gcc ttt aag tgg tcc tca     2142
Lys Pro Tyr Lys Cys Glu Glu Cys Gly Lys Ala Phe Lys Trp Ser Ser
648                 653                 658                 663

acc ctt act aaa cat aag ata att cat act gga gag aaa ccc tac aaa     2190
Thr Leu Thr Lys His Lys Ile Ile His Thr Gly Glu Lys Pro Tyr Lys
664                 669                 674                 679

tgt gaa gaa tgt ggc aaa gct ttt aaa ctg tcc tca acc ctt tct aca     2238
Cys Glu Glu Cys Gly Lys Ala Phe Lys Leu Ser Ser Thr Leu Ser Thr
680                 685                 690                 695

cat aag att att cat act gga gag aaa ccc tac aaa tgt gaa aaa tgt     2286
His Lys Ile Ile His Thr Gly Glu Lys Pro Tyr Lys Cys Glu Lys Cys
696                 701                 706                 711

ggc aaa gct ttt aac cga ccc tca aac ctt att gaa cat aag aaa att     2334
Gly Lys Ala Phe Asn Arg Pro Ser Asn Leu Ile Glu His Lys Lys Ile
712                 717                 722                 727

cat act gga gag caa ccc tac aaa tgt gaa gaa tgt ggc aaa gca ttt     2382
His Thr Gly Glu Gln Pro Tyr Lys Cys Glu Glu Cys Gly Lys Ala Phe
728                 733                 738                 743

aac tat tcc tca cac ctt aat aca cat aag aga att cat act aaa gag     2430
Asn Tyr Ser Ser His Leu Asn Thr His Lys Arg Ile His Thr Lys Glu
744                 749                 754                 759

caa ccc tac aaa tgt aaa gaa tgt ggc aaa gct ttc aac caa tat tca     2478
Gln Pro Tyr Lys Cys Lys Glu Cys Gly Lys Ala Phe Asn Gln Tyr Ser
760                 765                 770                 775

aac ctt act aca cat aac aaa att cat act gga gag aaa ctc tac aaa     2526
Asn Leu Thr Thr His Asn Lys Ile His Thr Gly Glu Lys Leu Tyr Lys
776                 781                 786                 791
```

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cct gaa gat gtg aca gtg att ttg aca aca cct caa act ttt tca aac     2574
Pro Glu Asp Val Thr Val Ile Leu Thr Thr Pro Gln Thr Phe Ser Asn
792                 797                 802                 807

ata aaa taa attatac tggtgagaaa ttctagaaat gtaaagaatg tgataaaggc     2630
Ile Lys  *
808

tttacatggt tgtcacactt gattgtaggt aagataattt acattggagt aaacttctac   2690

aagtgtgaag aatgtggcaa aacttttaat taatgctcat accttattgc acaggaaaga   2750

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tcaaaagatc tttcagaaaa taaaagcctt taaagtgaag aagataattc attctgaaga   2930

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09/15/2006 12:36:30 PM

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cac caa acc caa aaa aag aga tct ctc gag gat ccg aat tcg cgg ccg      96
His Gln Thr Gln Lys Lys Arg Ser Leu Glu Asp Pro Asn Ser Arg Pro
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cgt cga ccg cgg ccg cgt cga cgc cag tct agc tgc tgc aca ggc tgg      144
Arg Arg Pro Arg Pro Arg Arg Arg Gln Ser Ser Cys Cys Thr Gly Trp
 29                  34                  39                  44

ctg gct ggc tgg ctg cta agg gct gct cca cgc ttt tgc cgg agg aca      192
Leu Ala Gly Trp Leu Leu Arg Ala Ala Pro Arg Phe Cys Arg Arg Thr
 45                  50                  55                  60

gag act gac atg gaa cag ggg aag ggc ctg gct gtc ctc atc ctg gct      240
Glu Thr Asp Met Glu Gln Gly Lys Gly Leu Ala Val Leu Ile Leu Ala
 61                  66                  71                  76

atc att ctt ctt caa ggt act ttg gcc cag tca atc aaa gga aac cac      288
Ile Ile Leu Leu Gln Gly Thr Leu Ala Gln Ser Ile Lys Gly Asn His
 77                  82                  87                  92

ttg gtt aag gtg tat gac tat caa gaa gat ggt tcg gta ctt ctg act      336
Leu Val Lys Val Tyr Asp Tyr Gln Glu Asp Gly Ser Val Leu Leu Thr
 93                  98                  103                 108

tgt gat gca gaa gcc aaa aat atc aca tgg ttt aaa gat ggg aag atg      384
Cys Asp Ala Glu Ala Lys Asn Ile Thr Trp Phe Lys Asp Gly Lys Met
109                 114                 119                 124

atc ggc ttc cta act gaa gat aaa aaa aaa tgg aat ctg gga agt aat      432
Ile Gly Phe Leu Thr Glu Asp Lys Lys Lys Trp Asn Leu Gly Ser Asn
125                 130                 135                 140

gcc aag gac cct cga ggg atg tat cag tgt aaa gga tca cag aac aag      480
Ala Lys Asp Pro Arg Gly Met Tyr Gln Cys Lys Gly Ser Gln Asn Lys
141                 146                 151                 156

tca aaa cca ctc caa gtg tat tac aga atg tgt cag aac tgc att gaa      528
Ser Lys Pro Leu Gln Val Tyr Tyr Arg Met Cys Gln Asn Cys Ile Glu
157                 162                 167                 172

cta aat gca gcc acc ata tct ggc ttt ctc ttt gct gaa atc gtc agc      576
Leu Asn Ala Ala Thr Ile Ser Gly Phe Leu Phe Ala Glu Ile Val Ser
173                 178                 183                 188

att ttc gtc ctt gcc ttt ggg gtc tac ttc att gct gga cag gat gga      624
Ile Phe Val Leu Ala Phe Gly Val Tyr Phe Ile Ala Gly Gln Asp Gly
189                 194                 199                 204

gtt cgc cag tcg aga gct tca gac aag cag act ctg ttg ccc aat gac      672
Val Arg Gln Ser Arg Ala Ser Asp Lys Gln Thr Leu Leu Pro Asn Asp
205                 210                 215                 220

cag ctc tac cag ccc ctc aag gat cga gaa gat gac cag tac agc cac      720
Gln Leu Tyr Gln Pro Leu Lys Asp Arg Glu Asp Asp Gln Tyr Ser His
221                 226                 231                 236

ctt caa gga aac cag ttg agg agg aat tga a ctcaggactc agagtagtcc      771
Leu Gln Gly Asn Gln Leu Arg Arg Asn  *
237                 242
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agtctgaacc ctgggggcag tcccaggagc cacccacc    atg ccc caa cgg ctt    2873
                                                Met Pro Gln Arg Leu
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ccc cat gcc agg cag cac aca ccc ctc cct ctg gga tca gca gac tac     2921
Pro His Ala Arg Gln His Thr Pro Leu Pro Leu Gly Ser Ala Asp Tyr
  6                  11                  16                  21

agg cgt gtc gtc agt gtc aga cca cag ggg cca cac aga gac ccc aag     2969
Arg Arg Val Val Ser Val Arg Pro Gln Gly Pro His Arg Asp Pro Lys
 22                  27                  32                  37

gac tcc aga gat gca gcc aaa cgc gag caa ggg tcc ttg gca ccc agg     3017
Asp Ser Arg Asp Ala Ala Lys Arg Glu Gln Gly Ser Leu Ala Pro Arg
 38                  43                  48                  53

cct gtg ccg gct tca cgt ggt ggg aag acc ctc tgc aag ggg tat agg     3065
Pro Val Pro Ala Ser Arg Gly Gly Lys Thr Leu Cys Lys Gly Tyr Arg
 54                  59                  64                  69

cag gcc cct cca ggc cca cca gcc cag ttc cag cgg ccc att tgc tca     3113
Gln Ala Pro Pro Gly Pro Pro Ala Gln Phe Gln Arg Pro Ile Cys Ser
 70                  75                  80                  85

gct tcc ccg cca tgg gca tct cgt ttt tcc acg ccc tgt cct ggt ggg     3161
Ala Ser Pro Pro Trp Ala Ser Arg Phe Ser Thr Pro Cys Pro Gly Gly
 86                  91                  96                 101

gct gtc cgg gaa gac acg tac cct gtg ggc act cag ggt gtg ccc agc     3209
Ala Val Arg Glu Asp Thr Tyr Pro Val Gly Thr Gln Gly Val Pro Ser
102                 107                 112                 117

ctg gcc ctg gct cag gga gga cct cag ggt tcc tgg aga ttc ctg gag     3257
Leu Ala Leu Ala Gln Gly Gly Pro Gln Gly Ser Trp Arg Phe Leu Glu
118                 123                 128                 133

tgg aag tca atg ccc cgg ctc cca acg gac ctg gat ata ggg ggc cct     3305
Trp Lys Ser Met Pro Arg Leu Pro Thr Asp Leu Asp Ile Gly Gly Pro
134                 139                 144                 149

tgg ttc ccc cat tat gat ttt gaa cgg agc tgc tgg gtc cgt gcc ata     3353
Trp Phe Pro His Tyr Asp Phe Glu Arg Ser Cys Trp Val Arg Ala Ile
150                 155                 160                 165

tcc cag gag gac cag ctg gcc acc tgc tgg cag gct gaa cac tgc gga     3401
Ser Gln Glu Asp Gln Leu Ala Thr Cys Trp Gln Ala Glu His Cys Gly
166                 171                 176                 181
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gag gtt cac aac aaa gat atg agt tgg cct gag gag atg tct ttt aca     3449
Glu Val His Asn Lys Asp Met Ser Trp Pro Glu Glu Met Ser Phe Thr
182                 187                 192                 197

gca aat agt agt aaa ata gat aga caa aag gtt ccc aca gaa aag gga     3497
Ala Asn Ser Ser Lys Ile Asp Arg Gln Lys Val Pro Thr Glu Lys Gly
198                 203                 208                 213

gcc aca ggt cta agc aac ctg gga aac aca tgc ttc atg aac tca agc     3545
Ala Thr Gly Leu Ser Asn Leu Gly Asn Thr Cys Phe Met Asn Ser Ser
214                 219                 224                 229

atc cag tgc gtt agt aac aca cag cca ctg aca cag tat ttt atc tca     3593
Ile Gln Cys Val Ser Asn Thr Gln Pro Leu Thr Gln Tyr Phe Ile Ser
230                 235                 240                 245

ggg aga cat ctt tat gaa ctc aac agg aca aat ccc att ggt atg aag     3641
Gly Arg His Leu Tyr Glu Leu Asn Arg Thr Asn Pro Ile Gly Met Lys
246                 251                 256                 261

ggg cat atg gct aaa tgc tat ggt gat tta gtg cag gaa ctc tgg agt     3689
Gly His Met Ala Lys Cys Tyr Gly Asp Leu Val Gln Glu Leu Trp Ser
262                 267                 272                 277

gga act cag aag agt gtt gcc cca tta aag ctt cgg cgg acc ata gca     3737
Gly Thr Gln Lys Ser Val Ala Pro Leu Lys Leu Arg Arg Thr Ile Ala
278                 283                 288                 293

aaa tat gct ccc aag ttt gat ggg ttt cag caa caa gac tcc caa gaa     3785
Lys Tyr Ala Pro Lys Phe Asp Gly Phe Gln Gln Gln Asp Ser Gln Glu
294                 299                 304                 309

ctt ctg gct ttt ctc ttg gat ggt ctt cat gaa gat ctc aac cga gtc     3833
Leu Leu Ala Phe Leu Leu Asp Gly Leu His Glu Asp Leu Asn Arg Val
310                 315                 320                 325

cat gaa aag cca tat gtg gaa ctg aag gac agt gat ggc cga cca gac     3881
His Glu Lys Pro Tyr Val Glu Leu Lys Asp Ser Asp Gly Arg Pro Asp
326                 331                 336                 341

tgg gaa gta gct gca gag gcc tgg gac aac cat cta aga aga aat aga     3929
Trp Glu Val Ala Ala Glu Ala Trp Asp Asn His Leu Arg Arg Asn Arg
342                 347                 352                 357

tca att att gtg gat ttg ttc cat ggg cag cta aga tct caa gtc aaa     3977
Ser Ile Ile Val Asp Leu Phe His Gly Gln Leu Arg Ser Gln Val Lys
358                 363                 368                 373

tgc aag aca tgt ggg cat ata agt gtc cga ttt gac cct ttc aat ttt     4025
Cys Lys Thr Cys Gly His Ile Ser Val Arg Phe Asp Pro Phe Asn Phe
374                 379                 384                 389

ttg tct ttg cca cta cca atg gac agt tac atg gac tta gaa ata aca     4073
Leu Ser Leu Pro Leu Pro Met Asp Ser Tyr Met Asp Leu Glu Ile Thr
390                 395                 400                 405
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gtg att aag tta gat ggt act acc cct gta cgg tat gga cta aga ctg     4121
Val Ile Lys Leu Asp Gly Thr Thr Pro Val Arg Tyr Gly Leu Arg Leu
406                 411                 416                 421

aat atg gat gaa aag tac aca ggt tta aaa aaa cag ctg agg gat ctc     4169
Asn Met Asp Glu Lys Tyr Thr Gly Leu Lys Lys Gln Leu Arg Asp Leu
422                 427                 432                 437

tgt gga ctt aat tca gaa caa atc cta cta gca gaa gta cat gat tcc     4217
Cys Gly Leu Asn Ser Glu Gln Ile Leu Leu Ala Glu Val His Asp Ser
438                 443                 448                 453

aac ata aag aac ttt cct cag gat aac caa aaa gta caa ctc tca gtg     4265
Asn Ile Lys Asn Phe Pro Gln Asp Asn Gln Lys Val Gln Leu Ser Val
454                 459                 464                 469

agc gga ttt ttg tgt gca ttt gaa att cct gtc cct tca tct cca att     4313
Ser Gly Phe Leu Cys Ala Phe Glu Ile Pro Val Pro Ser Ser Pro Ile
470                 475                 480                 485

tca gct tct agt cca aca caa ata gat ttc tcc tct tca cca tct aca     4361
Ser Ala Ser Ser Pro Thr Gln Ile Asp Phe Ser Ser Ser Pro Ser Thr
486                 491                 496                 501

aat gga atg ttc acc cta act acc aat ggg gac cta ccc aaa cca ata     4409
Asn Gly Met Phe Thr Leu Thr Thr Asn Gly Asp Leu Pro Lys Pro Ile
502                 507                 512                 517

ttc atc ccc aat gga atg cca aac act gtt gtg cca tgt gga act gag     4457
Phe Ile Pro Asn Gly Met Pro Asn Thr Val Val Pro Cys Gly Thr Glu
518                 523                 528                 533

aag aac ttc aca aat gga atg gtt aat ggt cac atg cca tct ctt cct     4505
Lys Asn Phe Thr Asn Gly Met Val Asn Gly His Met Pro Ser Leu Pro
534                 539                 544                 549

gac agc ccc ttt aca ggt tac atc att gca gtc cac cga aaa atg atg     4553
Asp Ser Pro Phe Thr Gly Tyr Ile Ile Ala Val His Arg Lys Met Met
550                 555                 560                 565

agg aca gaa ctg tat ttc ctg tca cct cag gag aat cgc ccc agc ctc     4601
Arg Thr Glu Leu Tyr Phe Leu Ser Pro Gln Glu Asn Arg Pro Ser Leu
566                 571                 576                 581

ttt gga atg cca ttg att gtt cca tgc act gtg cat acc cag aag aaa     4649
Phe Gly Met Pro Leu Ile Val Pro Cys Thr Val His Thr Gln Lys Lys
582                 587                 592                 597

gac cta tat gat gcg gtt tgg att caa gta tcc tgg tta gca aga cca     4697
Asp Leu Tyr Asp Ala Val Trp Ile Gln Val Ser Trp Leu Ala Arg Pro
598                 603                 608                 613

ctc cca cct cag gaa gct agt att cat gcc cag gat cgt gat aac tgt     4745
Leu Pro Pro Gln Glu Ala Ser Ile His Ala Gln Asp Arg Asp Asn Cys
614                 619                 624                 629

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Ile Ser Cys Ala Trp Cys Pro Gln Tyr Arg Phe Cys Arg Gly Cys Lys
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att gat tgt ggg gaa gac aga gct ttc att gga aat gcc tat att gct     4889
Ile Asp Cys Gly Glu Asp Arg Ala Phe Ile Gly Asn Ala Tyr Ile Ala
662                 667                 672                 677

gtg gat tgg cac ccc aca gcc ctt cac ctt cgc tat caa aca tcc cag     4937
Val Asp Trp His Pro Thr Ala Leu His Leu Arg Tyr Gln Thr Ser Gln
678                 683                 688                 693

gaa agg gtt gta gat aag cat gag agt gtg gag cag agt cgg cga gcg     4985
Glu Arg Val Val Asp Lys His Glu Ser Val Glu Gln Ser Arg Arg Ala
694                 699                 704                 709

caa gcc gag ccc atc aac ctg gac agc tgt ctc cgt gct ttc acc agt     5033
Gln Ala Glu Pro Ile Asn Leu Asp Ser Cys Leu Arg Ala Phe Thr Ser
710                 715                 720                 725

gag gaa gag cta ggg gaa agt gag atg tac tac tgt tcc aag tgt aag     5081
Glu Glu Glu Leu Gly Glu Ser Glu Met Tyr Tyr Cys Ser Lys Cys Lys
726                 731                 736                 741

acc cac tgc tta gca aca aag aag ctg gat ctc tgg agg ctt cca ccc     5129
Thr His Cys Leu Ala Thr Lys Lys Leu Asp Leu Trp Arg Leu Pro Pro
742                 747                 752                 757

ttc ctg att att cac ctt aag cga ttt caa ttt gta aat gat cag tgg     5177
Phe Leu Ile Ile His Leu Lys Arg Phe Gln Phe Val Asn Asp Gln Trp
758                 763                 768                 773

ata aaa tca cag aaa att gtc aga ttt ctt cgg gaa agt ttt gat ccg     5225
Ile Lys Ser Gln Lys Ile Val Arg Phe Leu Arg Glu Ser Phe Asp Pro
774                 779                 784                 789

agt gct ttt ttg gta cca cga gac ccg gcc ctc tgc cag cat aaa cca     5273
Ser Ala Phe Leu Val Pro Arg Asp Pro Ala Leu Cys Gln His Lys Pro
790                 795                 800                 805

ctc aca ccc cag ggg gat gag ctc tcc aag ccc agg att ctg gca aga     5321
Leu Thr Pro Gln Gly Asp Glu Leu Ser Lys Pro Arg Ile Leu Ala Arg
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Glu Val Lys Lys Val Asp Ala Gln Ser Ser Ala Gly Lys Glu Asp Met
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Leu Leu Ser Lys Ser Pro Ser Ser Leu Ser Ala Asn Ile Ser Ser Ser
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Pro Lys Gly Ser Pro Ser Ser Ser Arg Lys Ser Gly Thr Ser Cys Pro
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Ser Ser Lys Asn Ser Ser Pro Asn Ser Ser Pro Arg Thr Leu Gly Arg
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agc aaa ggg agg ctc cgg ctg ccc cag att ggc agc aaa aat aag ccg     5561
Ser Lys Gly Arg Leu Arg Leu Pro Gln Ile Gly Ser Lys Asn Lys Pro
886                 891                 896                 901

tca agt agt aag aag aac ttg gat gcc agc aaa gag aat ggg gct ggg     5609
Ser Ser Ser Lys Lys Asn Leu Asp Ala Ser Lys Glu Asn Gly Ala Gly
902                 907                 912                 917

cag atc tgt gag ctg gct gac gcc ttg agc cga ggg cat atg cgg ggg     5657
Gln Ile Cys Glu Leu Ala Asp Ala Leu Ser Arg Gly His Met Arg Gly
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Gly Ser Gln Pro Glu Leu Val Thr Pro Gln Asp His Glu Val Ala Leu
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Ala Asn Gly Phe Leu Tyr Glu His Glu Ala Cys Gly Asn Gly Cys Gly
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gat ggc tac agc aat ggt cag ctt gga aac cac agt gaa gaa gac agc     5801
Asp Gly Tyr Ser Asn Gly Gln Leu Gly Asn His Ser Glu Glu Asp Ser
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act gat gac caa aga gaa gac act cat att aag cct att tat aat cta     5849
Thr Asp Asp Gln Arg Glu Asp Thr His Ile Lys Pro Ile Tyr Asn Leu
982                 987                 992                 997

tat gca att tca tgc cat tca gga att ctg agt ggg ggc cat tac atc     5897
Tyr Ala Ile Ser Cys His Ser Gly Ile Leu Ser Gly Gly His Tyr Ile
998                1003                1008                1013

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Thr Tyr Ala Lys Asn Pro Asn Cys Lys Trp Tyr Cys Tyr Asn Asp Ser
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agc tgt gag gaa ctt cac cct gat gaa att gac acc gac tct gcc tac     5993
Ser Cys Glu Glu Leu His Pro Asp Glu Ile Asp Thr Asp Ser Ala Tyr
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Ile Leu Phe Tyr Glu Gln Gln Gly Ile Asp Tyr Ala Gln Phe Leu Pro
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aag att gat ggc aaa aag atg gca gac aca agc agt acg gat gaa gac     6089
Lys Ile Asp Gly Lys Lys Met Ala Asp Thr Ser Ser Thr Asp Glu Asp
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Ser Glu Ser Asp Tyr Glu Lys Tyr Ser Met Leu Gln  *
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ccc cat gcc agg cag cac aca ccc ctc cct ctg gga tca gca gac tac     2921
Pro His Ala Arg Gln His Thr Pro Leu Pro Leu Gly Ser Ala Asp Tyr
  6                  11                  16                  21

agg cgt gtc gtc agt gtc aga cca cag ggg cca cac aga gac ccc aag     2969
Arg Arg Val Val Ser Val Arg Pro Gln Gly Pro His Arg Asp Pro Lys
 22                  27                  32                  37

gac tcc aga gat gca gcc aaa cgc gag caa ggg tcc ttg gca ccc agg     3017
Asp Ser Arg Asp Ala Ala Lys Arg Glu Gln Gly Ser Leu Ala Pro Arg
 38                  43                  48                  53

cct gtg ccg gct tca cgt ggt ggg aag acc ctc tgc aag ggg tat agg     3065
Pro Val Pro Ala Ser Arg Gly Gly Lys Thr Leu Cys Lys Gly Tyr Arg
 54                  59                  64                  69

cag gcc cct cca ggc cca cca gcc cag ttc cag cgg ccc att tgc tca     3113
Gln Ala Pro Pro Gly Pro Pro Ala Gln Phe Gln Arg Pro Ile Cys Ser
 70                  75                  80                  85

gct tcc ccg cca tgg gca tct cgt ttt tcc acg ccc tgt cct ggt ggg     3161
Ala Ser Pro Pro Trp Ala Ser Arg Phe Ser Thr Pro Cys Pro Gly Gly
 86                  91                  96                 101

gct gtc cgg gaa gac acg tac cct gtg ggc act cag ggt gtg ccc agc     3209
Ala Val Arg Glu Asp Thr Tyr Pro Val Gly Thr Gln Gly Val Pro Ser
102                 107                 112                 117

ctg gcc ctg gct cag gga gga cct cag ggt tcc tgg aga ttc ctg gag     3257
Leu Ala Leu Ala Gln Gly Gly Pro Gln Gly Ser Trp Arg Phe Leu Glu
118                 123                 128                 133

tgg aag tca atg ccc cgg ctc cca acg gac ctg gat ata ggg ggc cct     3305
Trp Lys Ser Met Pro Arg Leu Pro Thr Asp Leu Asp Ile Gly Gly Pro
134                 139                 144                 149

tgg ttc ccc cat tat gat ttt gaa cgg agc tgc tgg gtc cgt gcc ata     3353
Trp Phe Pro His Tyr Asp Phe Glu Arg Ser Cys Trp Val Arg Ala Ile
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Ser Gln Glu Asp Gln Leu Ala Thr Cys Trp Gln Ala Glu His Cys Gly
166                 171                 176                 181

gag gtt cac aac aaa gat atg agt tgg cct gag gag atg tct ttt aca     3449
Glu Val His Asn Lys Asp Met Ser Trp Pro Glu Glu Met Ser Phe Thr
182                 187                 192                 197

gca aat agt agt aaa ata gat aga caa aag gtt ccc aca gaa aag gga     3497
Ala Asn Ser Ser Lys Ile Asp Arg Gln Lys Val Pro Thr Glu Lys Gly
198                 203                 208                 213

gcc aca ggt cta agc aac ctg gga aac aca tgc ttc atg aac tca agc     3545
Ala Thr Gly Leu Ser Asn Leu Gly Asn Thr Cys Phe Met Asn Ser Ser
214                 219                 224                 229

atc cag tgc gtt agt aac aca cag cca ctg aca cag tat ttt atc tca     3593
Ile Gln Cys Val Ser Asn Thr Gln Pro Leu Thr Gln Tyr Phe Ile Ser
230                 235                 240                 245

ggg aga cat ctt tat gaa ctc aac agg aca aat ccc att ggt atg aag     3641
Gly Arg His Leu Tyr Glu Leu Asn Arg Thr Asn Pro Ile Gly Met Lys
246                 251                 256                 261

ggg cat atg gct aaa tgc tat ggt gat tta gtg cag gaa ctc tgg agt     3689
Gly His Met Ala Lys Cys Tyr Gly Asp Leu Val Gln Glu Leu Trp Ser
262                 267                 272                 277

gga act cag aag agt gtt gcc cca tta aag ctt cgg cgg acc ata gca     3737
Gly Thr Gln Lys Ser Val Ala Pro Leu Lys Leu Arg Arg Thr Ile Ala
278                 283                 288                 293

aaa tat gct ccc aag ttt gat ggg ttt cag caa caa gac tcc caa gaa     3785
Lys Tyr Ala Pro Lys Phe Asp Gly Phe Gln Gln Gln Asp Ser Gln Glu
294                 299                 304                 309

ctt ctg gct ttt ctc ttg gat ggt ctt cat gaa gat ctc aac cga gtc     3833
Leu Leu Ala Phe Leu Leu Asp Gly Leu His Glu Asp Leu Asn Arg Val
310                 315                 320                 325

cat gaa aag cca tat gtg gaa ctg aag gac agt gat ggc cga cca gac     3881
His Glu Lys Pro Tyr Val Glu Leu Lys Asp Ser Asp Gly Arg Pro Asp
326                 331                 336                 341

tgg gaa gta gct gca gag gcc tgg gac aac cat cta aga aga aat aga     3929
Trp Glu Val Ala Ala Glu Ala Trp Asp Asn His Leu Arg Arg Asn Arg
342                 347                 352                 357

tca att att gtg gat ttg ttc cat ggg cag cta aga tct caa gtc aaa     3977
Ser Ile Ile Val Asp Leu Phe His Gly Gln Leu Arg Ser Gln Val Lys
358                 363                 368                 373

tgc aag aca tgt ggg cat ata agt gtc cga ttt gac cct ttc aat ttt     4025
Cys Lys Thr Cys Gly His Ile Ser Val Arg Phe Asp Pro Phe Asn Phe
374                 379                 384                 389
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gtg att aag tta gat ggt act acc cct gta cgg tat gga cta aga ctg     4121
Val Ile Lys Leu Asp Gly Thr Thr Pro Val Arg Tyr Gly Leu Arg Leu
406                 411                 416                 421

aat atg gat gaa aag tac aca ggt tta aaa aaa cag ctg agg gat ctc     4169
Asn Met Asp Glu Lys Tyr Thr Gly Leu Lys Lys Gln Leu Arg Asp Leu
422                 427                 432                 437

tgt gga ctt aat tca gaa caa atc cta cta gca gaa gta cat gat tcc     4217
Cys Gly Leu Asn Ser Glu Gln Ile Leu Leu Ala Glu Val His Asp Ser
438                 443                 448                 453

aac ata aag aac ttt cct cag gat aac caa aaa gta caa ctc tca gtg     4265
Asn Ile Lys Asn Phe Pro Gln Asp Asn Gln Lys Val Gln Leu Ser Val
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agc gga ttt ttg tgt gca ttt gaa att cct gtc cct tca tct cca att     4313
Ser Gly Phe Leu Cys Ala Phe Glu Ile Pro Val Pro Ser Ser Pro Ile
470                 475                 480                 485

tca gct tct agt cca aca caa ata gat ttc tcc tct tca cca tct aca     4361
Ser Ala Ser Ser Pro Thr Gln Ile Asp Phe Ser Ser Ser Pro Ser Thr
486                 491                 496                 501

aat gga atg ttc acc cta act acc aat ggg gac cta ccc aaa cca ata     4409
Asn Gly Met Phe Thr Leu Thr Thr Asn Gly Asp Leu Pro Lys Pro Ile
502                 507                 512                 517

ttc atc ccc aat gga atg cca aac act gtt gtg cca tgt gga act gag     4457
Phe Ile Pro Asn Gly Met Pro Asn Thr Val Val Pro Cys Gly Thr Glu
518                 523                 528                 533

aag aac ttc aca aat gga atg gtt aat ggt cac atg cca tct ctt cct     4505
Lys Asn Phe Thr Asn Gly Met Val Asn Gly His Met Pro Ser Leu Pro
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gac agc ccc ttt aca ggt tac atc att gca gtc cac cga aaa atg atg     4553
Asp Ser Pro Phe Thr Gly Tyr Ile Ile Ala Val His Arg Lys Met Met
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agg aca gaa ctg tat ttc ctg tca cct cag gag aat cgc ccc agc ctc     4601
Arg Thr Glu Leu Tyr Phe Leu Ser Pro Gln Glu Asn Arg Pro Ser Leu
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Phe Gly Met Pro Leu Ile Val Pro Cys Thr Val His Thr Gln Lys Lys
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gac cta tat gat gcg gtt tgg att caa gta tcc tgg tta gca aga cca     4697
Asp Leu Tyr Asp Ala Val Trp Ile Gln Val Ser Trp Leu Ala Arg Pro
598                 603                 608                 613
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atg ggc tat caa tat cca ttc act cta cga gtt gtg cag aaa gat ggg     4793
Met Gly Tyr Gln Tyr Pro Phe Thr Leu Arg Val Val Gln Lys Asp Gly
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atc tcc tgt gct tgg tgc cca cag tat aga ttt tgc aga ggc tgt aaa     4841
Ile Ser Cys Ala Trp Cys Pro Gln Tyr Arg Phe Cys Arg Gly Cys Lys
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Ile Asp Cys Gly Glu Asp Arg Ala Phe Ile Gly Asn Ala Tyr Ile Ala
662                 667                 672                 677

gtg gat tgg cac ccc aca gcc ctt cac ctt cgc tat caa aca tcc cag     4937
Val Asp Trp His Pro Thr Ala Leu His Leu Arg Tyr Gln Thr Ser Gln
678                 683                 688                 693

gaa agg gtt gta gat aag cat gag agt gtg gag cag agt cgg cga gcg     4985
Glu Arg Val Val Asp Lys His Glu Ser Val Glu Gln Ser Arg Arg Ala
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Gln Ala Glu Pro Ile Asn Leu Asp Ser Cys Leu Arg Ala Phe Thr Ser
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Glu Glu Glu Leu Gly Glu Ser Glu Met Tyr Tyr Cys Ser Lys Cys Lys
726                 731                 736                 741

acc cac tgc tta gca aca aag aag ctg gat ctc tgg agg ctt cca ccc     5129
Thr His Cys Leu Ala Thr Lys Lys Leu Asp Leu Trp Arg Leu Pro Pro
742                 747                 752                 757

ttc ctg att att cac ctt aag cga ttt caa ttt gta aat gat cag tgg     5177
Phe Leu Ile Ile His Leu Lys Arg Phe Gln Phe Val Asn Asp Gln Trp
758                 763                 768                 773

ata aaa tca cag aaa att gtc aga ttt ctt cgg gaa agt ttt gat ccg     5225
Ile Lys Ser Gln Lys Ile Val Arg Phe Leu Arg Glu Ser Phe Asp Pro
774                 779                 784                 789

agt gct ttt ttg gta cca cga gac ccg gcc ctc tgc cag cat aaa cca     5273
Ser Ala Phe Leu Val Pro Arg Asp Pro Ala Leu Cys Gln His Lys Pro
790                 795                 800                 805

ctc aca ccc cag ggg gat gag ctc tcc aag ccc agg att ctg gca aga     5321
Leu Thr Pro Gln Gly Asp Glu Leu Ser Lys Pro Arg Ile Leu Ala Arg
806                 811                 816                 821

gag gtg aag aaa gtg gat gcg cag agt tcg gct gga aaa gag gac atg     5369
Glu Val Lys Lys Val Asp Ala Gln Ser Ser Ala Gly Lys Glu Asp Met
822                 827                 832                 837

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Leu Leu Ser Lys Ser Pro Ser Ser Leu Ser Ala Asn Ile Ser Ser Ser
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Pro Lys Gly Ser Pro Ser Ser Ser Arg Lys Ser Gly Thr Ser Cys Pro
854                 859                 864                 869

tcc agc aaa aac agc agc cct aat agc agc cca cgg act ttg ggg agg     5513
Ser Ser Lys Asn Ser Ser Pro Asn Ser Ser Pro Arg Thr Leu Gly Arg
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agc aaa ggg agg ctc cgg ctg ccc cag att ggc agc aaa aat aag ccg     5561
Ser Lys Gly Arg Leu Arg Leu Pro Gln Ile Gly Ser Lys Asn Lys Pro
886                 891                 896                 901

tca agt agt aag aag aac ttg gat gcc agc aaa gag aat ggg gct ggg     5609
Ser Ser Ser Lys Lys Asn Leu Asp Ala Ser Lys Glu Asn Gly Ala Gly
902                 907                 912                 917

cag atc tgt gag ctg gct gac gcc ttg agc cga ggg cat atg cgg ggg     5657
Gln Ile Cys Glu Leu Ala Asp Ala Leu Ser Arg Gly His Met Arg Gly
918                 923                 928                 933

ggc agc caa cca gag ctg gtc act cct cag gac cat gag gta gct ttg     5705
Gly Ser Gln Pro Glu Leu Val Thr Pro Gln Asp His Glu Val Ala Leu
934                 939                 944                 949

gcc aat gga ttc ctt tat gag cat gaa gca tgt ggc aat ggc tac agc     5753
Ala Asn Gly Phe Leu Tyr Glu His Glu Ala Cys Gly Asn Gly Tyr Ser
950                 955                 960                 965

aat ggt cag ctt gga aac cac agt gaa gaa gac agc act gat gac caa     5801
Asn Gly Gln Leu Gly Asn His Ser Glu Glu Asp Ser Thr Asp Asp Gln
966                 971                 976                 981

aga gaa gac act cat att aag cct att tat aat cta tat gca att tca     5849
Arg Glu Asp Thr His Ile Lys Pro Ile Tyr Asn Leu Tyr Ala Ile Ser
982                 987                 992                 997

tgc cat tca gga att ctg agt ggg ggc cat tac atc act tat gcc aaa     5897
Cys His Ser Gly Ile Leu Ser Gly Gly His Tyr Ile Thr Tyr Ala Lys
998                1003                1008                1013

aac cca aac tgc aag tgg tac tgt tat aat gac agc agc tgt gag gaa     5945
Asn Pro Asn Cys Lys Trp Tyr Cys Tyr Asn Asp Ser Ser Cys Glu Glu
1014                1019                1024                1029

ctt cac cct gat gaa att gac acc gac tct gcc tac att ctt ttc tat     5993
Leu His Pro Asp Glu Ile Asp Thr Asp Ser Ala Tyr Ile Leu Phe Tyr
1030                1035                1040                1045

gag cag cag ggg ata gac tac gca caa ttt ctg cca aag att gat ggc     6041
Glu Gln Gln Gly Ile Asp Tyr Ala Gln Phe Leu Pro Lys Ile Asp Gly
1046                1051                1056                1061

aaa aag atg gca gac aca agc agt acg gat gaa gac tct gag tct gat     6089
Lys Lys Met Ala Asp Thr Ser Ser Thr Asp Glu Asp Ser Glu Ser Asp
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1062                1067                1072                1077

 tac gaa aag tac tct atg tta cag taa agcta ccactctggc tgctagacag     6141
 Tyr Glu Lys Tyr Ser Met Leu Gln  *
1078                1083

 cttggtggcg agggagatga ctccttgtag ctgatacttg gcaaaagtgt cactgaaaga   6201

 caagctaaat gtagttattt tatcctgtta gaacaaaaat tctaattaaa atagttaact   6261

 tgaagagtag aaacaattgt attttgaagt ctcatacaag ctgtctgata gagaactttc   6321

 aggcagatcc caccattagc ctgtaaacaa aaggtgtggc accagccacc tgggaccaaa   6381

 taagaattga attgtgcttg tccagatatg aacaaatatg tagtgagtat agagtttacc   6441

 aataatcata acaaatatta aagatttcct tggagtcaga ggaaaaaaca aacaattata   6501

 atgttgtcta gggacgacat gatacgctac ctccttttttc ctgaagtttt attccattat   6561

 attgacaaga tggagaaagc aagatcatga aggtgtgcaa atgattctta cggcatggac   6621

 aaggattttt caatttattt tttaaactgt ttccataccc tttctttttc ttgctttttg   6681

 tttttgccat tgtgtttacg tttgagacac aaccagtcat tggtggcagg ggcatagagt   6741

 ggtcagtctg aaagggaggc tctcttaaga gctatgtgcc ttccaaccag agggagaccc   6801

 agtagaaaga aaaacatcct gggaaatcca gctaccaggg ccctcccagt ggaggcatct   6861

 tacatttagg ctacttcaag tatcctcaga aatgtattct gcacccccgg ccccgcccat   6921

 gctgagggaa ggggagcagt tgccaatatt tgcaccatct tcacatgcac atgttgcaac   6981

 aagagcttct gggaaggtaa gcggcatcgg agctagatca cgtttcacaa ttagtggtta   7041

 ttcttttctg tgtttgtttt gcactttaaa aaagagagaa cacatgcaaa tgaacttgct   7101

 tgtgtgtatt tgatggctct aagggctata aattacaaac aaaacacatc ccagacatta   7161

 ggagttcata agtatattta atgaaattgg tggttttagg aagtcaactt tagttttgct   7221

 ttgtttgcat gtccactggt ttttttattt tgatatttgt ctttttttaa attttacagt   7281

 agtcattgaa agttatgttt ctttgcttac ttcatttttt ccctctaatt atttaagatt   7341

 ggaacaaaag tataaatatt atttatttga ggtagaattt ttttcatgta gtttcttaat   7401

 atatacttga aggaaatgtt tcaccttatt tttggtcttt gtttattcat ttagaccctg   7461

 caagttgatt ctcattgcca gattccatta ccctttcttc ctcataggta gtaattacca   7521

 atgtaactaa gcatttgtgt tctgatatct gaggccagta actattaata tctagttctc   7581

 agaggcattt ggaaaggtta tcttaaatgg ctacctaaat tgaaatcctt ttcagaaaaa   7641

 atataattgc aagtaggtag gagtggccta aattgtctaa tgtaataaag tcagacaaaa   7701
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tgcacacttt atagtttcaa gattttcagt aaataaaatc tgtccattcc tacctggaca   7761

tgtcccatta aaaagtggaa gattttaaat aatttcttta cagatgtttt atttaaacag   7821

gtagcacaat ctactaatgt tgtgtgattt gtgttatact ggttgtaatt aatttttta   7881

attcatgaac tagcggaaaa tttattaaat taactattaa ctacattcac cttgtaaatt   7941

actgtataaa acttgttgac aatgcactga ctttagaaag atgttaatgt acataaatag   8001

agtgtaaata aaatagtgtt gatgtactga aatatgaact gtatcaaaag tattggtaat   8061

tgtatatggg gtgtacctgt ttatctgtta actattatcc aaacaaatta aatactgtgg   8121

ttgcctctat gtgctgtttt tcctcataca agtaaacaca gaaagtcaaa ttcttcagcc   8181

tccctctctg tgatcctgtt ttaattctcc tacttgaata atttctttct gacttgtata   8241

cagaggggat gcttcatctc tgaggttgga aactctgtag agcaggattc cccaactcct   8301

gggctacaga ccagtactgt ccatggcctg ttaggaaccg ggctgcgcag caagaggtga   8361

gtggcgagct gtatttatag ccgctccccc ttgctcccat taccgcc                 8408
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gccggccgcc agg   atg cag gcc ccg cac aag gag cac ctg tac aag ttg     109
                 Met Gln Ala Pro His Lys Glu His Leu Tyr Lys Leu
                   1               5                  10

ctg gtg att ggc gac ctg ggc gtg ggg aag acc agt atc atc aag cgc     157
Leu Val Ile Gly Asp Leu Gly Val Gly Lys Thr Ser Ile Ile Lys Arg
 13                  18                  23                  28

tac gtg cac cag aac ttc tcc tcg cac tac cgg gcc aca atc ggc gtg     205
Tyr Val His Gln Asn Phe Ser Ser His Tyr Arg Ala Thr Ile Gly Val
 29                  34                  39                  44

gac ttc gcg ctc aag gtg ctc cac tgg gac ccg gag act gtg gtg cgc     253
Asp Phe Ala Leu Lys Val Leu His Trp Asp Pro Glu Thr Val Val Arg
 45                  50                  55                  60

ctg cag ctc tgg gat atc gca ggt caa gaa aga ttt gga aac atg acg     301
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Leu Gln Leu Trp Asp Ile Ala Gly Gln Glu Arg Phe Gly Asn Met Thr
 61                  66                  71                  76

agg gtc tat tac cga gaa gct atg ggt gca ttt att gtc ttc gat gtc      349
Arg Val Tyr Tyr Arg Glu Ala Met Gly Ala Phe Ile Val Phe Asp Val
 77                  82                  87                  92

acc agg cca gcc aca ttt gaa gca gtg gca aag tgg aaa aat gat ttg      397
Thr Arg Pro Ala Thr Phe Glu Ala Val Ala Lys Trp Lys Asn Asp Leu
 93                  98                 103                 108

gac tcc aag tta agt ctc cct aat ggc aaa ccg gtt tca gtg gtt ttg      445
Asp Ser Lys Leu Ser Leu Pro Asn Gly Lys Pro Val Ser Val Val Leu
109                 114                 119                 124

ttg gcc aac aaa tgt gac cag ggg aag gat gtg ctc atg aac aat ggc      493
Leu Ala Asn Lys Cys Asp Gln Gly Lys Asp Val Leu Met Asn Asn Gly
125                 130                 135                 140

ctc aag atg gac cag ttc tgc aag gag cac ggt ttc gta gga tgg ttt      541
Leu Lys Met Asp Gln Phe Cys Lys Glu His Gly Phe Val Gly Trp Phe
141                 146                 151                 156

gaa aca tca gca aag gaa aat ata aac att gat gaa gcc tcc aga tgc      589
Glu Thr Ser Ala Lys Glu Asn Ile Asn Ile Asp Glu Ala Ser Arg Cys
157                 162                 167                 172

ctg gtg aaa cac ata ctt gca aat gag tgt gac cta atg gag tct att      637
Leu Val Lys His Ile Leu Ala Asn Glu Cys Asp Leu Met Glu Ser Ile
173                 178                 183                 188

gag ccg gac gtc gtg aag ccc cat ctc aca tca acc aag gtt gcc agc      685
Glu Pro Asp Val Val Lys Pro His Leu Thr Ser Thr Lys Val Ala Ser
189                 194                 199                 204

tgc tct ggc tgt gcc aaa tcc tag taggcacctt tgctggtgtc tggtaggaat     739
Cys Ser Gly Cys Ala Lys Ser  *
205                 210

gacctcattg ttccacaaat tgtgcctcca ttttttccat tttgggtaaa cgtgcgggg     798
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gcctgggatg taaaccggac cagccgctgc gggcagaagg aaggctcttg gctccttcgg    120
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gaaacccagc cccgtcaccg ggctccgagc ggctcgcagg cgacggacac gtccgtcagc    180

cccggcagcg cctagcgtcg gctgcggaaa gcggagggag tccgacgcgg gcgcgggcgg    240

ggagcgtgcg tccgttcgca caggcagcgg gaggaggggc ggccgaacc    atg gcc     295
                                                         Met Ala
                                                           1

ggg gac agc gag cag acc ctg cag aac cac cag cag ccc aac ggc ggc      343
Gly Asp Ser Glu Gln Thr Leu Gln Asn His Gln Gln Pro Asn Gly Gly
  3                   8                  13                  18

gag ccc ttc ctt ata ggc gtc agc ggg gga aca gct agc ggc aag tct      391
Glu Pro Phe Leu Ile Gly Val Ser Gly Gly Thr Ala Ser Gly Lys Ser
 19                  24                  29                  34

tcc gtg tgt gct aag atc gtg cag ctc ctg ggg cag aat gag gtg gac      439
Ser Val Cys Ala Lys Ile Val Gln Leu Leu Gly Gln Asn Glu Val Asp
 35                  40                  45                  50

tat cgc cag aag cag gtg gtc atc ctg agc cag gat agc ttc tac cgt      487
Tyr Arg Gln Lys Gln Val Val Ile Leu Ser Gln Asp Ser Phe Tyr Arg
 51                  56                  61                  66

gtc ctt acc tcg gag cag aag gcc aaa gcc ctg aag ggc cag ttc aac      535
Val Leu Thr Ser Glu Gln Lys Ala Lys Ala Leu Lys Gly Gln Phe Asn
 67                  72                  77                  82

ttt gac cac ccg gat gcc ttt gac aat gaa ctc att ctc aaa aca ctc      583
Phe Asp His Pro Asp Ala Phe Asp Asn Glu Leu Ile Leu Lys Thr Leu
 83                  88                  93                  98

aaa gaa atc act gaa ggg aaa aca gtc cag atc ccc gtg tat gac ttt      631
Lys Glu Ile Thr Glu Gly Lys Thr Val Gln Ile Pro Val Tyr Asp Phe
 99                 104                 109                 114

gtc tcc cat tcc cgg aag gag gag aca gtt act gtc tat ccc gca gac      679
Val Ser His Ser Arg Lys Glu Glu Thr Val Thr Val Tyr Pro Ala Asp
115                 120                 125                 130

gtg gtg ctc ttt gaa ggg atc ctg gcc ttc tac tcc cag gag gta cga      727
Val Val Leu Phe Glu Gly Ile Leu Ala Phe Tyr Ser Gln Glu Val Arg
131                 136                 141                 146

gac ctg ttc cag atg aag ctt ttt gtg gat aca gat gcg gac acc cgg      775
Asp Leu Phe Gln Met Lys Leu Phe Val Asp Thr Asp Ala Asp Thr Arg
147                 152                 157                 162

ctc tca cgc aga gta tta agg gac atc agc gag aga ggc agg gat ctt      823
Leu Ser Arg Arg Val Leu Arg Asp Ile Ser Glu Arg Gly Arg Asp Leu
163                 168                 173                 178

gag cag att tta tct cag tac att acg ttc gtc aag cct gcc ttt gag      871
Glu Gln Ile Leu Ser Gln Tyr Ile Thr Phe Val Lys Pro Ala Phe Glu
179                 184                 189                 194
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gaa ttc tgc ttg cca aca aag aag tat gct gat gtg atc atc cct aga      919
Glu Phe Cys Leu Pro Thr Lys Lys Tyr Ala Asp Val Ile Ile Pro Arg
195                 200                 205                 210

ggt gca gat aat ctg gtg gcc atc aac ctc atc gtg cag cac atc cag      967
Gly Ala Asp Asn Leu Val Ala Ile Asn Leu Ile Val Gln His Ile Gln
211                 216                 221                 226

gac atc ctg aat gga ggg ccc tcc aaa cgg cag acc aat ggc tgt ctc     1015
Asp Ile Leu Asn Gly Gly Pro Ser Lys Arg Gln Thr Asn Gly Cys Leu
227                 232                 237                 242

aac ggc tac acc cct tca cgc aag agg cag gca tcg gag tcc agc agc     1063
Asn Gly Tyr Thr Pro Ser Arg Lys Arg Gln Ala Ser Glu Ser Ser Ser
243                 248                 253                 258

agg ccg cat tga ccc gtctccatcg gaccccagcc cctatctcca agagacagag     1118
Arg Pro His  *
259

gaggggtcag gaggcactgc tcatctgtac atactgtttc ctatgacatt actgtattta   1178

agaaaacacc atggagatga aatgcctttg attttttttt tctttttgta ctttggaacg   1238

acaaaatgaa acagaacttg accctgagct taaataacaa aactgtgcca actactactg   1298

gtgatgccta attatgaatc caacgtgtaa ccagttataa atacatatat atataaaaaa   1358

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ccgctctttg ttggacacta acaaggcata tccaacttct ttcacaaaga ggccaacttc    180

tggtttgagg tcagtggata cctgatatcc ccactgcgaa gccctttgt ggatcctgca    240

ctcgaatgga gtcta atg gct tct cca tgg aat aaa atg gaa gga gaa tca      291
               Met Ala Ser Pro Trp Asn Lys Met Glu Gly Glu Ser
                 1               5                  10

agc aga ttt gaa atc cac act cca gtt tct gac aag aaa aag aaa aag      339
Ser Arg Phe Glu Ile His Thr Pro Val Ser Asp Lys Lys Lys Lys Lys
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 13                  18                  23                  28

tgt tct ata cat aag gaa aga cct cag aaa cat tcc cac gaa att ttc      387
Cys Ser Ile His Lys Glu Arg Pro Gln Lys His Ser His Glu Ile Phe
 29                  34                  39                  44

aga gac tcc tcc ctg gtg aat gaa cag tct caa ata act agg agg aaa      435
Arg Asp Ser Ser Leu Val Asn Glu Gln Ser Gln Ile Thr Arg Arg Lys
 45                  50                  55                  60

aag agg aaa aaa gat ttc cag cat ctc att tct tct cct ttg aaa aaa      483
Lys Arg Lys Lys Asp Phe Gln His Leu Ile Ser Ser Pro Leu Lys Lys
 61                  66                  71                  76

tcc aga atc tgt gat gag act gca aat gcc act tcc aca ctc aaa aag      531
Ser Arg Ile Cys Asp Glu Thr Ala Asn Ala Thr Ser Thr Leu Lys Lys
 77                  82                  87                  92

aga aaa aag aga aga tat agt gct ttg gag gtg gac gag gaa gca ggt      579
Arg Lys Lys Arg Arg Tyr Ser Ala Leu Glu Val Asp Glu Glu Ala Gly
 93                  98                 103                 108

gtt aca gtt gtc ctt gtg gat aaa gaa aat att aac aac aca cca aag      627
Val Thr Val Val Leu Val Asp Lys Glu Asn Ile Asn Asn Thr Pro Lys
109                 114                 119                 124

cat ttt aga aag gat gtt gat gtt gtt tgt gtt gat atg agc ata gaa      675
His Phe Arg Lys Asp Val Asp Val Val Cys Val Asp Met Ser Ile Glu
125                 130                 135                 140

cag aag tta cca aga aag cct aaa aca gac aaa ttt cag gta ctt gct      723
Gln Lys Leu Pro Arg Lys Pro Lys Thr Asp Lys Phe Gln Val Leu Ala
141                 146                 151                 156

aag tca cat gca cat aaa tca gaa gcc ctg cac agt aaa gtt agg gag      771
Lys Ser His Ala His Lys Ser Glu Ala Leu His Ser Lys Val Arg Glu
157                 162                 167                 172

aaa aag aat aaa aag cat cag agg aaa gct gca tcc tgg gag agc cag      819
Lys Lys Asn Lys Lys His Gln Arg Lys Ala Ala Ser Trp Glu Ser Gln
173                 178                 183                 188

cgg gca agg gac acc ctg cct cag tca gaa tcc cac cag gag gag tcc      867
Arg Ala Arg Asp Thr Leu Pro Gln Ser Glu Ser His Gln Glu Glu Ser
189                 194                 199                 204

tgg ctt tct gtg ggt cca ggg ggt gaa att aca gaa cta cca gca tct      915
Trp Leu Ser Val Gly Pro Gly Gly Glu Ile Thr Glu Leu Pro Ala Ser
205                 210                 215                 220

gct cat aaa aac aag tct aag aaa aaa aag aaa aag tcc agt aac cgg      963
Ala His Lys Asn Lys Ser Lys Lys Lys Lys Lys Lys Ser Ser Asn Arg
221                 226                 231                 236

gaa tat gag aca ctg gcc atg cct gaa gga tcg caa gca ggc aga gag     1011
Glu Tyr Glu Thr Leu Ala Met Pro Glu Gly Ser Gln Ala Gly Arg Glu
237                 242                 247                 252
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gcc ggg act gat atg cag gaa tcc cag cct act gtg ggc ttg gat gat     1059
Ala Gly Thr Asp Met Gln Glu Ser Gln Pro Thr Val Gly Leu Asp Asp
253                 258                 263                 268

gaa act cca caa cta cta gga cct act cac aaa aaa aag tct aag aaa     1107
Glu Thr Pro Gln Leu Leu Gly Pro Thr His Lys Lys Lys Ser Lys Lys
269                 274                 279                 284

aaa aag aag aaa aag tcc aat cac cag gaa ttt gag gca ttg gcc atg     1155
Lys Lys Lys Lys Lys Ser Asn His Gln Glu Phe Glu Ala Leu Ala Met
285                 290                 295                 300

cct gaa gga tca caa gtg ggc agt gag gtt ggg gct gat atg cag gaa     1203
Pro Glu Gly Ser Gln Val Gly Ser Glu Val Gly Ala Asp Met Gln Glu
301                 306                 311                 316

tcc cgg cct gct gtg ggc ctg cat ggt gaa act gca gga ata cca gca     1251
Ser Arg Pro Ala Val Gly Leu His Gly Glu Thr Ala Gly Ile Pro Ala
317                 322                 327                 332

cct gct tat aaa aac aag tct aag aaa aaa aag aaa aag tcc aat cac     1299
Pro Ala Tyr Lys Asn Lys Ser Lys Lys Lys Lys Lys Lys Ser Asn His
333                 338                 343                 348

cag gaa ttt gag gca gtg gcc atg cct gag agc ctc gag agt gca tac     1347
Gln Glu Phe Glu Ala Val Ala Met Pro Glu Ser Leu Glu Ser Ala Tyr
349                 354                 359                 364

cct gaa gga tca cag gtg ggc agt gag gtt ggg act gtg gaa ggc agt     1395
Pro Glu Gly Ser Gln Val Gly Ser Glu Val Gly Thr Val Glu Gly Ser
365                 370                 375                 380

aca gct ctt aaa ggg ttc aag gaa tcc aac agt aca aag aag aag tct     1443
Thr Ala Leu Lys Gly Phe Lys Glu Ser Asn Ser Thr Lys Lys Lys Ser
381                 386                 391                 396

aag aaa agg aag ctt acg tct gtc aaa agg gca cga gtg tct ggt gat     1491
Lys Lys Arg Lys Leu Thr Ser Val Lys Arg Ala Arg Val Ser Gly Asp
397                 402                 407                 412

gat ttt tca gtg ccc agt aag aac tct gag agc aca ctc ttt gat tca     1539
Asp Phe Ser Val Pro Ser Lys Asn Ser Glu Ser Thr Leu Phe Asp Ser
413                 418                 423                 428

gta gaa ggt gat ggc gcc atg atg gaa gaa ggt gtg aaa tct agg ccc     1587
Val Glu Gly Asp Gly Ala Met Met Glu Glu Gly Val Lys Ser Arg Pro
429                 434                 439                 444

cga caa aag aaa acc cag gcc tgt ttg gca agc aag cac gtg caa gag     1635
Arg Gln Lys Lys Thr Gln Ala Cys Leu Ala Ser Lys His Val Gln Glu
445                 450                 455                 460

gcg cca agg tta gaa cct gca aat gaa gaa cac aat gtg gaa aca gct     1683
Ala Pro Arg Leu Glu Pro Ala Asn Glu Glu His Asn Val Glu Thr Ala
461                 466                 471                 476
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09650-0050-US1 Patent

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gaa gat tcc gaa ata aga tac tta tct gca gat tca gga gat gcc gat     1731
Glu Asp Ser Glu Ile Arg Tyr Leu Ser Ala Asp Ser Gly Asp Ala Asp
477                 482                 487                 492

gat tca gat gcg gat ttg ggt tct gcc gtg aaa cag ctt cag gag ttc     1779
Asp Ser Asp Ala Asp Leu Gly Ser Ala Val Lys Gln Leu Gln Glu Phe
493                 498                 503                 508

att cct aac atc aag gac agg gcc acc agc aca atc aag cgg atg tac     1827
Ile Pro Asn Ile Lys Asp Arg Ala Thr Ser Thr Ile Lys Arg Met Tyr
509                 514                 519                 524

cgg gac gac ttg gaa cgg ttt aag gaa ttt aaa gca caa ggt gtc gct     1875
Arg Asp Asp Leu Glu Arg Phe Lys Glu Phe Lys Ala Gln Gly Val Ala
525                 530                 535                 540

att aaa ttt ggc aag ttt tct gta aag gaa aat aag cag tta gag aaa     1923
Ile Lys Phe Gly Lys Phe Ser Val Lys Glu Asn Lys Gln Leu Glu Lys
541                 546                 551                 556

aat gtg gaa gac ttt cta gcc ctg aca ggc att gag agt gca gac aag     1971
Asn Val Glu Asp Phe Leu Ala Leu Thr Gly Ile Glu Ser Ala Asp Lys
557                 562                 567                 572

ctc ctg tac acg gac aga tat cct gag gaa aaa tct gtg atc acc aac     2019
Leu Leu Tyr Thr Asp Arg Tyr Pro Glu Glu Lys Ser Val Ile Thr Asn
573                 578                 583                 588

tta aaa agg aga tac tcg ttt aga tta cac att ggt agg aac att gcc     2067
Leu Lys Arg Arg Tyr Ser Phe Arg Leu His Ile Gly Arg Asn Ile Ala
589                 594                 599                 604

cgg ccc tgg aaa ctt ata tac tat cga gca aag aag atg ttc gat gtc     2115
Arg Pro Trp Lys Leu Ile Tyr Tyr Arg Ala Lys Lys Met Phe Asp Val
605                 610                 615                 620

aac aat tac aaa ggc agg tat agc gaa gga gat act gag aag tta aag     2163
Asn Asn Tyr Lys Gly Arg Tyr Ser Glu Gly Asp Thr Glu Lys Leu Lys
621                 626                 631                 636

atg tac cat tct ctc ctt ggg aat gac tgg aag acg att ggt gag atg     2211
Met Tyr His Ser Leu Leu Gly Asn Asp Trp Lys Thr Ile Gly Glu Met
637                 642                 647                 652

gtg gcc cga agt agc ctc tcc gtg gcc ctc aag ttc tca cag atc agc     2259
Val Ala Arg Ser Ser Leu Ser Val Ala Leu Lys Phe Ser Gln Ile Ser
653                 658                 663                 668

agt caa aga aat cgt ggt gct tgg agt aag tct gaa acc cgg aaa cta     2307
Ser Gln Arg Asn Arg Gly Ala Trp Ser Lys Ser Glu Thr Arg Lys Leu
669                 674                 679                 684

atc aag gct gtc gaa gaa gtg att ctg aag aag atg tct ccc cag gag     2355
Ile Lys Ala Val Glu Glu Val Ile Leu Lys Lys Met Ser Pro Gln Glu
685                 690                 695                 700

tta aaa gag gtg gat tcc aaa ctc caa gaa aat cct gaa agt tgc cta     2403
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Leu Lys Glu Val Asp Ser Lys Leu Gln Glu Asn Pro Glu Ser Cys Leu
701                 706                 711                 716

tca att gtt cgg gaa aaa ctc tac aag ggc ata tct tgg gta gaa gta     2451
Ser Ile Val Arg Glu Lys Leu Tyr Lys Gly Ile Ser Trp Val Glu Val
717                 722                 727                 732

gaa gct aaa gtg caa acc aga aat tgg atg cag tgt aaa agt aag tgg     2499
Glu Ala Lys Val Gln Thr Arg Asn Trp Met Gln Cys Lys Ser Lys Trp
733                 738                 743                 748

aca gaa att cta acc aag agg atg act aat ggt cgg cgt ata tac tat     2547
Thr Glu Ile Leu Thr Lys Arg Met Thr Asn Gly Arg Arg Ile Tyr Tyr
749                 754                 759                 764

ggc atg aat gcc ctg cgg gcc aag gtc agc ctt att gaa agg ttg tat     2595
Gly Met Asn Ala Leu Arg Ala Lys Val Ser Leu Ile Glu Arg Leu Tyr
765                 770                 775                 780

gaa ata aat gtg gaa gat act aat gaa ata gac tgg gaa gat ctt gct     2643
Glu Ile Asn Val Glu Asp Thr Asn Glu Ile Asp Trp Glu Asp Leu Ala
781                 786                 791                 796

agt gcc ata ggt gat gtt cct cca tct tac gtt caa act aaa ttt tct     2691
Ser Ala Ile Gly Asp Val Pro Pro Ser Tyr Val Gln Thr Lys Phe Ser
797                 802                 807                 812

agg ctg aaa gct gtc tat gtt cca ttt tgg cag aaa aag act ttt cca     2739
Arg Leu Lys Ala Val Tyr Val Pro Phe Trp Gln Lys Lys Thr Phe Pro
813                 818                 823                 828

gag atc atc gac tac ctt tat gag acg act cta cct ttg ctg aag gaa     2787
Glu Ile Ile Asp Tyr Leu Tyr Glu Thr Thr Leu Pro Leu Leu Lys Glu
829                 834                 839                 844

aag tta gaa aaa atg atg gag aaa aaa ggc act aaa atc cag act cct     2835
Lys Leu Glu Lys Met Met Glu Lys Lys Gly Thr Lys Ile Gln Thr Pro
845                 850                 855                 860

gca gca ccc aag caa gtt ttc cca ttt cga gac atc ttt tat tat gaa     2883
Ala Ala Pro Lys Gln Val Phe Pro Phe Arg Asp Ile Phe Tyr Tyr Glu
861                 866                 871                 876

gac gat agt gaa gga gag gac ata gaa aaa gaa agc gaa ggc cag gcg     2931
Asp Asp Ser Glu Gly Glu Asp Ile Glu Lys Glu Ser Glu Gly Gln Ala
877                 882                 887                 892

cca tgc atg gct cac gcc tgt aat tcc agt act ttg gga ggc caa ggc     2979
Pro Cys Met Ala His Ala Cys Asn Ser Ser Thr Leu Gly Gly Gln Gly
893                 898                 903                 908

cgg tgg atc atc tga ggtcaggagt tcgagaccgg cctgaccaac atggtgaaga     3034
Arg Trp Ile Ile  *
909

cctgtcacta ttaaaaatgc gaaaattagc cgggtgtggt agtgcacacc tgtaatttca   3094
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actacttggg aggctgaggc aggagaattg cttgaaccca ggaggtggag gttgcagtga 3154

gccaagatcg caccaccgca tgagagagag agattactat ttcttgtccc tttttctcag 3214

tttgattata tttatataca tatgtcagta aatctgtttt cagtattgat gtttaataaa 3274

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Met Ala Asn Val Ser Lys Lys
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gtg tcc tgg tcc ggc cgg gac cgg gac gac gag gag gcg gcg ccg ctg 102
Val Ser Trp Ser Gly Arg Asp Arg Asp Asp Glu Glu Ala Ala Pro Leu
8 13 18 23

ctg cgg agg acg gcg cgg ccc ggc ggg ggg acg ccg ctg ctg aac ggg 150
Leu Arg Arg Thr Ala Arg Pro Gly Gly Gly Thr Pro Leu Leu Asn Gly
24 29 34 39

gct ggg ccc ggg gct gcg cgc cag tca cca cgt tct gcg ctt ttc cga 198
Ala Gly Pro Gly Ala Ala Arg Gln Ser Pro Arg Ser Ala Leu Phe Arg
40 45 50 55

gtc gga cat atg agc agc gtg gag ctg gat gat gaa ctt ttg gac ccg 246
Val Gly His Met Ser Ser Val Glu Leu Asp Asp Glu Leu Leu Asp Pro
56 61 66 71

gat atg gac cct cca cat ccc ttc ccc aag gag atc cca cac aac gag 294
Asp Met Asp Pro Pro His Pro Phe Pro Lys Glu Ile Pro His Asn Glu
72 77 82 87

aag ctc ctg tcc ctc aag tat gag agc ttg gac tat gac aac agt gag 342
Lys Leu Leu Ser Leu Lys Tyr Glu Ser Leu Asp Tyr Asp Asn Ser Glu
88 93 98 103

aac cag ctg ttc ctg gag gag gag cgg cgg atc aat cac acg gcc ttc 390
Asn Gln Leu Phe Leu Glu Glu Glu Arg Arg Ile Asn His Thr Ala Phe
104 109 114 119

cgg acg gtg gag atc aag cgc tgg gtc atc tgc gcc ctc att ggg atc 438
Arg Thr Val Glu Ile Lys Arg Trp Val Ile Cys Ala Leu Ile Gly Ile
120 125 130 135

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ctc acg ggc ctc gtg gcc tgc ttc att gac atc gtg gtg gaa aac ctg      486
Leu Thr Gly Leu Val Ala Cys Phe Ile Asp Ile Val Val Glu Asn Leu
136                 141                 146                 151

gct ggc ctc aag tac agg gtc atc aag ggc aat atc gac aag ttc aca      534
Ala Gly Leu Lys Tyr Arg Val Ile Lys Gly Asn Ile Asp Lys Phe Thr
152                 157                 162                 167

gag aag ggc gga ctg tcc ttc tcc ctg ttg ctg tgg gcc acg ctg aac      582
Glu Lys Gly Gly Leu Ser Phe Ser Leu Leu Leu Trp Ala Thr Leu Asn
168                 173                 178                 183

gcc gcc ttc gtg ctc gtg ggc tct gtg att gtg gct ttc ata gag ccg      630
Ala Ala Phe Val Leu Val Gly Ser Val Ile Val Ala Phe Ile Glu Pro
184                 189                 194                 199

gtg gct gct ggc agc gga atc ccc cag atc aag tgc ttc ctc aac ggg      678
Val Ala Ala Gly Ser Gly Ile Pro Gln Ile Lys Cys Phe Leu Asn Gly
200                 205                 210                 215

gtg aag atc ccc cac gtg gtg cgg ctc aag acg ttg gtg atc aaa gtg      726
Val Lys Ile Pro His Val Val Arg Leu Lys Thr Leu Val Ile Lys Val
216                 221                 226                 231

tcc ggt gtg atc ctg tcc gtg gtc ggg ggc ctg gcc gtg gga aag gaa      774
Ser Gly Val Ile Leu Ser Val Val Gly Gly Leu Ala Val Gly Lys Glu
232                 237                 242                 247

ggg ccg atg atc cac tca ggt tca gtg att gcc gcc ggg atc tct cag      822
Gly Pro Met Ile His Ser Gly Ser Val Ile Ala Ala Gly Ile Ser Gln
248                 253                 258                 263

gga agg tca acg tca ctg aaa cga gat ttc aag atc ttc gag tac ctc      870
Gly Arg Ser Thr Ser Leu Lys Arg Asp Phe Lys Ile Phe Glu Tyr Leu
264                 269                 274                 279

cgc aga gac aca gag aag cgg gac ttc gtc tcc gca ggg gct gcg gcc      918
Arg Arg Asp Thr Glu Lys Arg Asp Phe Val Ser Ala Gly Ala Ala Ala
280                 285                 290                 295

gga gtg tca gcg gcg ttt gga gcc ccc gtg ggt ggg gtc ctg ttc agc      966
Gly Val Ser Ala Ala Phe Gly Ala Pro Val Gly Gly Val Leu Phe Ser
296                 301                 306                 311

ttg gag gag ggt gcg tcc ttc tgg aac cag ttc ctg acc tgg agg atc     1014
Leu Glu Glu Gly Ala Ser Phe Trp Asn Gln Phe Leu Thr Trp Arg Ile
312                 317                 322                 327

ttc ttt gct tcc atg atc tcc acg ttc acc ctg aat ttt gtt ctg agc     1062
Phe Phe Ala Ser Met Ile Ser Thr Phe Thr Leu Asn Phe Val Leu Ser
328                 333                 338                 343

att tac cac ggg aac atg tgg gac ctg tcc agc cca ggc ctc atc aac     1110
Ile Tyr His Gly Asn Met Trp Asp Leu Ser Ser Pro Gly Leu Ile Asn
344                 349                 354                 359

ttc gga agg ttt gac tcg gag aaa atg gcc tac acg atc cac gag atc     1158
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Phe Gly Arg Phe Asp Ser Glu Lys Met Ala Tyr Thr Ile His Glu Ile
360                 365                 370                 375

ccg gtc ttc atc gcc atg ggc gtg gtg ggc ggt gtg ctt gga gcc gtg     1206
Pro Val Phe Ile Ala Met Gly Val Val Gly Gly Val Leu Gly Ala Val
376                 381                 386                 391

ttc aat gcc ttg aac tac tgg ctg acc atg ttt cga atc agg tac atc     1254
Phe Asn Ala Leu Asn Tyr Trp Leu Thr Met Phe Arg Ile Arg Tyr Ile
392                 397                 402                 407

cac cgg ccc tgc ctg cag gtg att gag gcc gtg ctg gtg gcc gcc gtc     1302
His Arg Pro Cys Leu Gln Val Ile Glu Ala Val Leu Val Ala Ala Val
408                 413                 418                 423

acg gcc aca gtt gcc ttc gtg ctg atc tac tcg tcg cgg gat tgc cag     1350
Thr Ala Thr Val Ala Phe Val Leu Ile Tyr Ser Ser Arg Asp Cys Gln
424                 429                 434                 439

ccc ctg cag ggg ggc tcc atg tcc tac ccg ctg cag ctc ttt tgt gca     1398
Pro Leu Gln Gly Gly Ser Met Ser Tyr Pro Leu Gln Leu Phe Cys Ala
440                 445                 450                 455

gat ggc gag tac aac tcc atg gct gcg gcc ttc ttc aac acc ccg gag     1446
Asp Gly Glu Tyr Asn Ser Met Ala Ala Ala Phe Phe Asn Thr Pro Glu
456                 461                 466                 471

aag agc gtg gtg agc ctc ttc cac gac ccg cca ggc tcc tac aac ccc     1494
Lys Ser Val Val Ser Leu Phe His Asp Pro Pro Gly Ser Tyr Asn Pro
472                 477                 482                 487

ctg acc ctc ggc ctg ttc acg ctg gtc tac ttc ttc ctg gcc tgc tgg     1542
Leu Thr Leu Gly Leu Phe Thr Leu Val Tyr Phe Phe Leu Ala Cys Trp
488                 493                 498                 503

acc tac ggg ctc acg gtg tct gcc ggg gtc ttc atc ccg tcc ctg ctc     1590
Thr Tyr Gly Leu Thr Val Ser Ala Gly Val Phe Ile Pro Ser Leu Leu
504                 509                 514                 519

atc ggg gct gcc tgg ggc cgg ctc ttt ggg atc tcc ctg tcc tac ctc     1638
Ile Gly Ala Ala Trp Gly Arg Leu Phe Gly Ile Ser Leu Ser Tyr Leu
520                 525                 530                 535

acg ggg gcg gcg atc tgg gcg gac ccc ggc aaa tac gcc ctg atg gga     1686
Thr Gly Ala Ala Ile Trp Ala Asp Pro Gly Lys Tyr Ala Leu Met Gly
536                 541                 546                 551

gct gct gcc cag ctg ggc ggg att gtg cgg atg aca ctg agc ctg acc     1734
Ala Ala Ala Gln Leu Gly Gly Ile Val Arg Met Thr Leu Ser Leu Thr
552                 557                 562                 567

gtc atc atg atg gag gcc acc agc aac gtg acc tac ggc ttc ccc atc     1782
Val Ile Met Met Glu Ala Thr Ser Asn Val Thr Tyr Gly Phe Pro Ile
568                 573                 578                 583

atg ctg gtg ctc atg acc gcc aag atc gtg ggc gac gtc ttc att gag     1830
Met Leu Val Leu Met Thr Ala Lys Ile Val Gly Asp Val Phe Ile Glu
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584                 589                 594                 599

ggc ctg tac gac atg cac att cag ctg cag agt gtg ccc ttc ctg cac     1878
Gly Leu Tyr Asp Met His Ile Gln Leu Gln Ser Val Pro Phe Leu His
600                 605                 610                 615

tgg gag gcc ccg gtc acc tca cac tca ctc act gcc agg gag gtg atg     1926
Trp Glu Ala Pro Val Thr Ser His Ser Leu Thr Ala Arg Glu Val Met
616                 621                 626                 631

agc aca cca gtg acc tgc ctg agg cgg cgt gag aag gtc ggc gtc att     1974
Ser Thr Pro Val Thr Cys Leu Arg Arg Arg Glu Lys Val Gly Val Ile
632                 637                 642                 647

gtg gac gtg ctg agc gac acg gcg tcc aat cac aac ggc ttc ccc gtg     2022
Val Asp Val Leu Ser Asp Thr Ala Ser Asn His Asn Gly Phe Pro Val
648                 653                 658                 663

gtg gag cat gcc gat gac acc cag cct gcc cgg ctc cag ggc ctg atc     2070
Val Glu His Ala Asp Asp Thr Gln Pro Ala Arg Leu Gln Gly Leu Ile
664                 669                 674                 679

ctg cgc tcc cag ctc atc gtt ctc cta aag cac aag gtg ttt gtg gag     2118
Leu Arg Ser Gln Leu Ile Val Leu Leu Lys His Lys Val Phe Val Glu
680                 685                 690                 695

cgg tcc aac ctg ggc ctg gta cag cgg cgc ctg agg ctg aag gac ttc     2166
Arg Ser Asn Leu Gly Leu Val Gln Arg Arg Leu Arg Leu Lys Asp Phe
696                 701                 706                 711

cga gac gcc tac ccg cgc ttc cca ccc atc cag tcc atc cac gtg tcc     2214
Arg Asp Ala Tyr Pro Arg Phe Pro Pro Ile Gln Ser Ile His Val Ser
712                 717                 722                 727

cag gac gag cgg gag tgc acc atg gac ctc tcc gag ttc atg aac ccc     2262
Gln Asp Glu Arg Glu Cys Thr Met Asp Leu Ser Glu Phe Met Asn Pro
728                 733                 738                 743

tcc ccc tac acg gtg ccc cag gag gcg tcg ctc cca cgg gtg ttc aag     2310
Ser Pro Tyr Thr Val Pro Gln Glu Ala Ser Leu Pro Arg Val Phe Lys
744                 749                 754                 759

ctg ttc cgg gcc ctg ggc ctg cgg cac ctg gtg gtg gtg gac aac cgc     2358
Leu Phe Arg Ala Leu Gly Leu Arg His Leu Val Val Val Asp Asn Arg
760                 765                 770                 775

aat cag gtt gtc ggg ttg gtg acc agg aag gac ctc gcc agg tac cgc     2406
Asn Gln Val Val Gly Leu Val Thr Arg Lys Asp Leu Ala Arg Tyr Arg
776                 781                 786                 791

ctg gga aag aga ggc ttg gag gag ctc tcg ctg gcc cag acg tga ggc     2454
Leu Gly Lys Arg Gly Leu Glu Glu Leu Ser Leu Ala Gln Thr  *
792                 797                 802

ccagccctgc ccataatggg cactggcgct ggcaccccgg cccttctgca tttcctcccg   2514

gagtcactgg tttctcggcc caaaccatgc tccccagcag tggcaatggc gagcaccctg   2574
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aagcgcaggt gcagcggggg ccagactcct gccggcctca gaggacacct ggcccagcac 3414

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gcccctggga ggctcctctg gcctggctgg gctgggtctg gggccgccac aggcccctca 3534

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agcccgctcc tgtccccgac atcacgtgta ttccgcacgt cccctccgcg ctgtgtgtct    180

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ggcaagctcc ccgtctccgg gcgcacttcc ctcgcctgtg ttcggtccat cctcctttct    300

ccagcctcct cccctcgcag gtgggatcgt cggtgggacc ggagcgcggg cgggcgcggc    360

ccccgggac c atg gcc ggg tcc gac acc gcg ccc ttc ctc agc cag gcg      410
             Met Ala Gly Ser Asp Thr Ala Pro Phe Leu Ser Gln Ala
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gat gac ccg gac gac ggg cca gtg cct ggc acc ccg ggg ttg cca ggg      458
Asp Asp Pro Asp Asp Gly Pro Val Pro Gly Thr Pro Gly Leu Pro Gly
 14                  19                  24                  29

tcc acg ggg aac ccg aag tcc gag gag ccc gag gtc ccg gac cag gag      506
Ser Thr Gly Asn Pro Lys Ser Glu Glu Pro Glu Val Pro Asp Gln Glu
 30                  35                  40                  45

ggg ctg cag cgc atc acc ggc ctg tct ccc ggc cgt tcg gct ctc ata      554
Gly Leu Gln Arg Ile Thr Gly Leu Ser Pro Gly Arg Ser Ala Leu Ile
 46                  51                  56                  61

gtg gcg gtg ctg tgc tac atc aat ctc ctg aac tac atg gac cgc ttc      602
Val Ala Val Leu Cys Tyr Ile Asn Leu Leu Asn Tyr Met Asp Arg Phe
 62                  67                  72                  77

acc gtg gct ggc gtc ctt ccc gac atc gag cag ttc ttc aac atc ggg      650
Thr Val Ala Gly Val Leu Pro Asp Ile Glu Gln Phe Phe Asn Ile Gly
 78                  83                  88                  93

gac agt agc tct ggg ctc atc cag acc gtg ttc atc tcc agt tac atg      698
Asp Ser Ser Ser Gly Leu Ile Gln Thr Val Phe Ile Ser Ser Tyr Met
 94                  99                 104                 109

gtg ttg gca cct gtg ttt ggc tac ctg ggt gac agg tac aat cgg aag      746
Val Leu Ala Pro Val Phe Gly Tyr Leu Gly Asp Arg Tyr Asn Arg Lys
110                 115                 120                 125

tat ctc atg tgc ggg ggc att gcc ttc tgg tcc ctg gtg aca ctg ggg      794
Tyr Leu Met Cys Gly Gly Ile Ala Phe Trp Ser Leu Val Thr Leu Gly
126                 131                 136                 141

tca tcc ttc atc ccc gga gag cat ttc tgg ctg ctc ctc ctg acc cgg      842
Ser Ser Phe Ile Pro Gly Glu His Phe Trp Leu Leu Leu Leu Thr Arg
142                 147                 152                 157

ggc ctg gtg ggg gtc ggg gag gcc agt tat tcc acc atc gcg ccc act      890
Gly Leu Val Gly Val Gly Glu Ala Ser Tyr Ser Thr Ile Ala Pro Thr
158                 163                 168                 173

ctc att gcc gac ctc ttt gtg gcc gac cag cgg agc cgg atg ctc agc      938
Leu Ile Ala Asp Leu Phe Val Ala Asp Gln Arg Ser Arg Met Leu Ser
174                 179                 184                 189
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atc ttc tac ttt gcc att ccg gtg ggc agt ggt ctg ggc tac att gca      986
Ile Phe Tyr Phe Ala Ile Pro Val Gly Ser Gly Leu Gly Tyr Ile Ala
190                 195                 200                 205

ggc tcc aaa gtg aag gat atg gct gga gac tgg cac tgg gct ctg agg     1034
Gly Ser Lys Val Lys Asp Met Ala Gly Asp Trp His Trp Ala Leu Arg
206                 211                 216                 221

gtg aca ccg ggt cta gga gtg gtg gcc gtt ctg ctg ctg ttc ctg gta     1082
Val Thr Pro Gly Leu Gly Val Val Ala Val Leu Leu Leu Phe Leu Val
222                 227                 232                 237

gtg cgg gag ccg cca agg gga gcc gtg gag cgc cac tca gat ttg cca     1130
Val Arg Glu Pro Pro Arg Gly Ala Val Glu Arg His Ser Asp Leu Pro
238                 243                 248                 253

ccc ctg aac ccc acc tcg tgg tgg gca gat ctg agg gct ctg gca aga     1178
Pro Leu Asn Pro Thr Ser Trp Trp Ala Asp Leu Arg Ala Leu Ala Arg
254                 259                 264                 269

aat cct agt ttc gtc ctg tct tcc ctg ggc ttc act gct gtg gcc ttt     1226
Asn Pro Ser Phe Val Leu Ser Ser Leu Gly Phe Thr Ala Val Ala Phe
270                 275                 280                 285

gtc acg ggc tcc ctg gct ctg tgg gct ccg gca ttc ctg ctg cgt tcc     1274
Val Thr Gly Ser Leu Ala Leu Trp Ala Pro Ala Phe Leu Leu Arg Ser
286                 291                 296                 301

cgc gtg gtc ctt ggg gag acc cca ccc tgc ctt ccc gga gac tcc tgc     1322
Arg Val Val Leu Gly Glu Thr Pro Pro Cys Leu Pro Gly Asp Ser Cys
302                 307                 312                 317

tct tcc tct gac agt ctc atc ttt gga ctc atc acc tgc ctg acc gga     1370
Ser Ser Ser Asp Ser Leu Ile Phe Gly Leu Ile Thr Cys Leu Thr Gly
318                 323                 328                 333

gtc ctg ggt gtg ggc ctg ggt gtg gag atc agc cgc cgg ctc cgc cac     1418
Val Leu Gly Val Gly Leu Gly Val Glu Ile Ser Arg Arg Leu Arg His
334                 339                 344                 349

tcc aac ccc cgg gct gat ccc ctg gtc tgt gcc act ggc ctc ctg ggc     1466
Ser Asn Pro Arg Ala Asp Pro Leu Val Cys Ala Thr Gly Leu Leu Gly
350                 355                 360                 365

tct gca ccc ttc ctc ttc ctg tcc ctt gcc tgc gcc cgt ggt agc atc     1514
Ser Ala Pro Phe Leu Phe Leu Ser Leu Ala Cys Ala Arg Gly Ser Ile
366                 371                 376                 381

gtg gcc act tat att ttc atc ttc att gga gag acc ctc ctg tcc atg     1562
Val Ala Thr Tyr Ile Phe Ile Phe Ile Gly Glu Thr Leu Leu Ser Met
382                 387                 392                 397

aac tgg gcc atc gtg gcc gac att ctg ctg tac gtg gtg atc cct acc     1610
Asn Trp Ala Ile Val Ala Asp Ile Leu Leu Tyr Val Val Ile Pro Thr
398                 403                 408                 413

cga cgc tcc acc gcc gag gcc ttc cag atc gtg ctg tcc cac ctg ctg     1658
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Arg Arg Ser Thr Ala Glu Ala Phe Gln Ile Val Leu Ser His Leu Leu
414                 419                 424                 429

ggt gat gct ggg agc ccc tac ctc att ggc ctg atc tct gac cgc ctg     1706
Gly Asp Ala Gly Ser Pro Tyr Leu Ile Gly Leu Ile Ser Asp Arg Leu
430                 435                 440                 445

cgc cgg aac tgg ccc ccc tcc ttc ttg tcc gag ttc cgg gct ctg cag     1754
Arg Arg Asn Trp Pro Pro Ser Phe Leu Ser Glu Phe Arg Ala Leu Gln
446                 451                 456                 461

ttc tcg ctc atg ctc tgc gcg ttt gtt ggg gca ctg ggc ggc gca gcc     1802
Phe Ser Leu Met Leu Cys Ala Phe Val Gly Ala Leu Gly Gly Ala Ala
462                 467                 472                 477

ttc ctg ggc acc gcc atc ttc att gag gcc gac cgc cgg cgg gca cag     1850
Phe Leu Gly Thr Ala Ile Phe Ile Glu Ala Asp Arg Arg Arg Ala Gln
478                 483                 488                 493

ctg cac gtg cag ggc ctg ctg cac gaa gca ggg tcc aca gac gac cgg     1898
Leu His Val Gln Gly Leu Leu His Glu Ala Gly Ser Thr Asp Asp Arg
494                 499                 504                 509

att gtg gtg ccc cag cgg ggc cgc tcc acc cgc gtg ccc gtg gcc agt     1946
Ile Val Val Pro Gln Arg Gly Arg Ser Thr Arg Val Pro Val Ala Ser
510                 515                 520                 525

gtg ctc atc tga gag gctgccgctc acctacctgc acatctgcca cagctggccc     2001
Val Leu Ile  *
526

tgggcccacc ccacgaaggg cctgggccta acccccttggc ctggcccagc ttccagaggg   2061

accctgggcc gtgtgccagc tcccagacac tacatgggta gctcagggga ggaggtgggg   2121

gtccaggagg gggatccctc tccacagggg cagccccaag ggctcggtgc tatttgtaac   2181

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gcgcccacag ggagccagga gcctgtgcgc aggccc  atg cgc aag tcc ttc tcc     234
                                         Met Arg Lys Ser Phe Ser
                                           1

cag ccc ggc ctg cgc tcg ctg gcc ttt agg aag gag ctg cag gat ggg     282
Gln Pro Gly Leu Arg Ser Leu Ala Phe Arg Lys Glu Leu Gln Asp Gly
  7                  12                  17                  22

ggc ctc cga agc agc ggc ttc ttc agc tcc ttc gag gag agc gac att     330
Gly Leu Arg Ser Ser Gly Phe Phe Ser Ser Phe Glu Glu Ser Asp Ile
 23                  28                  33                  38

gag aac cac ctc att agc gga cac aat att gtg cag ccc aca gat atc     378
Glu Asn His Leu Ile Ser Gly His Asn Ile Val Gln Pro Thr Asp Ile
 39                  44                  49                  54

gag gaa aat cga act atg ctc ttc acg att ggc cag tct gaa gtt tac     426
Glu Glu Asn Arg Thr Met Leu Phe Thr Ile Gly Gln Ser Glu Val Tyr
 55                  60                  65                  70

ctc atc agt cct gac acc aaa aaa ata gca ttg gag aaa aat ttt aag     474
Leu Ile Ser Pro Asp Thr Lys Lys Ile Ala Leu Glu Lys Asn Phe Lys
 71                  76                  81                  86

gag ata tcc ttt tgc tct cag ggc atc aga cac gtg gac cac ttt ggg     522
Glu Ile Ser Phe Cys Ser Gln Gly Ile Arg His Val Asp His Phe Gly
 87                  92                  97                 102

ttt atc tgt cgg gag tct tcc gga ggt ggc ggc ttt cat ttt gtc tgt     570
Phe Ile Cys Arg Glu Ser Ser Gly Gly Gly Gly Phe His Phe Val Cys
103                 108                 113                 118

tac gtg ttt cag tgc aca aat gag gct ctg gtt gat gaa att atg atg     618
Tyr Val Phe Gln Cys Thr Asn Glu Ala Leu Val Asp Glu Ile Met Met
119                 124                 129                 134

acc ctg aaa cag gcc ttc acg gtg gcc gca gtg cag cag aca gct aag     666
Thr Leu Lys Gln Ala Phe Thr Val Ala Ala Val Gln Gln Thr Ala Lys
135                 140                 145                 150

gcg cca gcc cag ctg tgt gag ggc tgc ccc ctg caa agc ctg cac aag     714
Ala Pro Ala Gln Leu Cys Glu Gly Cys Pro Leu Gln Ser Leu His Lys
151                 156                 161                 166

ctc tgt gag agg ata gag gga atg aat tct tcc aaa aca aaa cta gaa     762
Leu Cys Glu Arg Ile Glu Gly Met Asn Ser Ser Lys Thr Lys Leu Glu
167                 172                 177                 182

ctg caa aag cac ctg acg aca tta acc aat cag gag cag gcg act att     810
Leu Gln Lys His Leu Thr Thr Leu Thr Asn Gln Glu Gln Ala Thr Ile
183                 188                 193                 198

ttt gaa gag gtt cag aaa ttg aga ccg aga aat gag cag cga gag aat     858
Phe Glu Glu Val Gln Lys Leu Arg Pro Arg Asn Glu Gln Arg Glu Asn
199                 204                 209                 214
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gaa ttg att att tct ttt ctg aga tgt tta tat gaa gag aaa cag aaa      906
Glu Leu Ile Ile Ser Phe Leu Arg Cys Leu Tyr Glu Glu Lys Gln Lys
215                 220                 225                 230

gaa cac atc cat att ggg gag atg aag cag aca tcg cag atg gca gca      954
Glu His Ile His Ile Gly Glu Met Lys Gln Thr Ser Gln Met Ala Ala
231                 236                 241                 246

gag aat att gga agt gaa tta cca ccc agt gcc act cga ttt agg cta     1002
Glu Asn Ile Gly Ser Glu Leu Pro Pro Ser Ala Thr Arg Phe Arg Leu
247                 252                 257                 262

gat atg ctg aaa aac aaa gca aag aga tct tta aca gag tct tta gaa     1050
Asp Met Leu Lys Asn Lys Ala Lys Arg Ser Leu Thr Glu Ser Leu Glu
263                 268                 273                 278

agt att ttg tcc cgg ggt aat aaa gcc aga ggc ctg cag gaa cac tcc     1098
Ser Ile Leu Ser Arg Gly Asn Lys Ala Arg Gly Leu Gln Glu His Ser
279                 284                 289                 294

atc agt gtg gat ctg gat agc tcc ctg tct agt aca tta agt aac acc     1146
Ile Ser Val Asp Leu Asp Ser Ser Leu Ser Ser Thr Leu Ser Asn Thr
295                 300                 305                 310

agc aaa gag cca tct gtg tgt gaa aag gag gcc ttg ccc atc tct gag     1194
Ser Lys Glu Pro Ser Val Cys Glu Lys Glu Ala Leu Pro Ile Ser Glu
311                 316                 321                 326

agc tcc ttt aag ctc ctc ggc tcc tcg gag gac ctg tcc agt gac tcg     1242
Ser Ser Phe Lys Leu Leu Gly Ser Ser Glu Asp Leu Ser Ser Asp Ser
327                 332                 337                 342

gag agt cat ctc cca gaa gag cca gct ccg ctg tcg ccc cag cag gcc     1290
Glu Ser His Leu Pro Glu Glu Pro Ala Pro Leu Ser Pro Gln Gln Ala
343                 348                 353                 358

ttc agg agg cga gca aac acc ctg agt cac ttc ccc atc gaa tgc cag     1338
Phe Arg Arg Arg Ala Asn Thr Leu Ser His Phe Pro Ile Glu Cys Gln
359                 364                 369                 374

gaa cct cca caa cct gcc cgg ggg tcc ccg ggg gtt tcg caa agg aaa     1386
Glu Pro Pro Gln Pro Ala Arg Gly Ser Pro Gly Val Ser Gln Arg Lys
375                 380                 385                 390

ctt atg agg tat cac tca gtg agc aca gag acg cct cat gaa cga aag     1434
Leu Met Arg Tyr His Ser Val Ser Thr Glu Thr Pro His Glu Arg Lys
391                 396                 401                 406

gac ttt gaa tcc aaa gca aac cat ctt ggt gat tct ggt ggg act cct     1482
Asp Phe Glu Ser Lys Ala Asn His Leu Gly Asp Ser Gly Gly Thr Pro
407                 412                 417                 422

gtg aag acc cgg agg cat tcc tgg agg cag cag ata ttc ctc cga gta     1530
Val Lys Thr Arg Arg His Ser Trp Arg Gln Gln Ile Phe Leu Arg Val
423                 428                 433                 438

gcc acc ccg cag aag gcg tgc gat tct tcc agc aga tat gaa gat tat     1578
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Ala Thr Pro Gln Lys Ala Cys Asp Ser Ser Ser Arg Tyr Glu Asp Tyr
439                 444                 449                 454

tca gag ctg gga gag ctt ccc cca cga tct cct tta gaa cca gtt tgt     1626
Ser Glu Leu Gly Glu Leu Pro Pro Arg Ser Pro Leu Glu Pro Val Cys
455                 460                 465                 470

gaa gat ggg ccc ttt ggc ccc cca cca gag gaa aag aaa agg aca tct     1674
Glu Asp Gly Pro Phe Gly Pro Pro Pro Glu Glu Lys Lys Arg Thr Ser
471                 476                 481                 486

cgt gag ctc cga gag ctg tgg caa aag gct att ctt caa cag ata ctg     1722
Arg Glu Leu Arg Glu Leu Trp Gln Lys Ala Ile Leu Gln Gln Ile Leu
487                 492                 497                 502

ctg ctt aga atg gag aag gaa aat cag aag ctc caa gcc tct gaa aat     1770
Leu Leu Arg Met Glu Lys Glu Asn Gln Lys Leu Gln Ala Ser Glu Asn
503                 508                 513                 518

gat ttg ctg aac aag cgc ctg aag ctc gat tat gaa gaa att act ccc     1818
Asp Leu Leu Asn Lys Arg Leu Lys Leu Asp Tyr Glu Glu Ile Thr Pro
519                 524                 529                 534

tgt ctt aaa gaa gta act aca gtg tgg gaa aag atg ctt agc act cca     1866
Cys Leu Lys Glu Val Thr Thr Val Trp Glu Lys Met Leu Ser Thr Pro
535                 540                 545                 550

gga aga tca aaa att aag ttt gac atg gaa aaa atg cac tcg gct gtt     1914
Gly Arg Ser Lys Ile Lys Phe Asp Met Glu Lys Met His Ser Ala Val
551                 556                 561                 566

ggg caa ggt gtg cca cgt cat cac cga ggt gaa atc tgg aaa ttt cta     1962
Gly Gln Gly Val Pro Arg His His Arg Gly Glu Ile Trp Lys Phe Leu
567                 572                 577                 582

gct gag caa ttc cac ctt aaa cac cag ttt ccc agc aaa cag cag cca     2010
Ala Glu Gln Phe His Leu Lys His Gln Phe Pro Ser Lys Gln Gln Pro
583                 588                 593                 598

aag gat gtg cca tac aaa gaa ctc tta aag cag ctg act tcc cag cag     2058
Lys Asp Val Pro Tyr Lys Glu Leu Leu Lys Gln Leu Thr Ser Gln Gln
599                 604                 609                 614

cat gcg att ctt att gac ctt ggg cga acc ttt cct aca cac cca tac     2106
His Ala Ile Leu Ile Asp Leu Gly Arg Thr Phe Pro Thr His Pro Tyr
615                 620                 625                 630

ttc tct gcc cag ctt gga gca gga cag cta tcg ctt tac aac att ttg     2154
Phe Ser Ala Gln Leu Gly Ala Gly Gln Leu Ser Leu Tyr Asn Ile Leu
631                 636                 641                 646

aag gcc tac tca ctt cta gac cag gaa gtg gga tat tgc caa ggt ctc     2202
Lys Ala Tyr Ser Leu Leu Asp Gln Glu Val Gly Tyr Cys Gln Gly Leu
647                 652                 657                 662

agc ttt gta gca ggc att ttg ctt ctt cat atg agt gag gaa gag gcg     2250
Ser Phe Val Ala Gly Ile Leu Leu Leu His Met Ser Glu Glu Glu Ala
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663                 668                 673                 678

ttt aaa atg ctc aag ttt ctg atg ttt gac atg ggg ctg cgg aaa cag     2298
Phe Lys Met Leu Lys Phe Leu Met Phe Asp Met Gly Leu Arg Lys Gln
679                 684                 689                 694

tat cgg cca gac atg att att tta cag atc cag atg tac cag ctc tcg     2346
Tyr Arg Pro Asp Met Ile Ile Leu Gln Ile Gln Met Tyr Gln Leu Ser
695                 700                 705                 710

agg ttg ctt cat gat tac cac aga gac ctc tac aat cac ctg gag gag     2394
Arg Leu Leu His Asp Tyr His Arg Asp Leu Tyr Asn His Leu Glu Glu
711                 716                 721                 726

cac gag atc ggc ccc agc ctc tac gct gcc ccc tgg ttc ctc acc atg     2442
His Glu Ile Gly Pro Ser Leu Tyr Ala Ala Pro Trp Phe Leu Thr Met
727                 732                 737                 742

ttt gcc tca cag ttc ccg ctg gga ttc gta gcc aga gtc ttt gat atg     2490
Phe Ala Ser Gln Phe Pro Leu Gly Phe Val Ala Arg Val Phe Asp Met
743                 748                 753                 758

att ttt ctt cag gga aca gag gtc ata ttt aaa gtg gct tta agt ctg     2538
Ile Phe Leu Gln Gly Thr Glu Val Ile Phe Lys Val Ala Leu Ser Leu
759                 764                 769                 774

ttg gga agc cat aag ccc ttg att ctg cag cat gaa aac cta gaa acc     2586
Leu Gly Ser His Lys Pro Leu Ile Leu Gln His Glu Asn Leu Glu Thr
775                 780                 785                 790

ata gtt gac ttt ata aaa agc acg cta ccc aac ctt ggc ttg gta cag     2634
Ile Val Asp Phe Ile Lys Ser Thr Leu Pro Asn Leu Gly Leu Val Gln
791                 796                 801                 806

atg gaa aag acc atc aat cag gta ttt gaa atg gac atc gct aaa cag     2682
Met Glu Lys Thr Ile Asn Gln Val Phe Glu Met Asp Ile Ala Lys Gln
807                 812                 817                 822

tta caa gct tat gaa gtt gag tac cac gtc ctt caa gaa gaa ctt atc     2730
Leu Gln Ala Tyr Glu Val Glu Tyr His Val Leu Gln Glu Glu Leu Ile
823                 828                 833                 838

gat tcc tct cct ctc agt gac aac caa aga atg gat aaa tta gag aaa     2778
Asp Ser Ser Pro Leu Ser Asp Asn Gln Arg Met Asp Lys Leu Glu Lys
839                 844                 849                 854

acc aac agc agc tta cgc aaa cag aac ctt gac ctc ctt gaa cag ttg     2826
Thr Asn Ser Ser Leu Arg Lys Gln Asn Leu Asp Leu Leu Glu Gln Leu
855                 860                 865                 870

cag gtg gca aat ggt agg atc caa agc ctt gag gcc acc att gag aag     2874
Gln Val Ala Asn Gly Arg Ile Gln Ser Leu Glu Ala Thr Ile Glu Lys
871                 876                 881                 886

ctc ctg agc agt gag agc aag ctg aag cag gcc atg ctt acc tta gaa     2922
Leu Leu Ser Ser Glu Ser Lys Leu Lys Gln Ala Met Leu Thr Leu Glu
887                 892                 897                 902
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ctg gag cgg tcg gcc ctg ctg cag acg gtg gag gag ctg cgg cgg cgg     2970
Leu Glu Arg Ser Ala Leu Leu Gln Thr Val Glu Glu Leu Arg Arg Arg
903                 908                 913                 918

agc gca gag ccc agc gac cgg gag cct gag tgc acg cag ccc gag ccc     3018
Ser Ala Glu Pro Ser Asp Arg Glu Pro Glu Cys Thr Gln Pro Glu Pro
919                 924                 929                 934

acg ggc gac tga cag ctctgcagga gagattgcaa caccatccca cactgtccag     3073
Thr Gly Asp  *
935

gccttaactg agagggacag aagacgctgg aaggagagaa ggaagcggga agtgtgcttc   3133

tcagggagga aaccggcttg ccagcaagta gattcttacg aactccaact tgcaattcag   3193

ggggcatgtc ccagtgtttt ttttgttgtt tttagatact aaatcgtccc ttctccagtc   3253

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gcaaagcggg agtgaagaac acacattttc agaagatacc ggtttcctgt tttcattaag    120

aaaacaggga atgcggaaca gctgagtgcg gcgggggtgg tgtcactgca gccggaggga    180

gacctcgccg gtgaaagctc agcctatggc atccgagcgt ggccggccaa gtttacacga    240

atgttgaaac ttctcctcac ggggtgagga tcgagggcgc ccgaggccgg gtccggctga    300

gctggagcga gctgtgcggg gcagcgcggg ctggcgggga gcgcggcggg cgccacgtgg    360

aaaagcaggt gatattctca gtggagacca ggacaaggaa cagaaagacc cttactttgt    420

ggagaccccc tatggttatc aactagactt agatttcctc aaatatgtgg atgacataca    480

gaagggaaat accatcaaaa gactgaacat ccagaagagg cggaagccgt ccgtgccatg    540

cccagaaccc aggaccacat ctggtcagca aggtatatgg acttccactg aatccctctc    600

atcctccaac agtgatgaca acaagcagtg ccccaacttc ctcatagcca gaagtcaagt    660
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tacatcaact ccaatctcaa agccacctcc ccctctggag acctcactcc cttttcttac    720

catcccagaa aatcgacagc tgccacctcc ctcaccacaa ctcccaaagc ataaccttca    780

tgtcaccaag acactg    atg gag acc cgg aga aga ctg gaa cag gag aga     829
                     Met Glu Thr Arg Arg Arg Leu Glu Gln Glu Arg
                       1               5

gcc acc atg cag atg aca ccg ggt gag ttc aga agg ccc agg ctg gcc     877
Ala Thr Met Gln Met Thr Pro Gly Glu Phe Arg Arg Pro Arg Leu Ala
 12                  17                  22                  27

agt ttt gga ggc atg ggc acc aca agc tcc ctc cct tct ttt gtg ggt     925
Ser Phe Gly Gly Met Gly Thr Thr Ser Ser Leu Pro Ser Phe Val Gly
 28                  33                  38                  43

tct gga aac cac aat cct gcc aag cac cag ctt cag aat gga tac caa     973
Ser Gly Asn His Asn Pro Ala Lys His Gln Leu Gln Asn Gly Tyr Gln
 44                  49                  54                  59

ggt aat ggg gat tat ggt agc tat gcc cca gct gct ccc acc act tcc    1021
Gly Asn Gly Asp Tyr Gly Ser Tyr Ala Pro Ala Ala Pro Thr Thr Ser
 60                  65                  70                  75

tcc atg ggg agc tcc atc cgc cac agc ccc ctg agc tca ggg atc tcc    1069
Ser Met Gly Ser Ser Ile Arg His Ser Pro Leu Ser Ser Gly Ile Ser
 76                  81                  86                  91

acc cca gtg acc aac gtg agc ccc atg cac ctg cag cac atc cgc gag    1117
Thr Pro Val Thr Asn Val Ser Pro Met His Leu Gln His Ile Arg Glu
 92                  97                 102                 107

cag atg gcc att gct ctg aaa cgc ctg aag gag ctg gag gag cag gtg    1165
Gln Met Ala Ile Ala Leu Lys Arg Leu Lys Glu Leu Glu Glu Gln Val
108                 113                 118                 123

cga acc atc cct gtg ctc cag gta aag atc tct gtc ttg caa gaa gag    1213
Arg Thr Ile Pro Val Leu Gln Val Lys Ile Ser Val Leu Gln Glu Glu
124                 129                 134                 139

aaa agg cag ttg gtc tca cag ctg aaa aac caa agg gct gca tcc cag    1261
Lys Arg Gln Leu Val Ser Gln Leu Lys Asn Gln Arg Ala Ala Ser Gln
140                 145                 150                 155

atc aat gtc tgt ggt gtg agg aag cgg tcc tat agt gcg ggg aac gcc    1309
Ile Asn Val Cys Gly Val Arg Lys Arg Ser Tyr Ser Ala Gly Asn Ala
156                 161                 166                 171

tcc cag ctg gaa cag ctc tcc cgg gcc cga aga agt ggc ggg gaa tta    1357
Ser Gln Leu Glu Gln Leu Ser Arg Ala Arg Arg Ser Gly Gly Glu Leu
172                 177                 182                 187

tac att gac tat gag gag gaa gaa atg gag acc gta gaa cag agc acg    1405
Tyr Ile Asp Tyr Glu Glu Glu Glu Met Glu Thr Val Glu Gln Ser Thr
188                 193                 198                 203
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cag agg ata aag gag ttc cgg caa ctt aca gca gac atg caa gcc ctg     1453
Gln Arg Ile Lys Glu Phe Arg Gln Leu Thr Ala Asp Met Gln Ala Leu
204                 209                 214                 219

gag cag aag atc cag gac agc agc tgt gag gcc tcc tca gag ctc agg     1501
Glu Gln Lys Ile Gln Asp Ser Ser Cys Glu Ala Ser Ser Glu Leu Arg
220                 225                 230                 235

gag aat gga gag tgc cgg tct gtg gct gtg ggt gcc gag gag aac atg     1549
Glu Asn Gly Glu Cys Arg Ser Val Ala Val Gly Ala Glu Glu Asn Met
236                 241                 246                 251

aac gac atc gtc gtg tac cac aga ggc tcc agg tcc tgt aag gat gca     1597
Asn Asp Ile Val Val Tyr His Arg Gly Ser Arg Ser Cys Lys Asp Ala
252                 257                 262                 267

gct gta ggg aca ctt gtt gag atg aga aat tgt ggg gtc agc gtg aca     1645
Ala Val Gly Thr Leu Val Glu Met Arg Asn Cys Gly Val Ser Val Thr
268                 273                 278                 283

gag gcc atg ctt gga gtg atg act gaa gct gac aaa gaa att gag ctc     1693
Glu Ala Met Leu Gly Val Met Thr Glu Ala Asp Lys Glu Ile Glu Leu
284                 289                 294                 299

caa cag cag acc ata gaa tcc ttg aag gaa aag atc tat cgc cta gaa     1741
Gln Gln Gln Thr Ile Glu Ser Leu Lys Glu Lys Ile Tyr Arg Leu Glu
300                 305                 310                 315

gta cag ctt aga gaa acc acc cat gac cgg gag atg act aaa ctg aaa     1789
Val Gln Leu Arg Glu Thr Thr His Asp Arg Glu Met Thr Lys Leu Lys
316                 321                 326                 331

caa gag ctg cag gct gct gga tcg agg aaa aag gtt gac aaa gcc acg     1837
Gln Glu Leu Gln Ala Ala Gly Ser Arg Lys Lys Val Asp Lys Ala Thr
332                 337                 342                 347

atg gcc cag ccg ctt gtt ttc agt aag gtg gtg gag gca gtg gtg cag     1885
Met Ala Gln Pro Leu Val Phe Ser Lys Val Val Glu Ala Val Val Gln
348                 353                 358                 363

acc aga gac caa atg gtc ggc agt cac atg gac ctg gtg gac acg tgt     1933
Thr Arg Asp Gln Met Val Gly Ser His Met Asp Leu Val Asp Thr Cys
364                 369                 374                 379

gtt ggg acc tcc gtg gaa aca aac agt gta ggc atc tcc tgc cag cct     1981
Val Gly Thr Ser Val Glu Thr Asn Ser Val Gly Ile Ser Cys Gln Pro
380                 385                 390                 395

gaa tgt aag aat aaa gtc gta ggg cct gag ctg cct atg aat tgg tgg     2029
Glu Cys Lys Asn Lys Val Val Gly Pro Glu Leu Pro Met Asn Trp Trp
396                 401                 406                 411

att gtt aag gag agg gtg gaa atg cat gac cga tgt gct ggg agg tct     2077
Ile Val Lys Glu Arg Val Glu Met His Asp Arg Cys Ala Gly Arg Ser
412                 417                 422                 427

gtg gaa atg tgt gac aag agt gtg agt gtg gaa gtc agc gtc tgc gaa     2125
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Val Glu Met Cys Asp Lys Ser Val Ser Val Glu Val Ser Val Cys Glu
428                 433                 438                 443

aca ggc agc aac aca gag gag tct gtg aac gac ctc aca ctc ctc aag     2173
Thr Gly Ser Asn Thr Glu Glu Ser Val Asn Asp Leu Thr Leu Leu Lys
444                 449                 454                 459

aca aac ttg aat ctc aaa gaa gtg cgg tct atc ggt tgt gga gat tgt     2221
Thr Asn Leu Asn Leu Lys Glu Val Arg Ser Ile Gly Cys Gly Asp Cys
460                 465                 470                 475

tct gtt gac gtg acc gtc tgc tct cca aag gag tgc gcc tcc cgg ggc     2269
Ser Val Asp Val Thr Val Cys Ser Pro Lys Glu Cys Ala Ser Arg Gly
476                 481                 486                 491

gtg aac act gag gct gtt agc cag gtg gaa gct gcc gtc atg gca gtg     2317
Val Asn Thr Glu Ala Val Ser Gln Val Glu Ala Ala Val Met Ala Val
492                 497                 502                 507

cct cgt act gca gac cag gac act agc aca gat ttg gaa cag gtg cac     2365
Pro Arg Thr Ala Asp Gln Asp Thr Ser Thr Asp Leu Glu Gln Val His
508                 513                 518                 523

cag ttc acc aac acc gag acg gcc acc ctc ata gag tcc tgc acc aac     2413
Gln Phe Thr Asn Thr Glu Thr Ala Thr Leu Ile Glu Ser Cys Thr Asn
524                 529                 534                 539

act tgt cta agc act ttg gac aag cag acc agc acc cag act gtg gag     2461
Thr Cys Leu Ser Thr Leu Asp Lys Gln Thr Ser Thr Gln Thr Val Glu
540                 545                 550                 555

acg cgg aca gta gct gta gga gaa ggc cgt gtc aag gac atc aac tcc     2509
Thr Arg Thr Val Ala Val Gly Glu Gly Arg Val Lys Asp Ile Asn Ser
556                 561                 566                 571

tcc acc aag acg cgg tcc att ggt gtt gga acg ttg ctt tct ggc cat     2557
Ser Thr Lys Thr Arg Ser Ile Gly Val Gly Thr Leu Leu Ser Gly His
572                 577                 582                 587

tct ggg ttt gac agg cca tca gct gtg aag acc aaa gag tca ggt gtg     2605
Ser Gly Phe Asp Arg Pro Ser Ala Val Lys Thr Lys Glu Ser Gly Val
588                 593                 598                 603

ggg cag ata aat att aac gac aac tat ctg gtt ggt ctc aaa atg agg     2653
Gly Gln Ile Asn Ile Asn Asp Asn Tyr Leu Val Gly Leu Lys Met Arg
604                 609                 614                 619

act ata gct tgt ggg cca cca cag ttg act gtg ggg ctg aca gcc agc     2701
Thr Ile Ala Cys Gly Pro Pro Gln Leu Thr Val Gly Leu Thr Ala Ser
620                 625                 630                 635

aga agg agc gtg ggg gtt ggg gat gac cct gta ggg gaa tct ctg gag     2749
Arg Arg Ser Val Gly Val Gly Asp Asp Pro Val Gly Glu Ser Leu Glu
636                 641                 646                 651

aac ccc cag cct caa gct cca ctt gga atg atg act ggc ctg gat cac     2797
Asn Pro Gln Pro Gln Ala Pro Leu Gly Met Met Thr Gly Leu Asp His
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652                 657                 662                 667

tac att gag cgt atc cag aag ctg ctg gca gaa cag cag aca ctg ctg     2845
Tyr Ile Glu Arg Ile Gln Lys Leu Leu Ala Glu Gln Gln Thr Leu Leu
668                 673                 678                 683

gct gag aac tac agt gaa ctg gca gaa gct ttc ggg gaa cct cac tca     2893
Ala Glu Asn Tyr Ser Glu Leu Ala Glu Ala Phe Gly Glu Pro His Ser
684                 689                 694                 699

cag atg ggc tcc ctc aac tct cag ctc atc agc acc ctg tcg tct atc     2941
Gln Met Gly Ser Leu Asn Ser Gln Leu Ile Ser Thr Leu Ser Ser Ile
700                 705                 710                 715

aac tct gtc atg aaa tct gca agc act gaa gag ctg agg aac cct gac     2989
Asn Ser Val Met Lys Ser Ala Ser Thr Glu Glu Leu Arg Asn Pro Asp
716                 721                 726                 731

ttc cag aaa acc agt ctg ggt aaa atc aca ggc aat tat ttg gga tat     3037
Phe Gln Lys Thr Ser Leu Gly Lys Ile Thr Gly Asn Tyr Leu Gly Tyr
732                 737                 742                 747

acc tgt aag tgt ggg ggc ctt cag tca gga agt ccc tta agc tcc cag     3085
Thr Cys Lys Cys Gly Gly Leu Gln Ser Gly Ser Pro Leu Ser Ser Gln
748                 753                 758                 763

aca tcc cag cct gag caa gaa gtg ggg acc tca gaa gga aag cca atc     3133
Thr Ser Gln Pro Glu Gln Glu Val Gly Thr Ser Glu Gly Lys Pro Ile
764                 769                 774                 779

agc agc ctg gat gcc ttc ccc act cag gaa ggt acg ctg tct cca gtg     3181
Ser Ser Leu Asp Ala Phe Pro Thr Gln Glu Gly Thr Leu Ser Pro Val
780                 785                 790                 795

aac ctg aca gac gac cag atc gcc gct ggc ctc tat gca tgt aca aac     3229
Asn Leu Thr Asp Asp Gln Ile Ala Ala Gly Leu Tyr Ala Cys Thr Asn
796                 801                 806                 811

aat gaa agt aca ctg aag tcc atc atg aag aag aaa gat ggt aac aaa     3277
Asn Glu Ser Thr Leu Lys Ser Ile Met Lys Lys Lys Asp Gly Asn Lys
812                 817                 822                 827

gat tca aat ggc gca aaa aag aat ctt cag ttt gtt ggc att aat gga     3325
Asp Ser Asn Gly Ala Lys Lys Asn Leu Gln Phe Val Gly Ile Asn Gly
828                 833                 838                 843

ggg tat gaa aca act tca agt gat gat tcc agc tca gat gaa agc tct     3373
Gly Tyr Glu Thr Thr Ser Ser Asp Asp Ser Ser Ser Asp Glu Ser Ser
844                 849                 854                 859

tct tcc gag tca gat gac gag tgt gat gtc att gag tat cct ctt gaa     3421
Ser Ser Glu Ser Asp Asp Glu Cys Asp Val Ile Glu Tyr Pro Leu Glu
860                 865                 870                 875

gaa gag gag gag gag gag gat gaa gac act cgg gga atg gca gaa ggg     3469
Glu Glu Glu Glu Glu Glu Asp Glu Asp Thr Arg Gly Met Ala Glu Gly
876                 881                 886                 891
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cac cat gca gtt aat att gaa ggt ttg aag tct gcc agg gtg gaa gat     3517
His His Ala Val Asn Ile Glu Gly Leu Lys Ser Ala Arg Val Glu Asp
892                 897                 902                 907

gaa atg cag gtt caa gaa tgt gaa cct gag aag gtg gaa atc aga gag     3565
Glu Met Gln Val Gln Glu Cys Glu Pro Glu Lys Val Glu Ile Arg Glu
908                 913                 918                 923

agg tat gaa tta agt gaa aag atg ttg tct gca tgc aac tta ctg aaa     3613
Arg Tyr Glu Leu Ser Glu Lys Met Leu Ser Ala Cys Asn Leu Leu Lys
924                 929                 934                 939

aat act ata aat gac ccc aaa gct ttg acc agc aaa gat atg agg ttc     3661
Asn Thr Ile Asn Asp Pro Lys Ala Leu Thr Ser Lys Asp Met Arg Phe
940                 945                 950                 955

tgt ctg aac acc ctc cag cac gag tgg ttc cgc gtg tcc agt cag aag     3709
Cys Leu Asn Thr Leu Gln His Glu Trp Phe Arg Val Ser Ser Gln Lys
956                 961                 966                 971

tca gcc att cca gcc atg gtg ggg gac tac ata gct gct ttt gag gcc     3757
Ser Ala Ile Pro Ala Met Val Gly Asp Tyr Ile Ala Ala Phe Glu Ala
972                 977                 982                 987

att tcc cca gat gtc ctc cgc tat gtc atc aac ttg gca gac ggc aac     3805
Ile Ser Pro Asp Val Leu Arg Tyr Val Ile Asn Leu Ala Asp Gly Asn
988                 993                 998                1003

ggc aac aca gcc ctc cat tac agc gtg tcc cac tcc aac ttc gag att     3853
Gly Asn Thr Ala Leu His Tyr Ser Val Ser His Ser Asn Phe Glu Ile
1004                1009                1014                1019

gtg aag ctg ctg tta gat gcc gat gtg tgt aat gtg gat cac cag aac     3901
Val Lys Leu Leu Leu Asp Ala Asp Val Cys Asn Val Asp His Gln Asn
1020                1025                1030                1035

aag gca ggc tac acc ccc atc atg ttg gcg gcc ctc gcc gct gtg gaa     3949
Lys Ala Gly Tyr Thr Pro Ile Met Leu Ala Ala Leu Ala Ala Val Glu
1036                1041                1046                1051

gca gag aag gac atg cgg att gtg gaa gaa ctc ttc ggc tgt ggg gat     3997
Ala Glu Lys Asp Met Arg Ile Val Glu Glu Leu Phe Gly Cys Gly Asp
1052                1057                1062                1067

gtg aat gcc aaa gct agt cag gcg gga cag acg gcc ctc atg ctg gcg     4045
Val Asn Ala Lys Ala Ser Gln Ala Gly Gln Thr Ala Leu Met Leu Ala
1068                1073                1078                1083

gtc agt cac gga cgg ata gac atg gtg aag ggc ctt ctg gcc tgt ggg     4093
Val Ser His Gly Arg Ile Asp Met Val Lys Gly Leu Leu Ala Cys Gly
1084                1089                1094                1099

gct gat gtc aac atc cag gat gac gag ggc tcc acg gcc ctc atg tgt     4141
Ala Asp Val Asn Ile Gln Asp Asp Glu Gly Ser Thr Ala Leu Met Cys
1100                1105                1110                1115
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 gcc agc gag cac ggg cac gtg gag att gtc aag ctg ctg ctg gcc cag     4189
 Ala Ser Glu His Gly His Val Glu Ile Val Lys Leu Leu Leu Ala Gln
1116                1121                1126                1131

 ccc ggc tgc aac ggt cac cta gag gac aac gat ggc agc act gcg ctc     4237
 Pro Gly Cys Asn Gly His Leu Glu Asp Asn Asp Gly Ser Thr Ala Leu
1132                1137                1142                1147

 tca atc gcc ctg gaa gca gga cac aag gac atc gct gtt ctt ctg tat     4285
 Ser Ile Ala Leu Glu Ala Gly His Lys Asp Ile Ala Val Leu Leu Tyr
1148                1153                1158                1163

 gcc cat gtc aac ttt gca aaa gcc cag tct ccg ggc acc cct agg ctt     4333
 Ala His Val Asn Phe Ala Lys Ala Gln Ser Pro Gly Thr Pro Arg Leu
1164                1169                1174                1179

 gga agg aag acg tct cct ggc ccc acc cac cga ggt tca ttt gat tga     4381
 Gly Arg Lys Thr Ser Pro Gly Pro Thr His Arg Gly Ser Phe Asp  *
1180                1185                1190                1195

 ttgtatgcaa atagcccttt atttacatgc cactattaag ctgctaattg ttcctgttgg   4441

 ggtgacagat actgaatgta tacgtattgt gcctgagctc accagcaaac agaagcatca   4501

 agcccagggg taaaggctga agctttcaca gtgcagagac tgctagcctg ggcacacgca   4561

 cctcctttct ggccgtcttc tgtgtagggc acactttaac ccagtctctg ttgctgttga   4621

 gtctctgctc cgttttgtac agtcacaggg aattctgatc tgaaggggca ccttctgttc   4681

 actcccacaa agtggtgtct ggttctcact gagacgtttt aagatttttc cacaaatatt   4741

 tatatgtact aaatgtggaa ccattagaaa gttcttccaa aatctcattc cagcatagtt   4801

 ttggattttt cttttgtctt attttaaaat aaggaagtcg agatgacttt gatcattggt   4861

 aacttgggcc tgggccagac aaagtataaa acttacaaaa gaatattctc atttggtctt   4921

 aactaggtag atgtaatata tgacttttta taaaaagggt atctatatga acttgacaca   4981

 gtattttcag cttttgtatt ccatactaaa gccatgaaga actacacgta acatcatcat   5041

 ttgtattaat tgcacaactc caatgctaaa ggttggattg tgttagagga atcggctctg   5101

 tatttgcctc tagagaaaca cagtgttctc tttgtattta tggattcctt tttaccgtgt   5161

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aaaacaggga atgcggaaca gctgagtgcg gcgggggtgg tgtcactgca gccggaggga    180

gacctcgccg gtgaaagctc agcctatggc atccgagcgt ggccggccaa gtttacacga    240

atgttgaaac ttctcctcac ggggtgagga tcgagggcgc ccgaggccgg gtccggctga    300

gctggagcga gctgtgcggg gcagcgcggg ctggcgggga gcgcggcggg cgccacgtgg    360

aaaagcaggt gatattctca gtggagacca ggacaaggaa cagaaagacc cttactttgt    420

ggagaccccc tatggttatc aactagactt agatttcctc aaatatgtgg atgacataca    480

gaagggaaat accatcaaaa gactgaacat ccagaagagg cggaagccgt ccgtgccatg    540

cccagaaccc aggaccacat ctggtcagca aggtatatgg acttccactg aatccctctc    600

atcctccaac agtgatgaca acaagcagtg ccccaacttc ctcatagcca gaagtcaagt    660

tacatcaact ccaatctcaa agccacctcc ccctctggag acctcactcc cttttcttac    720

catcccagaa aatcgacagc tgccacctcc ctcaccacaa ctcccaaagc ataaccttca    780

tgtcaccaag acactg    atg gag acc cgg aga aga ctg gaa cag gag aga     829
                        Met Glu Thr Arg Arg Arg Leu Glu Gln Glu Arg
                          1               5

gcc acc atg cag atg aca ccg ggt gag ttc aga agg ccc agg ctg gcc     877
Ala Thr Met Gln Met Thr Pro Gly Glu Phe Arg Arg Pro Arg Leu Ala
 12                  17                  22                  27

agt ttt gga ggc atg ggc acc aca agc tcc ctc cct tct ttt gtg ggt     925
Ser Phe Gly Gly Met Gly Thr Thr Ser Ser Leu Pro Ser Phe Val Gly
 28                  33                  38                  43

tct gga aac cac aat cct gcc aag cac cag ctt cag aat gga tac caa     973
Ser Gly Asn His Asn Pro Ala Lys His Gln Leu Gln Asn Gly Tyr Gln
 44                  49                  54                  59

ggt aat ggg gat tat ggt agc tat gcc cca gct gct ccc acc act tcc    1021
Gly Asn Gly Asp Tyr Gly Ser Tyr Ala Pro Ala Ala Pro Thr Thr Ser
 60                  65                  70                  75

tcc atg ggg agc tcc atc cgc cac agc ccc ctg agc tca ggg atc tcc    1069
Ser Met Gly Ser Ser Ile Arg His Ser Pro Leu Ser Ser Gly Ile Ser
 76                  81                  86                  91

acc cca gtg acc aac gtg agc ccc atg cac ctg cag cac atc cgc gag    1117
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Thr Pro Val Thr Asn Val Ser Pro Met His Leu Gln His Ile Arg Glu
 92                  97                  102                 107

cag atg gcc att gct ctg aaa cgc ctg aag gag ctg gag gag cag gtg     1165
Gln Met Ala Ile Ala Leu Lys Arg Leu Lys Glu Leu Glu Glu Gln Val
108                 113                 118                 123

cga acc atc cct gtg ctc cag gta aag atc tct gtc ttg caa gaa gag     1213
Arg Thr Ile Pro Val Leu Gln Val Lys Ile Ser Val Leu Gln Glu Glu
124                 129                 134                 139

aaa agg cag ttg gtc tca cag ctg aaa aac caa agg gct gca tcc cag     1261
Lys Arg Gln Leu Val Ser Gln Leu Lys Asn Gln Arg Ala Ala Ser Gln
140                 145                 150                 155

atc aat gtc tgt ggt gtg agg aag cgg tcc tat agt gcg ggg aac gcc     1309
Ile Asn Val Cys Gly Val Arg Lys Arg Ser Tyr Ser Ala Gly Asn Ala
156                 161                 166                 171

tcc cag ctg gaa cag ctc tcc cgg gcc cga aga agt ggc ggg gaa tta     1357
Ser Gln Leu Glu Gln Leu Ser Arg Ala Arg Arg Ser Gly Gly Glu Leu
172                 177                 182                 187

tac att gac tat gag gag gaa gaa atg gag acc gta gaa cag agc acg     1405
Tyr Ile Asp Tyr Glu Glu Glu Glu Met Glu Thr Val Glu Gln Ser Thr
188                 193                 198                 203

cag agg ata aag gag ttc cgg caa ctt aca gca gac atg caa gcc ctg     1453
Gln Arg Ile Lys Glu Phe Arg Gln Leu Thr Ala Asp Met Gln Ala Leu
204                 209                 214                 219

gag cag aag atc cag gac agc agc tgt gag gcc tcc tca gag ctc agg     1501
Glu Gln Lys Ile Gln Asp Ser Ser Cys Glu Ala Ser Ser Glu Leu Arg
220                 225                 230                 235

gag aat gga gag tgc cgg tct gtg gct gtg ggt gcc gag gag aac atg     1549
Glu Asn Gly Glu Cys Arg Ser Val Ala Val Gly Ala Glu Glu Asn Met
236                 241                 246                 251

aac gac atc gtc gtg tac cac aga ggc tcc agg tcc tgt aag gat gca     1597
Asn Asp Ile Val Val Tyr His Arg Gly Ser Arg Ser Cys Lys Asp Ala
252                 257                 262                 267

gct gta ggg aca ctt gtt gag atg aga aat tgt ggg gtc agc gtg aca     1645
Ala Val Gly Thr Leu Val Glu Met Arg Asn Cys Gly Val Ser Val Thr
268                 273                 278                 283

gag gcc atg ctt gga gtg atg act gaa gct gac aaa gaa att gag ctc     1693
Glu Ala Met Leu Gly Val Met Thr Glu Ala Asp Lys Glu Ile Glu Leu
284                 289                 294                 299

caa cag cag acc ata gaa tcc ttg aag gaa aag atc tat cgc cta gaa     1741
Gln Gln Gln Thr Ile Glu Ser Leu Lys Glu Lys Ile Tyr Arg Leu Glu
300                 305                 310                 315

gta cag ctt aga gaa acc acc cat gac cgg gag atg act aaa ctg aaa     1789
Val Gln Leu Arg Glu Thr Thr His Asp Arg Glu Met Thr Lys Leu Lys
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316                 321                 326                 331

caa gag ctg cag gct gct gga tcg agg aaa aag gtt gac aaa gcc acg     1837
Gln Glu Leu Gln Ala Ala Gly Ser Arg Lys Lys Val Asp Lys Ala Thr
332                 337                 342                 347

atg gcc cag ccg ctt gtt ttc agt aag gtg gtg gag gca gtg gtg cag     1885
Met Ala Gln Pro Leu Val Phe Ser Lys Val Val Glu Ala Val Val Gln
348                 353                 358                 363

acc aga gac caa atg gtc ggc agt cac atg gac ctg gtg gac acg tgt     1933
Thr Arg Asp Gln Met Val Gly Ser His Met Asp Leu Val Asp Thr Cys
364                 369                 374                 379

gtt ggg acc tcc gtg gaa aca aac agt gta ggc atc tcc tgc cag cct     1981
Val Gly Thr Ser Val Glu Thr Asn Ser Val Gly Ile Ser Cys Gln Pro
380                 385                 390                 395

gaa tgt aag aat aaa gtc gta ggg cct gag ctg cct atg aat tgg tgg     2029
Glu Cys Lys Asn Lys Val Val Gly Pro Glu Leu Pro Met Asn Trp Trp
396                 401                 406                 411

att gtt aag gag agg gtg gaa atg cat gac cga tgt gct ggg agg tct     2077
Ile Val Lys Glu Arg Val Glu Met His Asp Arg Cys Ala Gly Arg Ser
412                 417                 422                 427

gtg gaa atg tgt gac aag agt gtg agt gtg gaa gtc agc gtc tgc gaa     2125
Val Glu Met Cys Asp Lys Ser Val Ser Val Glu Val Ser Val Cys Glu
428                 433                 438                 443

aca ggc agc aac aca gag gag tct gtg aac gac ctc aca ctc ctc aag     2173
Thr Gly Ser Asn Thr Glu Glu Ser Val Asn Asp Leu Thr Leu Leu Lys
444                 449                 454                 459

aca aac ttg aat ctc aaa gaa gtg cgg tct atc ggt tgt gga gat tgt     2221
Thr Asn Leu Asn Leu Lys Glu Val Arg Ser Ile Gly Cys Gly Asp Cys
460                 465                 470                 475

tct gtt gac gtg acc gtc tgc tct cca aag gag tgc gcc tcc cgg ggc     2269
Ser Val Asp Val Thr Val Cys Ser Pro Lys Glu Cys Ala Ser Arg Gly
476                 481                 486                 491

gtg aac act gag gct gtt agc cag gtg gaa gct gcc gtc atg gca gtg     2317
Val Asn Thr Glu Ala Val Ser Gln Val Glu Ala Ala Val Met Ala Val
492                 497                 502                 507

cct cgt act gca gac cag gac act agc aca gat ttg gaa cag gtg cac     2365
Pro Arg Thr Ala Asp Gln Asp Thr Ser Thr Asp Leu Glu Gln Val His
508                 513                 518                 523

cag ttc acc aac acc gag acg gcc acc ctc ata gag tcc tgc acc aac     2413
Gln Phe Thr Asn Thr Glu Thr Ala Thr Leu Ile Glu Ser Cys Thr Asn
524                 529                 534                 539

act tgt cta agc act ttg gac aag cag acc agc acc cag act gtg gag     2461
Thr Cys Leu Ser Thr Leu Asp Lys Gln Thr Ser Thr Gln Thr Val Glu
540                 545                 550                 555
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acg cgg aca gta gct gta gga gaa ggc cgt gtc aag gac atc aac tcc     2509
Thr Arg Thr Val Ala Val Gly Glu Gly Arg Val Lys Asp Ile Asn Ser
556                 561                 566                 571

tcc acc aag acg cgg tcc att ggt gtt gga acg ttg ctt tct ggc cat     2557
Ser Thr Lys Thr Arg Ser Ile Gly Val Gly Thr Leu Leu Ser Gly His
572                 577                 582                 587

tct ggg ttt gac agg cca tca gct gtg aag acc aaa gag tca ggt gtg     2605
Ser Gly Phe Asp Arg Pro Ser Ala Val Lys Thr Lys Glu Ser Gly Val
588                 593                 598                 603

ggg cag ata aat att aac gac aac tat ctg gtt ggt ctc aaa atg agg     2653
Gly Gln Ile Asn Ile Asn Asp Asn Tyr Leu Val Gly Leu Lys Met Arg
604                 609                 614                 619

act ata gct tgt ggg cca cca cag ttg act gtg ggg ctg aca gcc agc     2701
Thr Ile Ala Cys Gly Pro Pro Gln Leu Thr Val Gly Leu Thr Ala Ser
620                 625                 630                 635

aga agg agc gtg ggg gtt ggg gat gac cct gta ggg gaa tct ctg gag     2749
Arg Arg Ser Val Gly Val Gly Asp Asp Pro Val Gly Glu Ser Leu Glu
636                 641                 646                 651

aac ccc cag cct caa gct cca ctt gga atg atg act ggc ctg gat cac     2797
Asn Pro Gln Pro Gln Ala Pro Leu Gly Met Met Thr Gly Leu Asp His
652                 657                 662                 667

tac att gag cgt atc cag aag ctg ctg gca gaa cag cag aca ctg ctg     2845
Tyr Ile Glu Arg Ile Gln Lys Leu Leu Ala Glu Gln Gln Thr Leu Leu
668                 673                 678                 683

gct gag aac tac agt gaa ctg gca gaa gct ttc ggg gaa cct cac tca     2893
Ala Glu Asn Tyr Ser Glu Leu Ala Glu Ala Phe Gly Glu Pro His Ser
684                 689                 694                 699

cag atg ggc tcc ctc aac tct cag ctc atc agc acc ctg tcg tct atc     2941
Gln Met Gly Ser Leu Asn Ser Gln Leu Ile Ser Thr Leu Ser Ser Ile
700                 705                 710                 715

aac tct gtc atg aaa tct gca agc act gaa gag ctg agg aac cct gac     2989
Asn Ser Val Met Lys Ser Ala Ser Thr Glu Glu Leu Arg Asn Pro Asp
716                 721                 726                 731

ttc cag aaa acc agt ctg ggt aaa atc aca ggc aat tat ttg gga tat     3037
Phe Gln Lys Thr Ser Leu Gly Lys Ile Thr Gly Asn Tyr Leu Gly Tyr
732                 737                 742                 747

acc tgt aag tgt ggg ggc ctt cag tca gga agt ccc tta agc tcc cag     3085
Thr Cys Lys Cys Gly Gly Leu Gln Ser Gly Ser Pro Leu Ser Ser Gln
748                 753                 758                 763

aca tcc cag cct gag caa gaa gtg ggg acc tca gaa gga aag cca atc     3133
Thr Ser Gln Pro Glu Gln Glu Val Gly Thr Ser Glu Gly Lys Pro Ile
764                 769                 774                 779
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agc agc ctg gat gcc ttc ccc act cag gaa gca tgt aca aac aat gaa     3181
Ser Ser Leu Asp Ala Phe Pro Thr Gln Glu Ala Cys Thr Asn Asn Glu
780                 785                 790                 795

agt aca ctg aag tcc atc atg aag aag aaa gat ggt aac aaa gat tca     3229
Ser Thr Leu Lys Ser Ile Met Lys Lys Lys Asp Gly Asn Lys Asp Ser
796                 801                 806                 811

aat ggc gca aaa aag aat ctt cag ttt gtt ggc att aat gga ggg tat     3277
Asn Gly Ala Lys Lys Asn Leu Gln Phe Val Gly Ile Asn Gly Gly Tyr
812                 817                 822                 827

gaa aca act tca agt gat gat tcc agc tca gat gaa agc tct tct tcc     3325
Glu Thr Thr Ser Ser Asp Asp Ser Ser Ser Asp Glu Ser Ser Ser Ser
828                 833                 838                 843

gag tca gat gac gag tgt gat gtc att gag tat cct ctt gaa gaa gag     3373
Glu Ser Asp Asp Glu Cys Asp Val Ile Glu Tyr Pro Leu Glu Glu Glu
844                 849                 854                 859

gag gag gag gag gat gaa gac act cgg gga atg gca gaa ggg cac cat     3421
Glu Glu Glu Glu Asp Glu Asp Thr Arg Gly Met Ala Glu Gly His His
860                 865                 870                 875

gca gtt aat att gaa ggt ttg aag tct gcc agg gtg gaa gat gaa atg     3469
Ala Val Asn Ile Glu Gly Leu Lys Ser Ala Arg Val Glu Asp Glu Met
876                 881                 886                 891

cag gtt caa gaa tgt gaa cct gag aag gtg gaa atc aga gag agg tat     3517
Gln Val Gln Glu Cys Glu Pro Glu Lys Val Glu Ile Arg Glu Arg Tyr
892                 897                 902                 907

gaa tta agt gaa aag atg ttg tct gca tgc aac tta ctg aaa aat act     3565
Glu Leu Ser Glu Lys Met Leu Ser Ala Cys Asn Leu Leu Lys Asn Thr
908                 913                 918                 923

ata aat gac ccc aaa gct ttg acc agc aaa gat atg agg ttc tgt ctg     3613
Ile Asn Asp Pro Lys Ala Leu Thr Ser Lys Asp Met Arg Phe Cys Leu
924                 929                 934                 939

aac acc ctc cag cac gag tgg ttc cgc gtg tcc agt cag aag tca gcc     3661
Asn Thr Leu Gln His Glu Trp Phe Arg Val Ser Ser Gln Lys Ser Ala
940                 945                 950                 955

att cca gcc atg gtg ggg gac tac ata gct gct ttt gag gcc att tcc     3709
Ile Pro Ala Met Val Gly Asp Tyr Ile Ala Ala Phe Glu Ala Ile Ser
956                 961                 966                 971

cca gat gtc ctc cgc tat gtc atc aac ttg gca gac ggc aac ggc aac     3757
Pro Asp Val Leu Arg Tyr Val Ile Asn Leu Ala Asp Gly Asn Gly Asn
972                 977                 982                 987

aca gcc ctc cat tac agc gtg tcc cac tcc aac ttc gag att gtg aag     3805
Thr Ala Leu His Tyr Ser Val Ser His Ser Asn Phe Glu Ile Val Lys
988                 993                 998                1003

ctg ctg tta gat gcc gat gtg tgt aat gtg gat cac cag aac aag gca     3853
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 Leu Leu Leu Asp Ala Asp Val Cys Asn Val Asp His Gln Asn Lys Ala
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 Gly Tyr Thr Pro Ile Met Leu Ala Ala Leu Ala Ala Val Glu Ala Glu
1020                1025                1030                1035

 aag gac atg cgg att gtg gaa gaa ctc ttc ggc tgt ggg gat gtg aat     3949
 Lys Asp Met Arg Ile Val Glu Glu Leu Phe Gly Cys Gly Asp Val Asn
1036                1041                1046                1051

 gcc aaa gct agt cag gcg gga cag acg gcc ctc atg ctg gcg gtc agt     3997
 Ala Lys Ala Ser Gln Ala Gly Gln Thr Ala Leu Met Leu Ala Val Ser
1052                1057                1062                1067

 cac gga cgg ata gac atg gtg aag ggc ctt ctg gcc tgt ggg gct gat     4045
 His Gly Arg Ile Asp Met Val Lys Gly Leu Leu Ala Cys Gly Ala Asp
1068                1073                1078                1083

 gtc aac atc cag gat gac gag ggc tcc acg gcc ctc atg tgt gcc agc     4093
 Val Asn Ile Gln Asp Asp Glu Gly Ser Thr Ala Leu Met Cys Ala Ser
1084                1089                1094                1099

 gag cac ggg cac gtg gag att gtc aag ctg ctg ctg gcc cag ccc ggc     4141
 Glu His Gly His Val Glu Ile Val Lys Leu Leu Leu Ala Gln Pro Gly
1100                1105                1110                1115

 tgc aac ggt cac cta gag gac aac gat ggc agc act gcg ctc tca atc     4189
 Cys Asn Gly His Leu Glu Asp Asn Asp Gly Ser Thr Ala Leu Ser Ile
1116                1121                1126                1131

 gcc ctg gaa gca gga cac aag gac atc gct gtt ctt ctg tat gcc cat     4237
 Ala Leu Glu Ala Gly His Lys Asp Ile Ala Val Leu Leu Tyr Ala His
1132                1137                1142                1147

 gtc aac ttt gca aaa gcc cag tct ccg ggc acc cct agg ctt gga agg     4285
 Val Asn Phe Ala Lys Ala Gln Ser Pro Gly Thr Pro Arg Leu Gly Arg
1148                1153                1158                1163

 aag acg tct cct ggc ccc acc cac cga ggt tca ttt gat tga ttgtatg     4334
 Lys Thr Ser Pro Gly Pro Thr His Arg Gly Ser Phe Asp  *
1164                1169                1174

 caaatagccc tttatttaca tgccactatt aagctgctaa ttgttcctgt tggggtgaca   4394

 gatactgaat gtatacgtat tgtgcctgag ctcaccagca aacagaagca tcaagcccag   4454

 gggtaaaggc tgaagctttc acagtgcaga gactgctagc ctgggcacac gcacctcctt   4514

 tctggccgtc ttctgtgtag ggcacacttt aacccagtct ctgttgctgt tgagtctctg   4574

 ctccgttttg tacagtcaca gggaattctg atctgaaggg gcaccttctg ttcactccca   4634

 caaagtggtg tctggttctc actgagacgt tttaagattt ttccacaaat atttatatgt   4694

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Application No. 10/552,060

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tttcttttgt cttattttaa aataaggaag tcgagatgac tttgatcatt ggtaacttgg   4814

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tagatgtaat atatgacttt ttataaaaag ggtatctata tgaacttgac acagtatttt   4934

cagcttttgt attccatact aaagccatga agaactacac gtaacatcat catttgtatt   4994

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ctctagagaa acacagtgtt ctctttgtat ttatggattc ctttttaccg tgtcacattt   5114

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                Met Glu Thr Gly Ala Ala Glu Leu Tyr Asp Gln Ala
                  1               5                  10

ctt ttg ggc atc ctg cag cac gtg ggc aac gtc cag gat ttc ctg cgc     159
Leu Leu Gly Ile Leu Gln His Val Gly Asn Val Gln Asp Phe Leu Arg
 13                  18                  23                  28

gtt ctc ttt ggc ttc ctc tac cgc aag aca gac ttc tat cgc ttg ctg     207
Val Leu Phe Gly Phe Leu Tyr Arg Lys Thr Asp Phe Tyr Arg Leu Leu
 29                  34                  39                  44

cgc cac cca tcg gac cgc atg ggc ttc ccg ccc ggg gcc gcg cag gcc     255
Arg His Pro Ser Asp Arg Met Gly Phe Pro Pro Gly Ala Ala Gln Ala
 45                  50                  55                  60

ttg gtg ctg cag gta ttc aaa acc ttt gac cac atg gcc cgt cag gat     303
Leu Val Leu Gln Val Phe Lys Thr Phe Asp His Met Ala Arg Gln Asp
 61                  66                  71                  76

gat gag aag aga agg cag gaa ctt gaa gag aaa atc aga aga aag gaa     351
Asp Glu Lys Arg Arg Gln Glu Leu Glu Glu Lys Ile Arg Arg Lys Glu
 77                  82                  87                  92

gag gaa gag gcc aag act gtg tca gct gct gca gct gag aag gag cca     399
Glu Glu Glu Ala Lys Thr Val Ser Ala Ala Ala Ala Glu Lys Glu Pro
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 93                  98                  103                 108

gtc cca gtt cca gtc cag gaa ata gag att gac tcc acc aca gaa ttg      447
Val Pro Val Pro Val Gln Glu Ile Glu Ile Asp Ser Thr Thr Glu Leu
109                 114                 119                 124

gat ggg cat cag gaa gta gag aaa gtg cag cct cca ggc cct gtg aag      495
Asp Gly His Gln Glu Val Glu Lys Val Gln Pro Pro Gly Pro Val Lys
125                 130                 135                 140

gaa atg gcc cat ggt tca cag gag gca gaa gct cca gga gca gtt gct      543
Glu Met Ala His Gly Ser Gln Glu Ala Glu Ala Pro Gly Ala Val Ala
141                 146                 151                 156

ggt gct gct gaa gtc cct agg gaa cca cca att ctt ccc agg att cag      591
Gly Ala Ala Glu Val Pro Arg Glu Pro Pro Ile Leu Pro Arg Ile Gln
157                 162                 167                 172

gag cag ttc cag aaa aat ccc gac agt tac aat ggt gct gtc cga gag      639
Glu Gln Phe Gln Lys Asn Pro Asp Ser Tyr Asn Gly Ala Val Arg Glu
173                 178                 183                 188

aac tac acc tgg tca cag gac tat act gac ctg gag gtc agg gtg cca      687
Asn Tyr Thr Trp Ser Gln Asp Tyr Thr Asp Leu Glu Val Arg Val Pro
189                 194                 199                 204

gta ccc aag cac gtg gtg aag gga aag cag gtc tca gtg gcc ctt agc      735
Val Pro Lys His Val Val Lys Gly Lys Gln Val Ser Val Ala Leu Ser
205                 210                 215                 220

agc agc tcc att cgt gtg gcc atg ctg gag gaa aat ggg gag cgc gtc      783
Ser Ser Ser Ile Arg Val Ala Met Leu Glu Glu Asn Gly Glu Arg Val
221                 226                 231                 236

ctc atg gaa ggg aag ctc acc cac aag atc aac act gag agt tct ctc      831
Leu Met Glu Gly Lys Leu Thr His Lys Ile Asn Thr Glu Ser Ser Leu
237                 242                 247                 252

tgg agt ctc gag ccc ggg aag tgc gtt ttg gtg aac ctg agc aag gtg      879
Trp Ser Leu Glu Pro Gly Lys Cys Val Leu Val Asn Leu Ser Lys Val
253                 258                 263                 268

ggc gag tat tgg tgg aac gcc atc ctg gag gga gaa gag ccc atc gac      927
Gly Glu Tyr Trp Trp Asn Ala Ile Leu Glu Gly Glu Glu Pro Ile Asp
269                 274                 279                 284

att gac aag atc aac aag gag cgc tcc atg gcc acc gtg gat gag gag      975
Ile Asp Lys Ile Asn Lys Glu Arg Ser Met Ala Thr Val Asp Glu Glu
285                 290                 295                 300

gaa cag gcg gtg ttg gac agg ctt acc ttt gac tac cac cag aag ctg     1023
Glu Gln Ala Val Leu Asp Arg Leu Thr Phe Asp Tyr His Gln Lys Leu
301                 306                 311                 316

cag ggc aag cca cag agc cat gag ctg aaa gtc cat gag atg ctg aag     1071
Gln Gly Lys Pro Gln Ser His Glu Leu Lys Val His Glu Met Leu Lys
317                 322                 327                 332
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aag ggg tgg gat gct gaa ggt tct ccc ttc cga ggc cag cga ttc gac     1119
Lys Gly Trp Asp Ala Glu Gly Ser Pro Phe Arg Gly Gln Arg Phe Asp
333                 338                 343                 348

cct gcc atg ttc aac atc tcc ccg ggg gct gtg cag ttt taa tgaccag     1168
Pro Ala Met Phe Asn Ile Ser Pro Gly Ala Val Gln Phe  *
349                 354                 359

aaggaaagga aaccctcgcc ggtggggagg cagagcctta tcctcggctg cccttcttgg   1228

ctccctgcat tccagggact tgctcgtctt gtttacccct agccatcctt tctttcaagg   1288

gtgaaccagg ccttccaccc tgaccttgca tctccagact gttccagaga aggtgcgggg   1348

ccagctgcta tgtggtggcc gctgtggctg acactgagtg aaggtgtttg aaatgcagga   1408

gaggatatcc cagcaaattg ggatcacatg cttttgtctc cacagcaacc agccactgca   1468

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agccctgttt gcacgttcta gttgttcgga gaaagcctag gttctgggct caggtccaga   1828

tgcagcgggg attctgttct ctgactgtgg cgaccttgct ttggttcttg ttgaagtgaa   1888

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tgcttcgccc cacaaatcct ctccgcagcc cttggtggcc acacccagcc agcatcacca 180

gcagcagcag cagcagatca aacggtcagc ccgcatgtgt ggtgagtgtg aggcatgtcg 240

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caacaagatc cggcagaagt gccggctgcg ccagtgccag ctgcgggccc gggaatcgta 360

caagtacttc ccttcctcgc tctcaccagt gacgccctca gagtccctgc caaggccccg 420

cgaccactgc ccacccaaca gcagccacag ccatcacaga agttagggcg catccgtgaa 480

gatgaggggg cagtggcgtc atcaacagtc aaggagcctc ctgaggctac agccacacct 540

gagccactct cagatgagag cgatgaccca gatggctagc gtttaaactt aagcttggta 600

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ccgagctcgg atccactagt ccagtgtggt ggaattcgac acagaagagt ccccattcct    660

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agtctgagaa gaagaaggag gagcgataca agcggcatcg gcagaagcag aagcacaagg    780

ataaatggaa acacccagag agggctgatg ccaaggaccc tgcgtcactg ccccagtgcc    840

tggggcccgg ctgtgtgcgc cccgcccagc ccagctccaa gtattgctca gatgactgtg    900

gc   atg aag ctg gca gcc aac cgc atc tac gag atc ctc ccc cag cgc      947
     Met Lys Leu Ala Ala Asn Arg Ile Tyr Glu Ile Leu Pro Gln Arg
       1               5                  10

atc cag cag tgg cag cag agc cct tgc att gct gaa gag cac ggc aag      995
Ile Gln Gln Trp Gln Gln Ser Pro Cys Ile Ala Glu Glu His Gly Lys
 16                  21                  26                  31

aag ctg ctc gaa cgc att cgc cga gag cag cag agt gcc cgc acc cgc     1043
Lys Leu Leu Glu Arg Ile Arg Arg Glu Gln Gln Ser Ala Arg Thr Arg
 32                  37                  42                  47

ctt cag gaa atg gaa cgc cga ttc cat gag ctt gag gcc atc att cta     1091
Leu Gln Glu Met Glu Arg Arg Phe His Glu Leu Glu Ala Ile Ile Leu
 48                  53                  58                  63

cgt gcc aag cag cag gct gtg cgc gag gat gag gag agc aac gag ggt     1139
Arg Ala Lys Gln Gln Ala Val Arg Glu Asp Glu Glu Ser Asn Glu Gly
 64                  69                  74                  79

gac agt gat gac aca gac ctg cag atc ttc tgt gtt tcc tgt ggg cac     1187
Asp Ser Asp Asp Thr Asp Leu Gln Ile Phe Cys Val Ser Cys Gly His
 80                  85                  90                  95

ccc atc aac cca cgt gtt gcc ttg cgc cac atg gag cgc tgc tac gcc     1235
Pro Ile Asn Pro Arg Val Ala Leu Arg His Met Glu Arg Cys Tyr Ala
 96                 101                 106                 111

aag tat gag agc cag acg tcc ttt ggg tcc atg tac ccc aca cgc att     1283
Lys Tyr Glu Ser Gln Thr Ser Phe Gly Ser Met Tyr Pro Thr Arg Ile
112                 117                 122                 127

gaa ggg gcc aca cga ctc ttc tgt gat gtg tat aat cct cag agc aaa     1331
Glu Gly Ala Thr Arg Leu Phe Cys Asp Val Tyr Asn Pro Gln Ser Lys
128                 133                 138                 143

aca tac tgt aag cgg ctc cag gtg ctg tgc ccc gag cac tca cgg gac     1379
Thr Tyr Cys Lys Arg Leu Gln Val Leu Cys Pro Glu His Ser Arg Asp
144                 149                 154                 159

ccc aaa gtg cca gct gac gag gta tgc ggg tgc ccc ctt gta cgt gat     1427
Pro Lys Val Pro Ala Asp Glu Val Cys Gly Cys Pro Leu Val Arg Asp
160                 165                 170                 175

gtc ttt gag ctc acg ggt gac ttc tgc cgc ctg ccc aag cgc cag tgc     1475
Val Phe Glu Leu Thr Gly Asp Phe Cys Arg Leu Pro Lys Arg Gln Cys
176                 181                 186                 191
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aat cgc cat tac tgc tgg gag aag ctg cgg cgt gcg gaa gtg gac ttg     1523
Asn Arg His Tyr Cys Trp Glu Lys Leu Arg Arg Ala Glu Val Asp Leu
192                 197                 202                 207

gag cgc gtg cgt gtg tgg tac aag ctg gac gag ctg ttt gag cag gag     1571
Glu Arg Val Arg Val Trp Tyr Lys Leu Asp Glu Leu Phe Glu Gln Glu
208                 213                 218                 223

cgc aat gtg cgc aca gcc atg aca aac cgc gcg gga ttg ctg gcc ctg     1619
Arg Asn Val Arg Thr Ala Met Thr Asn Arg Ala Gly Leu Leu Ala Leu
224                 229                 234                 239

atg ctg cac cag acg atc cag cac gat ccc ctc act acc gac ctg cgc     1667
Met Leu His Gln Thr Ile Gln His Asp Pro Leu Thr Thr Asp Leu Arg
240                 245                 250                 255

tcc agt gcc gac cgc tga gcctcc tggcccggac cccttacacc ctgcattcca     1721
Ser Ser Ala Asp Arg  *
256                 261

gatgggggag ccgcccggtg cccgtgtgtc cgttcctcca ctcatctgtt tctccggttc   1781

tccctgtgcc catccaccgg ttgaccgccc atctgccttt atcagaggga ctgtccccgt   1841

cgacatgttc agtgcctggt ggggctgcgg agtccactca tccttgcctc ctctccctgg   1901

gttttgttaa taaaattttg aagaaaccaa aaaaaaaaaa                         1941
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caaagggagg acagagccct ttaaaacgag gcgggtggtg cctgcccctt taagggcggg    180

gcgtccggac gactgtatct gagccccaga ctgccccgag tttctgtcgc aggctgcgag    240

gaaaggcccc taggctgggt ctgggtgctt ggcggcggcg gcttcctccc cgctcgtcct    300

ccccgggccc agaggcacct cggcttcagt catgctgagc agagt    atg gaa gca     354
                                                     Met Glu Ala
                                                       1

cct gac tac gaa gtg cta tcc gtg cga gaa cag cta ttc cac gag agg      402
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```
Pro Asp Tyr Glu Val Leu Ser Val Arg Glu Gln Leu Phe His Glu Arg
  4                   9                  14                  19

atc cgc gag tgt att ata tca aca ctt ctg ttt gca aca ctg tac atc      450
Ile Arg Glu Cys Ile Ile Ser Thr Leu Leu Phe Ala Thr Leu Tyr Ile
 20                  25                  30                  35

ctc tgc cac atc ttc ctg acc cgc ttc aag aag cct gct gag ttc acc      498
Leu Cys His Ile Phe Leu Thr Arg Phe Lys Lys Pro Ala Glu Phe Thr
 36                  41                  46                  51

aca gtg gat gat gaa gat gcc acc gtc aac aag att gcg ctc gag ctg      546
Thr Val Asp Asp Glu Asp Ala Thr Val Asn Lys Ile Ala Leu Glu Leu
 52                  57                  62                  67

tgc acc ttt acc ctg gca att gcc ctg ggt gct gtc ctg ctc ctg ccc      594
Cys Thr Phe Thr Leu Ala Ile Ala Leu Gly Ala Val Leu Leu Leu Pro
 68                  73                  78                  83

ttc tcc atc atc agc aat gag gtg ctg ctc tcc ctg cct cgg aac tac      642
Phe Ser Ile Ile Ser Asn Glu Val Leu Leu Ser Leu Pro Arg Asn Tyr
 84                  89                  94                  99

tac atc cag tgg ctc aac ggc tcc ctc atc cat ggc ctc tgg aac ctt      690
Tyr Ile Gln Trp Leu Asn Gly Ser Leu Ile His Gly Leu Trp Asn Leu
100                 105                 110                 115

gtt ttt ctc ttc tcc aac ctg tcc ctc atc ttc ctc atg ccc ttt gca      738
Val Phe Leu Phe Ser Asn Leu Ser Leu Ile Phe Leu Met Pro Phe Ala
116                 121                 126                 131

tat ttc ttc act gag tct gag ggc ttt gct ggc tcc aga aag ggt gtc      786
Tyr Phe Phe Thr Glu Ser Glu Gly Phe Ala Gly Ser Arg Lys Gly Val
132                 137                 142                 147

ctg ggc cgg gtc tat gag aca gtg gtg atg ttg atg ctc ctc act ctg      834
Leu Gly Arg Val Tyr Glu Thr Val Val Met Leu Met Leu Leu Thr Leu
148                 153                 158                 163

ctg gtg cta ggt atg gtg tgg gtg gca tca gcc att gtg gac aag aac      882
Leu Val Leu Gly Met Val Trp Val Ala Ser Ala Ile Val Asp Lys Asn
164                 169                 174                 179

aag gcc aac aga gag tca ctc tat gac ttt tgg gag tac tat ctc ccc      930
Lys Ala Asn Arg Glu Ser Leu Tyr Asp Phe Trp Glu Tyr Tyr Leu Pro
180                 185                 190                 195

tac ctc tac tca tgc atc tcc ttc ctt ggg gtt ctg ctg ctc ctg gtg      978
Tyr Leu Tyr Ser Cys Ile Ser Phe Leu Gly Val Leu Leu Leu Leu Val
196                 201                 206                 211

tgt act cca ctg ggt ctc gcc cgc atg ttc tcc gtc act ggg aag ctg     1026
Cys Thr Pro Leu Gly Leu Ala Arg Met Phe Ser Val Thr Gly Lys Leu
212                 217                 222                 227

cta gtc aag ccc cgg ctg ctg gaa gac ctg gag gag cag ctg tac tgc     1074
Leu Val Lys Pro Arg Leu Leu Glu Asp Leu Glu Glu Gln Leu Tyr Cys
```

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228                 233                 238                 243

tca gcc ttt gag gag gca gcc ctg acc cgc agg atc tgt aat cct act     1122
Ser Ala Phe Glu Glu Ala Ala Leu Thr Arg Arg Ile Cys Asn Pro Thr
244                 249                 254                 259

tcc tgc tgg ctg cct tta gac atg gag ctg cta cac aga cag gtc ctg     1170
Ser Cys Trp Leu Pro Leu Asp Met Glu Leu Leu His Arg Gln Val Leu
260                 265                 270                 275

gct ctg cag aca cag agg gtc ctg ctg gag aag agg cgg aag gct tca     1218
Ala Leu Gln Thr Gln Arg Val Leu Leu Glu Lys Arg Arg Lys Ala Ser
276                 281                 286                 291

gcc tgg caa cgg aac ctg ggc tac ccc ctg gct atg ctg tgc ttg ctg     1266
Ala Trp Gln Arg Asn Leu Gly Tyr Pro Leu Ala Met Leu Cys Leu Leu
292                 297                 302                 307

gtg ctg acg ggc ctg tct gtg ctc att gtg gcc atc cac atc ctg gag     1314
Val Leu Thr Gly Leu Ser Val Leu Ile Val Ala Ile His Ile Leu Glu
308                 313                 318                 323

ctg ctc atc gat gag gct gcc atg ccc cga ggc atg cag ggt acc tcc     1362
Leu Leu Ile Asp Glu Ala Ala Met Pro Arg Gly Met Gln Gly Thr Ser
324                 329                 334                 339

tta ggc cag gtc tcc ttc tcc aag ctg ggc tcc ttt ggt gcc gtc att     1410
Leu Gly Gln Val Ser Phe Ser Lys Leu Gly Ser Phe Gly Ala Val Ile
340                 345                 350                 355

cag gtt gta ctc atc ttt tac cta atg gtg tcc tca gtt gtg ggc ttc     1458
Gln Val Val Leu Ile Phe Tyr Leu Met Val Ser Ser Val Val Gly Phe
356                 361                 366                 371

tat agc tct cca ctc ttc cgg agc ctg cgg ccc aga tgg cac gac act     1506
Tyr Ser Ser Pro Leu Phe Arg Ser Leu Arg Pro Arg Trp His Asp Thr
372                 377                 382                 387

gcc atg acg cag ata att ggg aac tgt gtc tgt ctc ctg gtc cta agc     1554
Ala Met Thr Gln Ile Ile Gly Asn Cys Val Cys Leu Leu Val Leu Ser
388                 393                 398                 403

tca gca ctt cct gtc ttc tct cga acc ctg ggg ctc act cgc ttt gac     1602
Ser Ala Leu Pro Val Phe Ser Arg Thr Leu Gly Leu Thr Arg Phe Asp
404                 409                 414                 419

ctg ctg ggt gac ttt gga cgc ttc aac tgg ctg ggc aat ttc tac att     1650
Leu Leu Gly Asp Phe Gly Arg Phe Asn Trp Leu Gly Asn Phe Tyr Ile
420                 425                 430                 435

gtg ttc ctc tac aac gca gcc ttt gca ggc ctc acc aca ctc tgt ctg     1698
Val Phe Leu Tyr Asn Ala Ala Phe Ala Gly Leu Thr Thr Leu Cys Leu
436                 441                 446                 451

gtg aag acc ttc act gca gct gtg cgg gca gag ctg atc cgg gcc ttt     1746
Val Lys Thr Phe Thr Ala Ala Val Arg Ala Glu Leu Ile Arg Ala Phe
452                 457                 462                 467
```

```
ggg ctg gac aga ctg ccg ctg ccc gtc tcc ggt ttc ccc cag gca tct     1794
Gly Leu Asp Arg Leu Pro Leu Pro Val Ser Gly Phe Pro Gln Ala Ser
468                 473                 478                 483

agg aag acc cag cac cag tga cc tccagctggg ggtgggaagg aaaaaactgg     1847
Arg Lys Thr Gln His Gln  *
484                 489

acactgccat ctgctgccta ggcctggagg gaagcccaag gctacttgga cctcaggacc   1907

tggaatctga gagggtgggt ggcagagggg agcagagcca tctgcactat tgcataatct   1967

gagccagagt ttgggaccag gacctcctgc ttttccatac ttaactgtgg cctcagcatg   2027

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gcctagtggc gggtgtttgc attgaaacgt gagcgcgacc cgaccttaaa gagtggggag    120

caaagggagg acagagccct ttaaaacgag gcgggtggtg cctgcccctt taagggcggg    180

gcgtccggac gactgtatct gagccccaga ctgccccgag tttctgtcgc aggctgcgag    240

gaaaggcccc taggctgggt ctgggtgctt ggcggcggcg gcttcctccc cgctcgtcct    300

ccccgggccc agaggcacct cggcttcagt catgctgagc agagt    atg gaa gca     354
                                                     Met Glu Ala
                                                       1

cct gac tac gaa gtg cta tcc gtg cga gaa cag cta ttc cac gag agg      402
Pro Asp Tyr Glu Val Leu Ser Val Arg Glu Gln Leu Phe His Glu Arg
  4                   9                  14                  19
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atc cgc gag tgt att ata tca aca ctt ctg ttt gca aca ctg tac atc      450
Ile Arg Glu Cys Ile Ile Ser Thr Leu Leu Phe Ala Thr Leu Tyr Ile
 20                  25                  30                  35

ctc tgc cac atc ttc ctg acc cgc ttc aag aag cct gct gag ttc acc      498
Leu Cys His Ile Phe Leu Thr Arg Phe Lys Lys Pro Ala Glu Phe Thr
 36                  41                  46                  51

aca gtg gat gat gaa gat gcc acc gtc aac aag att gcg ctc gag ctg      546
Thr Val Asp Asp Glu Asp Ala Thr Val Asn Lys Ile Ala Leu Glu Leu
 52                  57                  62                  67

tgc acc ttt acc ctg gca att gcc ctg ggt gct gtc ctg ctc ctg ccc      594
Cys Thr Phe Thr Leu Ala Ile Ala Leu Gly Ala Val Leu Leu Leu Pro
 68                  73                  78                  83

ttc tcc atc atc agc aat gag gtg ctg ctc tcc ctg cct cgg aac tac      642
Phe Ser Ile Ile Ser Asn Glu Val Leu Leu Ser Leu Pro Arg Asn Tyr
 84                  89                  94                  99

tac atc cag tgg ctc aac ggc tcc ctc atc cat ggc ctc tgg aac ctt      690
Tyr Ile Gln Trp Leu Asn Gly Ser Leu Ile His Gly Leu Trp Asn Leu
100                 105                 110                 115

gtt ttt ctc ttc tcc aac ctg tcc ctc atc ttc ctc atg ccc ttt gca      738
Val Phe Leu Phe Ser Asn Leu Ser Leu Ile Phe Leu Met Pro Phe Ala
116                 121                 126                 131

tat ttc ttc act gag tct gag ggc ttt gct ggc tcc aga aag ggt gtc      786
Tyr Phe Phe Thr Glu Ser Glu Gly Phe Ala Gly Ser Arg Lys Gly Val
132                 137                 142                 147

ctg ggc cgg gtc tat gag aca gtg gtg atg ttg atg ctc ctc act ctg      834
Leu Gly Arg Val Tyr Glu Thr Val Val Met Leu Met Leu Leu Thr Leu
148                 153                 158                 163

ctg gtg cta ggt atg gtg tgg gtg gca tca gcc att gtg gac aag aac      882
Leu Val Leu Gly Met Val Trp Val Ala Ser Ala Ile Val Asp Lys Asn
164                 169                 174                 179

aag gcc aac aga gag tca ctc tat gac ttt tgg gag tac tat ctc ccc      930
Lys Ala Asn Arg Glu Ser Leu Tyr Asp Phe Trp Glu Tyr Tyr Leu Pro
180                 185                 190                 195

tac ctc tac tca tgc atc tcc ttc ctt ggg gtt ctg ctg ctc ctg gtg      978
Tyr Leu Tyr Ser Cys Ile Ser Phe Leu Gly Val Leu Leu Leu Leu Val
196                 201                 206                 211

tgt act cca ctg ggt ctc gcc cgc atg ttc tcc gtc act ggg aag ctg     1026
Cys Thr Pro Leu Gly Leu Ala Arg Met Phe Ser Val Thr Gly Lys Leu
212                 217                 222                 227

cta gtc aag ccc cgg ctg ctg gaa gac ctg gag gag cag ctg tac tgc     1074
Leu Val Lys Pro Arg Leu Leu Glu Asp Leu Glu Glu Gln Leu Tyr Cys
228                 233                 238                 243
```

```
tca gcc ttt gag gag gca gcc ctg acc cgc agg atc tgt aat cct act     1122
Ser Ala Phe Glu Glu Ala Ala Leu Thr Arg Arg Ile Cys Asn Pro Thr
244                 249                 254                 259

tcc tgc tgg ctg cct tta gac atg gag ctg cta cac aga cag gtc ctg     1170
Ser Cys Trp Leu Pro Leu Asp Met Glu Leu Leu His Arg Gln Val Leu
260                 265                 270                 275

gct ctg cag aca cag agg gtc ctg ctg gag aag agg cgg aag gct tca     1218
Ala Leu Gln Thr Gln Arg Val Leu Leu Glu Lys Arg Arg Lys Ala Ser
276                 281                 286                 291

gcc tgg caa cgg aac ctg ggc tac ccc ctg gct atg ctg tgc ttg ctg     1266
Ala Trp Gln Arg Asn Leu Gly Tyr Pro Leu Ala Met Leu Cys Leu Leu
292                 297                 302                 307

gtg ctg acg ggc ctg tct gtg ctc att gtg gcc atc cac atc ctg gag     1314
Val Leu Thr Gly Leu Ser Val Leu Ile Val Ala Ile His Ile Leu Glu
308                 313                 318                 323

ctg ctc atc gat gag gct gcc atg ccc cga ggc atg cag gtt gta ctc     1362
Leu Leu Ile Asp Glu Ala Ala Met Pro Arg Gly Met Gln Val Val Leu
324                 329                 334                 339

atc ttt tac cta atg gtg tcc tca gtt gtg ggc ttc tat agc tct cca     1410
Ile Phe Tyr Leu Met Val Ser Ser Val Val Gly Phe Tyr Ser Ser Pro
340                 345                 350                 355

ctc ttc cgg agc ctg cgg ccc aga tgg cac gac act gcc atg acg cag     1458
Leu Phe Arg Ser Leu Arg Pro Arg Trp His Asp Thr Ala Met Thr Gln
356                 361                 366                 371

ata att ggg aac tgt gtc tgt ctc ctg gtc cta agc tca gca ctt cct     1506
Ile Ile Gly Asn Cys Val Cys Leu Leu Val Leu Ser Ser Ala Leu Pro
372                 377                 382                 387

gtc ttc tct cga acc ctg ggg ctc act cgc ttt gac ctg ctg ggt gac     1554
Val Phe Ser Arg Thr Leu Gly Leu Thr Arg Phe Asp Leu Leu Gly Asp
388                 393                 398                 403

ttt gga cgc ttc aac tgg ctg ggc aat ttc tac att gtg ttc ctc tac     1602
Phe Gly Arg Phe Asn Trp Leu Gly Asn Phe Tyr Ile Val Phe Leu Tyr
404                 409                 414                 419

aac gca gcc ttt gca ggc ctc acc aca ctc tgt ctg gtg aag acc ttc     1650
Asn Ala Ala Phe Ala Gly Leu Thr Thr Leu Cys Leu Val Lys Thr Phe
420                 425                 430                 435

act gca gct gtg cgg gca gag ctg atc cgg gcc ttt ggg ctg gac aga     1698
Thr Ala Ala Val Arg Ala Glu Leu Ile Arg Ala Phe Gly Leu Asp Arg
436                 441                 446                 451

ctg ccg ctg ccc gtc tcc ggt ttc ccc cag gca tct agg aag acc cag     1746
Leu Pro Leu Pro Val Ser Gly Phe Pro Gln Ala Ser Arg Lys Thr Gln
452                 457                 462                 467

cac cag tga cctccag ctgggggtgg gaaggaaaaa actggacact gccatctgct     1802
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```
His Gln  *
468

gcctaggcct ggagggaagc ccaaggctac ttggacctca ggacctggaa tctgagaggg   1862

tgggtggcag aggggagcag agccatctgc actattgcat aatctgagcc agagtttggg   1922

accaggacct cctgcttttc catacttaac tgtggcctca gcatggggta gggctgggtg   1982

actgggtcta gcccctgatc ccaaatctgt ttacacatca atctgcctca ctgctgttct   2042

gggccatccc catagccatg tttacatgat ttgatgtgca atagggtggg gtaggggcag   2102

ggaaaggact gggccagggc aggctcggga gatagattgt ctcccttgcc tctggcccag   2162

cagagcctaa gcactgtgct atcctggagg ggctttggac cacctgaaag accaagggga   2222

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Confidential - Attorney Eyes Only

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acccgggcca gttttcaagg cgggctgtaa ctggtggcat ttgtcccggg accaggctgg    240

agtgcaacgg tgcgatctcg gctcatcaca acctccacct ctcgggttca aacgattctc    300

ctgccttagc ctcccaagta gctgggatta caggtccaca gttttatgtg tgagcaag   358

atg gag gct gac ctg tct ggc ttt aac atc gat gcc ccc cgt tgg gac      406
Met Glu Ala Asp Leu Ser Gly Phe Asn Ile Asp Ala Pro Arg Trp Asp
  1               5                  10                  15

cag cgc acc ttc ctg ggg aga gtg aag cac ttc cta aac atc acg gac      454
Gln Arg Thr Phe Leu Gly Arg Val Lys His Phe Leu Asn Ile Thr Asp
 17                  22                  27                  32

ccc cgc act gtc ttt gta tct gag cgg gag ctg gac tgg gcc aag gtg      502
Pro Arg Thr Val Phe Val Ser Glu Arg Glu Leu Asp Trp Ala Lys Val
 33                  38                  43                  48
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atg gtg gag aag agc agg atg ggg gtt gtg ccc cca ggc acc caa gtg      550
Met Val Glu Lys Ser Arg Met Gly Val Val Pro Pro Gly Thr Gln Val
 49                  54                  59                  64

gag cag ctg ctg tat gcc aag aag ctg tat gac tcg gcc ttc cac ccc      598
Glu Gln Leu Leu Tyr Ala Lys Lys Leu Tyr Asp Ser Ala Phe His Pro
 65                  70                  75                  80

gac act ggg gag aag atg aat gtc atc ggg cgc atg tct ttc cag ctt      646
Asp Thr Gly Glu Lys Met Asn Val Ile Gly Arg Met Ser Phe Gln Leu
 81                  86                  91                  96

cct ggc ggc atg atc atc acg ggc ttc atg ctc cag ttc tac agg acg      694
Pro Gly Gly Met Ile Ile Thr Gly Phe Met Leu Gln Phe Tyr Arg Thr
 97                 102                 107                 112

atg ccg gcg gtg atc ttc tgg cag tgg gtg aac cag tcc ttc aat gcc      742
Met Pro Ala Val Ile Phe Trp Gln Trp Val Asn Gln Ser Phe Asn Ala
113                 118                 123                 128

tta gtc aac tac acc aac agg aat gcg gct tcc ccc aca tca gtc agg      790
Leu Val Asn Tyr Thr Asn Arg Asn Ala Ala Ser Pro Thr Ser Val Arg
129                 134                 139                 144

cag atg gcc ctt tcc tac ttc aca gcc aca acc act gct gtg gcc acg      838
Gln Met Ala Leu Ser Tyr Phe Thr Ala Thr Thr Thr Ala Val Ala Thr
145                 150                 155                 160

gct gtg ggc atg aac atg ttg aca aag aaa gcg ccg ccc ttg gtg ggc      886
Ala Val Gly Met Asn Met Leu Thr Lys Lys Ala Pro Pro Leu Val Gly
161                 166                 171                 176

cgc tgg gtg ccc ttt gcc gct gtg gct gcg gct aac tgt gtc aat atc      934
Arg Trp Val Pro Phe Ala Ala Val Ala Ala Ala Asn Cys Val Asn Ile
177                 182                 187                 192

ccc atg atg cga cag cag gag ctc ata aag gga atc tgc gtg aag gac      982
Pro Met Met Arg Gln Gln Glu Leu Ile Lys Gly Ile Cys Val Lys Asp
193                 198                 203                 208

agg aat gaa aat gag att ggt cat tcc cgg aga gct gcg gcc ata ggc     1030
Arg Asn Glu Asn Glu Ile Gly His Ser Arg Arg Ala Ala Ala Ile Gly
209                 214                 219                 224

atc acc caa gta gtt att tct cgg atc acc atg tca gct cct ggg atg     1078
Ile Thr Gln Val Val Ile Ser Arg Ile Thr Met Ser Ala Pro Gly Met
225                 230                 235                 240

atc ttg ctg cca gtc atc atg gaa agg ctt gag aaa ttg cac ttc atg     1126
Ile Leu Leu Pro Val Ile Met Glu Arg Leu Glu Lys Leu His Phe Met
241                 246                 251                 256

cag aaa gtc aag gtc ctg cac gcc cca ttg cag gtc atg ctg agc ggg     1174
Gln Lys Val Lys Val Leu His Ala Pro Leu Gln Val Met Leu Ser Gly
257                 262                 267                 272
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tgc ttc ctc atc ttc atg gtg cca gtg gcg tgt ggg ctt ttc cca cag     1222
Cys Phe Leu Ile Phe Met Val Pro Val Ala Cys Gly Leu Phe Pro Gln
273                 278                 283                 288

aaa tgt gaa ttg cca gtt tcc tat ctg gaa ccg aag ctc caa gac act     1270
Lys Cys Glu Leu Pro Val Ser Tyr Leu Glu Pro Lys Leu Gln Asp Thr
289                 294                 299                 304

atc aag gcc aag tat gga gaa ctt gag cct tat gtc tac ttc aat aag     1318
Ile Lys Ala Lys Tyr Gly Glu Leu Glu Pro Tyr Val Tyr Phe Asn Lys
305                 310                 315                 320

ggt ctc taa atgcccc acttcagcaa ggaccagtct attcccatat tcaccagctc     1374
Gly Leu  *
321

ctccttagct acgtgcacac ttgtgtcctc cttccccttt gccaacaagg cctgaaggcc   1434

agggtagatt ggggggtggg acaatgaatg cctcatactt acaccctggt actggttgat   1494

tggacctcag gggaaaaaag tgaaaaaggg tagcaaaggc caatgttttc tagctgcttc   1554

ctcaacccct gtcccctgga gaccagaagc tgaggccctc tcagggagga gacatccaag   1614

caaatcattt ggaaaagtta ggaaaccttt aggattctgg ttccagccag ggttgaggaa   1674

aagaccttgg atcaaaagga agcttctata cctctttctt cttcgcttcc tcctctccca   1734

agcaatggaa acttttaccc atgtaattct agctgaactc aggaaaaaga aggggaaag    1794

gactctgtcc ccttggggct catcaccctt ccacatcctc ctcctcgttg ccccctggtc   1854

aggcagcttc ttttttttt tttaaaaagg gagttttgtt ttgcccccca ggcggaaagg   1914

caggggccca atttggttaa atggaaaatt tgccctcggg attaaaggaa attttctggc   1974

ttaaccttta aaggaagggg gaataagggg gccctggccc ccccccgggg aaaattttgg   2034

atttaaaggg aaaaggggtt taaccatggt ggccaaaagg ggtttaaacc cctgacctta   2094

gggggaaccc ccccccccaaa cctttgaaat tgggggggatt accgggttgg acccccaaac   2154

ccagcccgga aaggtttttt gggaggggggg gtaaccttgg aattttcaaa cccttagggg   2214

tttttagggc taaaaagggg accggcccag gccacaaaaa taacggggtt ttaaaaacat   2274

ggttgaacct aattttggaa attttttttta aaaaagggaa ggtttttttaa cccaatggcc   2334

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                          Met Gly Ser Gly Asp Leu Leu Leu Ser Gly
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gaa agc cag gtg gag aag acc aag ctt tct tcc tcc gag gag ttc cct      100
Glu Ser Gln Val Glu Lys Thr Lys Leu Ser Ser Ser Glu Glu Phe Pro
 11                  16                  21                  26

cag act ctg agc ctt ccc aga aca act att tgc tca gga cat gat gct      148
Gln Thr Leu Ser Leu Pro Arg Thr Thr Ile Cys Ser Gly His Asp Ala
 27                  32                  37                  42

gat acc gaa gat gat cca tcc cta gca gat ttg ccc cag gca ctg gac      196
Asp Thr Glu Asp Asp Pro Ser Leu Ala Asp Leu Pro Gln Ala Leu Asp
 43                  48                  53                  58

ctc agc cag cag cct cac agc tca ggt ctc tct tgc ctg tca cag tgg      244
Leu Ser Gln Gln Pro His Ser Ser Gly Leu Ser Cys Leu Ser Gln Trp
 59                  64                  69                  74

aag tcc gtg ctg agc cca ggt tcc gca gct cag cct tcc agc tgc agc      292
Lys Ser Val Leu Ser Pro Gly Ser Ala Ala Gln Pro Ser Ser Cys Ser
 75                  80                  85                  90

atc tct gct tcc tcc aca ggc agc agt ctc cag ggt cac cag gag agg      340
Ile Ser Ala Ser Ser Thr Gly Ser Ser Leu Gln Gly His Gln Glu Arg
 91                  96                 101                 106

gcg gag cct cgt ggt ggt tct ctg gcc aag gtc tcc tcc tcc ctg gag      388
Ala Glu Pro Arg Gly Gly Ser Leu Ala Lys Val Ser Ser Ser Leu Glu
107                 112                 117                 122

ccg gtc gtc ccc cag gaa cct tcc tct gtg gtg ggg cta gga cct cgg      436
Pro Val Val Pro Gln Glu Pro Ser Ser Val Val Gly Leu Gly Pro Arg
123                 128                 133                 138

ccc cag tgg tca cca cag cct gtg ttc tct ggg ggt gat gct tct ggg      484
Pro Gln Trp Ser Pro Gln Pro Val Phe Ser Gly Gly Asp Ala Ser Gly
139                 144                 149                 154

cta ggc agg aga cgc ctc tcc ttc cag gct gag tac tgg gcc tgt gtg      532
Leu Gly Arg Arg Arg Leu Ser Phe Gln Ala Glu Tyr Trp Ala Cys Val
155                 160                 165                 170

ctg cca gat tcc ctg cct cca tca ccc gac cgc cac tcc cct ctc tgg      580
Leu Pro Asp Ser Leu Pro Pro Ser Pro Asp Arg His Ser Pro Leu Trp
171                 176                 181                 186

aac cca aat aaa gag tat gaa gat ctg ctt gac tat act tac cca ctg      628
Asn Pro Asn Lys Glu Tyr Glu Asp Leu Leu Asp Tyr Thr Tyr Pro Leu
187                 192                 197                 202
```

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agg ccc ggg cct cag ctc cca aag cac ctt gat agc cgt gtg cca gct      676
Arg Pro Gly Pro Gln Leu Pro Lys His Leu Asp Ser Arg Val Pro Ala
203                 208                 213                 218

gac cct gtc ctg cag gac tcc ggg gta gac ctg gat agc ttc tct gtc      724
Asp Pro Val Leu Gln Asp Ser Gly Val Asp Leu Asp Ser Phe Ser Val
219                 224                 229                 234

tct cca gca agc acc ctc aaa tca cct act aat gtc tcc ccc aac tgc      772
Ser Pro Ala Ser Thr Leu Lys Ser Pro Thr Asn Val Ser Pro Asn Cys
235                 240                 245                 250

cca cca gca gag gcc act gcc ctg cca ttt tct ggg ccc aga gag cca      820
Pro Pro Ala Glu Ala Thr Ala Leu Pro Phe Ser Gly Pro Arg Glu Pro
251                 256                 261                 266

agc ctt aag cag tgg ccc tcc aga gta ccc cag aaa cag ggt ggc atg      868
Ser Leu Lys Gln Trp Pro Ser Arg Val Pro Gln Lys Gln Gly Gly Met
267                 272                 277                 282

ggc ttg gca tct tgg agc caa ctt gca tct acc ccc aga gcc cca ggc      916
Gly Leu Ala Ser Trp Ser Gln Leu Ala Ser Thr Pro Arg Ala Pro Gly
283                 288                 293                 298

agt agg gat gct cgt tgg gag cgc aga gag cca gcc ctg agg ggt gcg      964
Ser Arg Asp Ala Arg Trp Glu Arg Arg Glu Pro Ala Leu Arg Gly Ala
299                 304                 309                 314

aag gac cgg ctg act ata ggc aag cac ctt gat atg ggc tct ccc cag     1012
Lys Asp Arg Leu Thr Ile Gly Lys His Leu Asp Met Gly Ser Pro Gln
315                 320                 325                 330

cta agg aca cgg gac aga ggg tgg ccc tcg ccc agg cca gag agg gag     1060
Leu Arg Thr Arg Asp Arg Gly Trp Pro Ser Pro Arg Pro Glu Arg Glu
331                 336                 341                 346

aag agg acc agc cag agt gcc cgg cgc cct acc tgc aca gag tct agg     1108
Lys Arg Thr Ser Gln Ser Ala Arg Arg Pro Thr Cys Thr Glu Ser Arg
347                 352                 357                 362

tgg aaa tca gaa gag gaa gtg gaa agt gat gac gag tat ctt gcc ctc     1156
Trp Lys Ser Glu Glu Glu Val Glu Ser Asp Asp Glu Tyr Leu Ala Leu
363                 368                 373                 378

ccc gct cgg ctg aca cag gtt tct agc ctg gtt tcg tat cta gga tcc     1204
Pro Ala Arg Leu Thr Gln Val Ser Ser Leu Val Ser Tyr Leu Gly Ser
379                 384                 389                 394

att tct acc ttg gtt acc ctg ccc act ggg gat atc aaa ggg cag agc     1252
Ile Ser Thr Leu Val Thr Leu Pro Thr Gly Asp Ile Lys Gly Gln Ser
395                 400                 405                 410

ccc ttg gaa gtg tca gac agt gat ggg cca gct tcc ttc cct tca agc     1300
Pro Leu Glu Val Ser Asp Ser Asp Gly Pro Ala Ser Phe Pro Ser Ser
411                 416                 421                 426
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tcc agc caa agc cag ctt ccc cct gga gct gcc ctc caa gga tct ggg     1348
Ser Ser Gln Ser Gln Leu Pro Pro Gly Ala Ala Leu Gln Gly Ser Gly
427                 432                 437                 442

gat cct gag ggc cag aat ccc tgt ttc ctg cgc tcc ttc gtc cgt gcc     1396
Asp Pro Glu Gly Gln Asn Pro Cys Phe Leu Arg Ser Phe Val Arg Ala
443                 448                 453                 458

cac gac tcc gca ggg gaa ggc agt ctg ggg agc agc cag gcc ctc ggg     1444
His Asp Ser Ala Gly Glu Gly Ser Leu Gly Ser Ser Gln Ala Leu Gly
459                 464                 469                 474

gtc tcc tct gga ctg ctg aaa aca cgc ccc tcc ttg cca gct agg ttg     1492
Val Ser Ser Gly Leu Leu Lys Thr Arg Pro Ser Leu Pro Ala Arg Leu
475                 480                 485                 490

gac cgg tgg cca ttc tca gac cca gat gtt gaa ggg cag ctt ccc agg     1540
Asp Arg Trp Pro Phe Ser Asp Pro Asp Val Glu Gly Gln Leu Pro Arg
491                 496                 501                 506

aaa gga gga gaa cag gga aaa gaa tca ctg gtg caa tgt gtg aag aca     1588
Lys Gly Gly Glu Gln Gly Lys Glu Ser Leu Val Gln Cys Val Lys Thr
507                 512                 517                 522

ttt tgc tgt cag ctg gaa gag ctg atc tgc tgg ctg tat aat gtt gca     1636
Phe Cys Cys Gln Leu Glu Glu Leu Ile Cys Trp Leu Tyr Asn Val Ala
523                 528                 533                 538

gat gtt act gac cac ggg act gca gcc agg tcc aat ctt aca agt ctc     1684
Asp Val Thr Asp His Gly Thr Ala Ala Arg Ser Asn Leu Thr Ser Leu
539                 544                 549                 554

aag tct tct ctg cag ctt tac cgg caa ttt aag aaa gat ata gat gaa     1732
Lys Ser Ser Leu Gln Leu Tyr Arg Gln Phe Lys Lys Asp Ile Asp Glu
555                 560                 565                 570

cat cag tct ctg acg gag agt gtc tta cag aag ggg gag att ctt ctt     1780
His Gln Ser Leu Thr Glu Ser Val Leu Gln Lys Gly Glu Ile Leu Leu
571                 576                 581                 586

cag tgc ctg ttg gag aac acc cca gtt tta gag gat gtc ctt ggg agg     1828
Gln Cys Leu Leu Glu Asn Thr Pro Val Leu Glu Asp Val Leu Gly Arg
587                 592                 597                 602

atc gca aag cag tct ggt gag ctg gag agc cac gca gat cgc ctg tat     1876
Ile Ala Lys Gln Ser Gly Glu Leu Glu Ser His Ala Asp Arg Leu Tyr
603                 608                 613                 618

gac tct atc ttg gcc tct ctg gac atg ctg gct ggc tgc acc ctt atc     1924
Asp Ser Ile Leu Ala Ser Leu Asp Met Leu Ala Gly Cys Thr Leu Ile
619                 624                 629                 634

cct gac aaa aag ccc atg gcg gca atg gag cac cca tgt gaa ggg gtt     1972
Pro Asp Lys Lys Pro Met Ala Ala Met Glu His Pro Cys Glu Gly Val
635                 640                 645                 650

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651

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gaa agc cag gtg gag aag acc aag ctt tct tcc tcc gag gag ttc cct      100
Glu Ser Gln Val Glu Lys Thr Lys Leu Ser Ser Ser Glu Glu Phe Pro
 11                  16                  21                  26

cag act ctg agc ctt ccc aga aca act att tgc tca gga cat gat gct      148
Gln Thr Leu Ser Leu Pro Arg Thr Thr Ile Cys Ser Gly His Asp Ala
 27                  32                  37                  42

gat acc gaa gat gat cca tcc cta gca gat ttg ccc cag gca ctg gac      196
Asp Thr Glu Asp Asp Pro Ser Leu Ala Asp Leu Pro Gln Ala Leu Asp
 43                  48                  53                  58

ctc agc cag cag cct cac agc tca ggt ctc tct tgc ctg tca cag tgg      244
Leu Ser Gln Gln Pro His Ser Ser Gly Leu Ser Cys Leu Ser Gln Trp
 59                  64                  69                  74

aag tcc gtg ctg agc cca ggt tcc gca gct cag cct tcc agc tgc agc      292
Lys Ser Val Leu Ser Pro Gly Ser Ala Ala Gln Pro Ser Ser Cys Ser
 75                  80                  85                  90

atc tct gct tcc tcc aca ggc agc agt ctc cag ggt cac cag gag agg      340
Ile Ser Ala Ser Ser Thr Gly Ser Ser Leu Gln Gly His Gln Glu Arg
 91                  96                 101                 106

gcg gag cct cgt ggt ggt tct ctg gcc aag gtc tcc tcc tcc ctg gag      388
Ala Glu Pro Arg Gly Gly Ser Leu Ala Lys Val Ser Ser Ser Leu Glu
107                 112                 117                 122

ccg gtc gtc ccc cag gaa cct tcc tct gtg gtg ggg cta gga cct cgg      436
Pro Val Val Pro Gln Glu Pro Ser Ser Val Val Gly Leu Gly Pro Arg
123                 128                 133                 138

ccc cag tgg tca cca cag cct gtg ttc tct ggg ggt gat gct tct ggg      484
Pro Gln Trp Ser Pro Gln Pro Val Phe Ser Gly Gly Asp Ala Ser Gly
139                 144                 149                 154

cta ggc agg aga cgc ctc tcc ttc cag gct gag tac tgg gcc tgt gtg      532
Leu Gly Arg Arg Arg Leu Ser Phe Gln Ala Glu Tyr Trp Ala Cys Val
155                 160                 165                 170
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ctg cca gat tcc ctg cct cca tca ccc gac cgc cac tcc cct ctc tgg      580
Leu Pro Asp Ser Leu Pro Pro Ser Pro Asp Arg His Ser Pro Leu Trp
171                 176                 181                 186

aac cca aat aaa gag tat gaa gat ctg ctt gac tat act tac cca ctg      628
Asn Pro Asn Lys Glu Tyr Glu Asp Leu Leu Asp Tyr Thr Tyr Pro Leu
187                 192                 197                 202

agg ccc ggg cct cag ctc cca aag cac ctt gat agc cgt gtg cca gct      676
Arg Pro Gly Pro Gln Leu Pro Lys His Leu Asp Ser Arg Val Pro Ala
203                 208                 213                 218

gac cct gtc ctg cag gac tcc ggg gta gac ctg gat agc ttc tct gtc      724
Asp Pro Val Leu Gln Asp Ser Gly Val Asp Leu Asp Ser Phe Ser Val
219                 224                 229                 234

tct cca gca agc acc ctc aaa tca cct act aat gtc tcc ccc aac tgc      772
Ser Pro Ala Ser Thr Leu Lys Ser Pro Thr Asn Val Ser Pro Asn Cys
235                 240                 245                 250

cca cca gca gag gcc act gcc ctg cca ttt tct ggg ccc aga gag cca      820
Pro Pro Ala Glu Ala Thr Ala Leu Pro Phe Ser Gly Pro Arg Glu Pro
251                 256                 261                 266

agc ctt aag cag tgg ccc tcc aga gta ccc cag aaa cag ggt ggc atg      868
Ser Leu Lys Gln Trp Pro Ser Arg Val Pro Gln Lys Gln Gly Gly Met
267                 272                 277                 282

ggc ttg gca tct tgg agc caa ctt gca tct acc ccc aga gcc cca ggc      916
Gly Leu Ala Ser Trp Ser Gln Leu Ala Ser Thr Pro Arg Ala Pro Gly
283                 288                 293                 298

agt agg gat gct cgt tgg gag cgc aga gag cca gcc ctg agg ggt gcg      964
Ser Arg Asp Ala Arg Trp Glu Arg Arg Glu Pro Ala Leu Arg Gly Ala
299                 304                 309                 314

aag gac cgg ctg act ata ggc aag cac ctt gat atg ggc tct ccc cag     1012
Lys Asp Arg Leu Thr Ile Gly Lys His Leu Asp Met Gly Ser Pro Gln
315                 320                 325                 330

cta agg aca cgg gac aga ggg tgg ccc tcg ccc agg cca gag agg gag     1060
Leu Arg Thr Arg Asp Arg Gly Trp Pro Ser Pro Arg Pro Glu Arg Glu
331                 336                 341                 346

aag agg acc agc cag agt gcc cgg cgc cct acc tgc aca gag tct agg     1108
Lys Arg Thr Ser Gln Ser Ala Arg Arg Pro Thr Cys Thr Glu Ser Arg
347                 352                 357                 362

tgg aaa tca gaa gag gaa gtg gaa agt gat gac gag tat ctt gcc ctc     1156
Trp Lys Ser Glu Glu Glu Val Glu Ser Asp Asp Glu Tyr Leu Ala Leu
363                 368                 373                 378

ccc gct cgg ctg aca cag gtt tct agc ctg gtt tcg tat cta gga tcc     1204
Pro Ala Arg Leu Thr Gln Val Ser Ser Leu Val Ser Tyr Leu Gly Ser
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Ile Ser Thr Leu Val Thr Leu Pro Thr Gly Asp Ile Lys Gly Gln Ser
395                 400                 405                 410

ccc ttg gaa gtg tca gac agt gat ggg cca gct tcc ttc cct tca agc     1300
Pro Leu Glu Val Ser Asp Ser Asp Gly Pro Ala Ser Phe Pro Ser Ser
411                 416                 421                 426

tcc agc caa agc cag ctt ccc agg aaa gga gga gaa cag gga aaa gaa     1348
Ser Ser Gln Ser Gln Leu Pro Arg Lys Gly Gly Glu Gln Gly Lys Glu
427                 432                 437                 442

tca ctg gtg caa tgt gtg aag aca ttt tgc tgt cag ctg gaa gag ctg     1396
Ser Leu Val Gln Cys Val Lys Thr Phe Cys Cys Gln Leu Glu Glu Leu
443                 448                 453                 458

atc tgc tgg ctg tat aat gtt gca gat gtt act gac cac ggg act gca     1444
Ile Cys Trp Leu Tyr Asn Val Ala Asp Val Thr Asp His Gly Thr Ala
459                 464                 469                 474

gcc agg tcc aat ctt aca agt ctc aag tct tct ctg cag ctt tac cgg     1492
Ala Arg Ser Asn Leu Thr Ser Leu Lys Ser Ser Leu Gln Leu Tyr Arg
475                 480                 485                 490

caa ttt aag aaa gat ata gat gaa cat cag tct ctg acg gag agt gtc     1540
Gln Phe Lys Lys Asp Ile Asp Glu His Gln Ser Leu Thr Glu Ser Val
491                 496                 501                 506

tta cag aag ggg gag att ctt ctt cag tgc ctg ttg gag aac acc cca     1588
Leu Gln Lys Gly Glu Ile Leu Leu Gln Cys Leu Leu Glu Asn Thr Pro
507                 512                 517                 522

gtt tta gag gat gtc ctt ggg agg atc gca aag cag tct ggt gag ctg     1636
Val Leu Glu Asp Val Leu Gly Arg Ile Ala Lys Gln Ser Gly Glu Leu
523                 528                 533                 538

gag agc cac gca gat cgc ctg tat gac tct atc ttg gcc tct ctg gac     1684
Glu Ser His Ala Asp Arg Leu Tyr Asp Ser Ile Leu Ala Ser Leu Asp
539                 544                 549                 554

atg ctg gct ggc tgc acc ctt atc cct gac aaa aag ccc atg gcg gca     1732
Met Leu Ala Gly Cys Thr Leu Ile Pro Asp Lys Lys Pro Met Ala Ala
555                 560                 565                 570

atg gag cac cca tgt gaa ggg gtt taa cctgg catcttctca ggcagaggtg     1784
Met Glu His Pro Cys Glu Gly Val  *
571                 576

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tcctccctga atggagggct gagttactat ttttatttac aatgaatcct tccaaactaa   1964

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ccacc    atg tcg atg gct gtg gaa acc ttt ggc ttc ttc atg gca act      767
         Met Ser Met Ala Val Glu Thr Phe Gly Phe Phe Met Ala Thr
           1               5                  10

gtg ggg ctg ctg atg ctg ggg gtg act ctg cca aac agc tac tgg cga      815
Val Gly Leu Leu Met Leu Gly Val Thr Leu Pro Asn Ser Tyr Trp Arg
 15                  20                  25                  30

gtg tcc act gtg cac ggg aac gtc atc acc acc aac acc atc ttc gag      863
Val Ser Thr Val His Gly Asn Val Ile Thr Thr Asn Thr Ile Phe Glu
 31                  36                  41                  46

aac ctc tgg ttt agc tgt gcc acc gac tcc ctg ggc gtc tac aac tgc      911
Asn Leu Trp Phe Ser Cys Ala Thr Asp Ser Leu Gly Val Tyr Asn Cys
 47                  52                  57                  62

tgg gag ttc ccg tcc atg ctg gcc ctc tct ggg tat att cag gcc tgc      959
Trp Glu Phe Pro Ser Met Leu Ala Leu Ser Gly Tyr Ile Gln Ala Cys
 63                  68                  73                  78

cgg gca ctc atg atc acc gcc atc ctc ctg ggc ttc ctc ggc ctc ttg     1007
Arg Ala Leu Met Ile Thr Ala Ile Leu Leu Gly Phe Leu Gly Leu Leu
 79                  84                  89                  94

cta ggc ata gcg ggc ctg cgc tgc acc aac att ggg ggc ctg gag ctc     1055
Leu Gly Ile Ala Gly Leu Arg Cys Thr Asn Ile Gly Gly Leu Glu Leu
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tcc agg aaa gcc aag ctg gcg gcc acc gca ggg gcc ctc cac att ctg     1103
Ser Arg Lys Ala Lys Leu Ala Ala Thr Ala Gly Ala Leu His Ile Leu
111                 116                 121                 126

gcc ggt atc tgc ggg atg gtg gcc atc tcc tgg tac gcc ttc aac atc     1151
Ala Gly Ile Cys Gly Met Val Ala Ile Ser Trp Tyr Ala Phe Asn Ile
127                 132                 137                 142

acc cgg gac ttc ttc gac ccc ttg tac ccc gga acc aag tac gag ctg     1199
Thr Arg Asp Phe Phe Asp Pro Leu Tyr Pro Gly Thr Lys Tyr Glu Leu
143                 148                 153                 158

ggc ccc gcc ctc tac ctg ggg tgg agc gcc tca ctg atc tcc atc ctg     1247
Gly Pro Ala Leu Tyr Leu Gly Trp Ser Ala Ser Leu Ile Ser Ile Leu
159                 164                 169                 174

ggt ggc ctc tgc ctc tgc tcc gcc tgc tgc tgc ggc tct gac gag gac     1295
Gly Gly Leu Cys Leu Cys Ser Ala Cys Cys Cys Gly Ser Asp Glu Asp
175                 180                 185                 190

cca gcc gcc agc gcc cgg cgg ccc tac cag gct ccc gtg tcc gtg atg     1343
Pro Ala Ala Ser Ala Arg Arg Pro Tyr Gln Ala Pro Val Ser Val Met
191                 196                 201                 206

ccc gtc gcc acc tcg gac caa gaa ggc gac agc agc ttt ggc aaa tac     1391
Pro Val Ala Thr Ser Asp Gln Glu Gly Asp Ser Ser Phe Gly Lys Tyr
207                 212                 217                 222

ggc aga aac gcc tac gtg tag ca gctctggccc gtgggccccg ctgtcttccc     1444
Gly Arg Asn Ala Tyr Val  *
223                 228

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                                                     Met Glu Arg
                                                       1

tct cca gga gag ggc ccc agc ccc agc ccc atg gac cag ccc tct gct      162
Ser Pro Gly Glu Gly Pro Ser Pro Ser Pro Met Asp Gln Pro Ser Ala
  4                   9                  14                  19

ccc tcc gac ccc act gac cag ccc ccc gct gct cac gca aag cca gac      210
Pro Ser Asp Pro Thr Asp Gln Pro Pro Ala Ala His Ala Lys Pro Asp
 20                  25                  30                  35

cca ggt tct ggg ggc caa cct gct ggc cct ggc gcg gcg ggt gag gcc      258
Pro Gly Ser Gly Gly Gln Pro Ala Gly Pro Gly Ala Ala Gly Glu Ala
 36                  41                  46                  51

ctg gcg gtg ctg act tca ttc ggg agg cgg ttg ctg gtg ctg ata cct      306
Leu Ala Val Leu Thr Ser Phe Gly Arg Arg Leu Leu Val Leu Ile Pro
 52                  57                  62                  67

gtg tat ttg gcc ggg gca gtg gga ctc agc gtg ggt ttc gtg ctc ttc      354
Val Tyr Leu Ala Gly Ala Val Gly Leu Ser Val Gly Phe Val Leu Phe
 68                  73                  78                  83

ggc ctc gcc ctc tac ctg ggc tgg cgc cgg gtc cgc gac gag aaa gaa      402
Gly Leu Ala Leu Tyr Leu Gly Trp Arg Arg Val Arg Asp Glu Lys Glu
 84                  89                  94                  99

cgg agc ctt cga gca gcg agg cag cta ctg gac gac gag gag cag ctc      450
Arg Ser Leu Arg Ala Ala Arg Gln Leu Leu Asp Asp Glu Glu Gln Leu
100                 105                 110                 115

act gcg aaa act ctc tat atg agt cat cga gag cta cct gcc tgg gtc      498
Thr Ala Lys Thr Leu Tyr Met Ser His Arg Glu Leu Pro Ala Trp Val
116                 121                 126                 131

agc ttc cca gac gtg gaa aag gct gaa tgg ctc aat aag att gtg gcc      546
Ser Phe Pro Asp Val Glu Lys Ala Glu Trp Leu Asn Lys Ile Val Ala
132                 137                 142                 147

cag gtc tgg ccc ttc ctg ggc cag tat atg gag aag ctt ctg gct gaa      594
Gln Val Trp Pro Phe Leu Gly Gln Tyr Met Glu Lys Leu Leu Ala Glu
148                 153                 158                 163

act gtg gct ccg gct gtt agg gga tct aac ccc cat ctg caa aca ttt      642
Thr Val Ala Pro Ala Val Arg Gly Ser Asn Pro His Leu Gln Thr Phe
164                 169                 174                 179

aca ttt aca cga gtg gaa ctg ggt gaa aag cca ttg cgc atc att gga      690
Thr Phe Thr Arg Val Glu Leu Gly Glu Lys Pro Leu Arg Ile Ile Gly
180                 185                 190                 195

gtc aag gtt cac cca ggt cag aga aaa gag cag atc ctg ctg gac ttg      738
Val Lys Val His Pro Gly Gln Arg Lys Glu Gln Ile Leu Leu Asp Leu
196                 201                 206                 211
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aac atc agc tat gta ggt gat gtg cag att gat gtg gaa gtg aag aaa      786
Asn Ile Ser Tyr Val Gly Asp Val Gln Ile Asp Val Glu Val Lys Lys
212                 217                 222                 227

tat ttt tgc aaa gca gga gtc aag ggc atg cag cta cat ggc gtt ttg      834
Tyr Phe Cys Lys Ala Gly Val Lys Gly Met Gln Leu His Gly Val Leu
228                 233                 238                 243

cgg gtg ata ctg gag cca ctc att ggg gac ctt ccc ttc gtg ggg gct      882
Arg Val Ile Leu Glu Pro Leu Ile Gly Asp Leu Pro Phe Val Gly Ala
244                 249                 254                 259

gtg tca atg ttc ttc atc cga cgc ccg acc cta gac atc aac tgg aca      930
Val Ser Met Phe Phe Ile Arg Arg Pro Thr Leu Asp Ile Asn Trp Thr
260                 265                 270                 275

ggg atg acc aac ctg ctg gat atc cca gga ctt agc tca ctc tct gac      978
Gly Met Thr Asn Leu Leu Asp Ile Pro Gly Leu Ser Ser Leu Ser Asp
276                 281                 286                 291

acc atg atc atg gac tcc att gct gcc ttc ctc gtg ttg ccc aac cga     1026
Thr Met Ile Met Asp Ser Ile Ala Ala Phe Leu Val Leu Pro Asn Arg
292                 297                 302                 307

tta ctg gtg ccc ctt gtg cct gac ctt caa gat gtg gct cag ttg cgt     1074
Leu Leu Val Pro Leu Val Pro Asp Leu Gln Asp Val Ala Gln Leu Arg
308                 313                 318                 323

tcc cct ctg ccc agg ggc att att cga att cac ctg ctg gct gct cga     1122
Ser Pro Leu Pro Arg Gly Ile Ile Arg Ile His Leu Leu Ala Ala Arg
324                 329                 334                 339

ggg ctg agt tcc aag gac aaa tat gtg aag ggc ctg att gag ggc aag     1170
Gly Leu Ser Ser Lys Asp Lys Tyr Val Lys Gly Leu Ile Glu Gly Lys
340                 345                 350                 355

tca gac cca tat gca ctt gtg cgt ttg ggt acc cag aca ttc tgc agt     1218
Ser Asp Pro Tyr Ala Leu Val Arg Leu Gly Thr Gln Thr Phe Cys Ser
356                 361                 366                 371

cgt gtc att gat gaa gaa ctc aac cca cag tgg gga gag act tat gag     1266
Arg Val Ile Asp Glu Glu Leu Asn Pro Gln Trp Gly Glu Thr Tyr Glu
372                 377                 382                 387

gtg atg gta cac gag gtc cca ggg cag gag att gaa gtg gag gtg ttc     1314
Val Met Val His Glu Val Pro Gly Gln Glu Ile Glu Val Glu Val Phe
388                 393                 398                 403

gac aag gat cca gat aaa gat gac ttt ctg ggc aga atg aag ctg gat     1362
Asp Lys Asp Pro Asp Lys Asp Asp Phe Leu Gly Arg Met Lys Leu Asp
404                 409                 414                 419

gta ggg aag gtg tta cag gct agc gtt ctg gat gat tgg ttc cct cta     1410
Val Gly Lys Val Leu Gln Ala Ser Val Leu Asp Asp Trp Phe Pro Leu
420                 425                 430                 435
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caa ggt ggg caa ggc caa gtt cac ttg agg cta gaa tgg ctg tca ctt 1458
Gln Gly Gly Gln Gly Gln Val His Leu Arg Leu Glu Trp Leu Ser Leu
436 441 446 451

ttg tca gat gca gag aaa ctg gag cag gtt cta cag tgg aat tgg gga 1506
Leu Ser Asp Ala Glu Lys Leu Glu Gln Val Leu Gln Trp Asn Trp Gly
452 457 462 467

gtc tcc tct cga cca gat ccc ccg tca gct gcc atc tta gtt gtc tac 1554
Val Ser Ser Arg Pro Asp Pro Pro Ser Ala Ala Ile Leu Val Val Tyr
468 473 478 483

ctg gat cgg gcc cag gat ctt cct atg gtg acc tct gaa ttg tac cca 1602
Leu Asp Arg Ala Gln Asp Leu Pro Met Val Thr Ser Glu Leu Tyr Pro
484 489 494 499

cca cag ctg aag aag ggg aac aag gaa ccc aac cct atg gta caa ctg 1650
Pro Gln Leu Lys Lys Gly Asn Lys Glu Pro Asn Pro Met Val Gln Leu
500 505 510 515

tca att cag gat gtg act cag gag agc aag gct gtc tac agt acc aac 1698
Ser Ile Gln Asp Val Thr Gln Glu Ser Lys Ala Val Tyr Ser Thr Asn
516 521 526 531

tgc cca gtg tgg gag gaa gcg ttc cgg ttc ttc cta caa gac cct caa 1746
Cys Pro Val Trp Glu Glu Ala Phe Arg Phe Phe Leu Gln Asp Pro Gln
532 537 542 547

agc cag gag ctc gat gtg caa gtg aag gat gat tcc agg gcc ctg act 1794
Ser Gln Glu Leu Asp Val Gln Val Lys Asp Asp Ser Arg Ala Leu Thr
548 553 558 563

tta gga gca ctg acg ctg cct ctg gcc cgc ctg ctg act gcc cca gaa 1842
Leu Gly Ala Leu Thr Leu Pro Leu Ala Arg Leu Leu Thr Ala Pro Glu
564 569 574 579

ctc atc ctg gac cag tgg ttc cag ctc agc agc tct ggt cca aac tcc 1890
Leu Ile Leu Asp Gln Trp Phe Gln Leu Ser Ser Ser Gly Pro Asn Ser
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aga ctc tat atg aaa cta gtc atg agg atc ctg tac ttg gat tca tca 1938
Arg Leu Tyr Met Lys Leu Val Met Arg Ile Leu Tyr Leu Asp Ser Ser
596 601 606 611

gaa ata tgc ttc ccc acg gtg cct ggt tgt cct ggt gct tgg gac gtg 1986
Glu Ile Cys Phe Pro Thr Val Pro Gly Cys Pro Gly Ala Trp Asp Val
612 617 622 627

gac agt gag aat ccc cag aga ggc agc agt gtg gat gcc cca cct cga 2034
Asp Ser Glu Asn Pro Gln Arg Gly Ser Ser Val Asp Ala Pro Pro Arg
628 633 638 643

ccc tgt cac acg act cct gat agc cag ttt ggg act gag cat gtg ctt 2082
Pro Cys His Thr Thr Pro Asp Ser Gln Phe Gly Thr Glu His Val Leu
644 649 654 659

cgg atc cat gta tta gag gcc cag gac ctg att gcc aaa gac cgt ttc 2130

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Arg Ile His Val Leu Glu Ala Gln Asp Leu Ile Ala Lys Asp Arg Phe
660                 665                 670                 675

ttg ggg gga ctg gtg aag ggc aag tca gac ccc tat gtc aaa cta aag     2178
Leu Gly Gly Leu Val Lys Gly Lys Ser Asp Pro Tyr Val Lys Leu Lys
676                 681                 686                 691

ttg gca gga cga agc ttc cgg agc cat gtt gtt cgg gaa gat ctc aat     2226
Leu Ala Gly Arg Ser Phe Arg Ser His Val Val Arg Glu Asp Leu Asn
692                 697                 702                 707

ccc cgc tgg aat gag gtt ttt gag gtg atc gtc aca tca gtt cca ggc     2274
Pro Arg Trp Asn Glu Val Phe Glu Val Ile Val Thr Ser Val Pro Gly
708                 713                 718                 723

caa gag cta gag gtt gaa gtc ttt gac aag gac ttg gac aag gat gat     2322
Gln Glu Leu Glu Val Glu Val Phe Asp Lys Asp Leu Asp Lys Asp Asp
724                 729                 734                 739

ttt ctg ggc agg tgt aaa gtg cgt ctc acc aca gtc tta aac agt ggc     2370
Phe Leu Gly Arg Cys Lys Val Arg Leu Thr Thr Val Leu Asn Ser Gly
740                 745                 750                 755

ttc ctt gat gag tgg ctg acc ctg gag gat gtc cca tct ggc cgc ctg     2418
Phe Leu Asp Glu Trp Leu Thr Leu Glu Asp Val Pro Ser Gly Arg Leu
756                 761                 766                 771

cac ttg cgc ctg gag cgt ctc acc ccc cgt ccc act gct gct gag tta     2466
His Leu Arg Leu Glu Arg Leu Thr Pro Arg Pro Thr Ala Ala Glu Leu
772                 777                 782                 787

gag gag gtg ctg cag gtg aat agt ttg atc cag act cag aag agt gcg     2514
Glu Glu Val Leu Gln Val Asn Ser Leu Ile Gln Thr Gln Lys Ser Ala
788                 793                 798                 803

gag ctg gct gcg gcc ctg cta tcc atc tat atg gag cgg gca gag gac     2562
Glu Leu Ala Ala Ala Leu Leu Ser Ile Tyr Met Glu Arg Ala Glu Asp
804                 809                 814                 819

ctc ccg ctg cga aaa ggc acc aag cac ctc agc cct tat gct act ctc     2610
Leu Pro Leu Arg Lys Gly Thr Lys His Leu Ser Pro Tyr Ala Thr Leu
820                 825                 830                 835

act gtg gga gat agt tct cat aaa acc aag act att tcg caa act tca     2658
Thr Val Gly Asp Ser Ser His Lys Thr Lys Thr Ile Ser Gln Thr Ser
836                 841                 846                 851

gcc cct gtc tgg gat gag agt gcc tcc ttt ctc atc agg aaa cca cac     2706
Ala Pro Val Trp Asp Glu Ser Ala Ser Phe Leu Ile Arg Lys Pro His
852                 857                 862                 867

act gag agc cta gag ttg cag gtt cgg ggt gag ggc act ggc gtg ctg     2754
Thr Glu Ser Leu Glu Leu Gln Val Arg Gly Glu Gly Thr Gly Val Leu
868                 873                 878                 883

ggc tca tta tcc ctg ccc ctc tca gag ctc ctc gtg gct gac cag ctc     2802
Gly Ser Leu Ser Leu Pro Leu Ser Glu Leu Leu Val Ala Asp Gln Leu
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884                 889                 894                 899

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Cys Leu Asp Arg Trp Phe Thr Leu Ser Ser Gly Gln Gly Gln Val Leu
900                 905                 910                 915

ctg aga gca cag cta ggg atc ctg gtg tcc cag cac tcg gga gtg gaa     2898
Leu Arg Ala Gln Leu Gly Ile Leu Val Ser Gln His Ser Gly Val Glu
916                 921                 926                 931

gct cat agc cac agc tac agc cac agc tcc tca tcg ctg agt gaa gaa     2946
Ala His Ser His Ser Tyr Ser His Ser Ser Ser Ser Leu Ser Glu Glu
932                 937                 942                 947

cca gag ctc tcg ggg gga ccc cct cac atc acc tcc tca gcc cca gag     2994
Pro Glu Leu Ser Gly Gly Pro Pro His Ile Thr Ser Ser Ala Pro Glu
948                 953                 958                 963

ctc cgg cag cgc cta aca cat gtt gac agt ccc ctt gag gct cca gcc     3042
Leu Arg Gln Arg Leu Thr His Val Asp Ser Pro Leu Glu Ala Pro Ala
964                 969                 974                 979

ggg cct ctg ggc cag gtg aaa ctg act ctg tgg tac tac agt gaa gaa     3090
Gly Pro Leu Gly Gln Val Lys Leu Thr Leu Trp Tyr Tyr Ser Glu Glu
980                 985                 990                 995

cga aag ctg gtc agc att gtt cat ggt tgc cgg tcc ctt cga cag aat     3138
Arg Lys Leu Val Ser Ile Val His Gly Cys Arg Ser Leu Arg Gln Asn
996                1001                1006                1011

gga cgt gat cct cct gat ccc tat gtg tca ctg ttg cta ctg cca gac     3186
Gly Arg Asp Pro Pro Asp Pro Tyr Val Ser Leu Leu Leu Leu Pro Asp
1012                1017                1022                1027

aag aac cga ggc acc aag agg agg acc tca cag aag aag agg acc ctg     3234
Lys Asn Arg Gly Thr Lys Arg Arg Thr Ser Gln Lys Lys Arg Thr Leu
1028                1033                1038                1043

agt cct gaa ttt aat gaa cgg ttt gag tgg gaa ctc ccc ctg gat gag     3282
Ser Pro Glu Phe Asn Glu Arg Phe Glu Trp Glu Leu Pro Leu Asp Glu
1044                1049                1054                1059

gcc cag aga cga aag ctg gat gtc tct gtc aag tct aat tcc tcc ttc     3330
Ala Gln Arg Arg Lys Leu Asp Val Ser Val Lys Ser Asn Ser Ser Phe
1060                1065                1070                1075

atg tca aga gag cgt gag ctg ctg ggg aag gtg cag ctg gac cta gct     3378
Met Ser Arg Glu Arg Glu Leu Leu Gly Lys Val Gln Leu Asp Leu Ala
1076                1081                1086                1091

gag aca gac ctt tcc cag ggt gta gcc cgg tgg tat gac ctg atg gac     3426
Glu Thr Asp Leu Ser Gln Gly Val Ala Arg Trp Tyr Asp Leu Met Asp
1092                1097                1102                1107

aac aag gac aag ggc agc tcc tag gagctggcga gtcccagcct gactgctctg    3480
Asn Lys Asp Lys Gly Ser Ser  *
1108                1113
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cctgaccaaa gagaagaacc gtatgttccc tttactgcac ggcctttatc cttctgggcc   3660

cctggggcgg ggacctgagc tggctgtttc ctgctttgcc tgcacattgt tctcccttcc   3720

tcccaactcc tcagggcctt ctgtatctgt gcctggccag tggcagcact agcagtggta   3780

ttagcttatg ccaaatacag ctttggaagg atctttttt ctttaactag atggtcacct   3840

tcttccctac cacacatggg tgggaaggtg gacaggctaa cctctccagc tgtgagcctc   3900

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tcttggagct cctagctggt gatacggaga gggctttgga ggacttggga cagcagggcc   4140

aatttttttg cccaagtgcc taggctgcta actcactgac tagaacttaa tctggtactt   4200

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                                                     Met Glu Arg
                                                       1

tct cca gga gag ggc ccc agc ccc agc ccc atg gac cag ccc tct gct     162
Ser Pro Gly Glu Gly Pro Ser Pro Ser Pro Met Asp Gln Pro Ser Ala
  4                   9                  14                  19

ccc tcc gac ccc act gac cag ccc ccc gct gct cac gca aag cca gac     210
Pro Ser Asp Pro Thr Asp Gln Pro Pro Ala Ala His Ala Lys Pro Asp
 20                  25                  30                  35

cca ggt tct ggg ggc caa cct gct ggc cct ggc gcg gcg ggt gag gcc     258
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Pro Gly Ser Gly Gly Gln Pro Ala Gly Pro Gly Ala Ala Gly Glu Ala
 36                  41                  46                  51

ctg gcg gtg ctg act tca ttc ggg agg cgg ttg ctg gtg ctg ata cct      306
Leu Ala Val Leu Thr Ser Phe Gly Arg Arg Leu Leu Val Leu Ile Pro
 52                  57                  62                  67

gtg tat ttg gcc ggg gca gtg gga ctc agc gtg ggt ttc gtg ctc ttc      354
Val Tyr Leu Ala Gly Ala Val Gly Leu Ser Val Gly Phe Val Leu Phe
 68                  73                  78                  83

ggc ctc gcc ctc tac ctg ggc tgg cgc cgg gtc cgc gac gag aaa gaa      402
Gly Leu Ala Leu Tyr Leu Gly Trp Arg Arg Val Arg Asp Glu Lys Glu
 84                  89                  94                  99

cgg agc ctt cga gca gcg agg cag cta ctg gac gac gag gag cag ctc      450
Arg Ser Leu Arg Ala Ala Arg Gln Leu Leu Asp Asp Glu Glu Gln Leu
100                 105                 110                 115

act gcg aaa act ctc tat atg agt cat cga gag cta cct gcc tgg gtc      498
Thr Ala Lys Thr Leu Tyr Met Ser His Arg Glu Leu Pro Ala Trp Val
116                 121                 126                 131

agc ttc cca gac gtg gaa aag gct gaa tgg ctc aat aag att gtg gcc      546
Ser Phe Pro Asp Val Glu Lys Ala Glu Trp Leu Asn Lys Ile Val Ala
132                 137                 142                 147

cag gtc tgg ccc ttc ctg ggc cag tat atg gag aag ctt ctg gct gaa      594
Gln Val Trp Pro Phe Leu Gly Gln Tyr Met Glu Lys Leu Leu Ala Glu
148                 153                 158                 163

act gtg gct ccg gct gtt agg gga tct aac ccc cat ctg caa aca ttt      642
Thr Val Ala Pro Ala Val Arg Gly Ser Asn Pro His Leu Gln Thr Phe
164                 169                 174                 179

aca ttt aca cga gtg gaa ctg ggt gaa aag cca ttg cgc atc att gga      690
Thr Phe Thr Arg Val Glu Leu Gly Glu Lys Pro Leu Arg Ile Ile Gly
180                 185                 190                 195

gtc aag gtt cac cca ggt cag aga aaa gag cag atc ctg ctg gac ttg      738
Val Lys Val His Pro Gly Gln Arg Lys Glu Gln Ile Leu Leu Asp Leu
196                 201                 206                 211

aac atc agc tat gta ggt gat gtg cag att gat gtg gaa gtg aag aaa      786
Asn Ile Ser Tyr Val Gly Asp Val Gln Ile Asp Val Glu Val Lys Lys
212                 217                 222                 227

tat ttt tgc aaa gca gga gtc aag ggc atg cag cta cat ggc gtt ttg      834
Tyr Phe Cys Lys Ala Gly Val Lys Gly Met Gln Leu His Gly Val Leu
228                 233                 238                 243

cgg gtg ata ctg gag cca ctc att ggg gac ctt ccc ttc gtg ggg gct      882
Arg Val Ile Leu Glu Pro Leu Ile Gly Asp Leu Pro Phe Val Gly Ala
244                 249                 254                 259

gtg tca atg ttc ttc atc cga cgc ccg acc cta gac atc aac tgg aca      930
Val Ser Met Phe Phe Ile Arg Arg Pro Thr Leu Asp Ile Asn Trp Thr
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260                 265                 270                 275

ggg atg acc aac ctg ctg gat atc cca gga ctt agc tca ctc tct gac      978
Gly Met Thr Asn Leu Leu Asp Ile Pro Gly Leu Ser Ser Leu Ser Asp
276                 281                 286                 291

acc atg atc atg gac tcc att gct gcc ttc ctc gtg ttg ccc aac cga     1026
Thr Met Ile Met Asp Ser Ile Ala Ala Phe Leu Val Leu Pro Asn Arg
292                 297                 302                 307

tta ctg gtg ccc ctt gtg cct gac ctt caa gat gtg gct cag ttg cgt     1074
Leu Leu Val Pro Leu Val Pro Asp Leu Gln Asp Val Ala Gln Leu Arg
308                 313                 318                 323

tcc cct ctg ccc agg ggc att att cga att cac ctg ctg gct gct cga     1122
Ser Pro Leu Pro Arg Gly Ile Ile Arg Ile His Leu Leu Ala Ala Arg
324                 329                 334                 339

ggg ctg agt tcc aag gac aaa tat gtg aag ggc ctg att gag ggc aag     1170
Gly Leu Ser Ser Lys Asp Lys Tyr Val Lys Gly Leu Ile Glu Gly Lys
340                 345                 350                 355

tca gac cca tat gca ctt gtg cgt ttg ggt acc cag aca ttc tgc agt     1218
Ser Asp Pro Tyr Ala Leu Val Arg Leu Gly Thr Gln Thr Phe Cys Ser
356                 361                 366                 371

cgt gtc att gat gaa gaa ctc aac cca cag tgg gga gag act tat gag     1266
Arg Val Ile Asp Glu Glu Leu Asn Pro Gln Trp Gly Glu Thr Tyr Glu
372                 377                 382                 387

gtg atg gta cac gag gtc cca ggg cag gag att gaa gtg gag gtg ttc     1314
Val Met Val His Glu Val Pro Gly Gln Glu Ile Glu Val Glu Val Phe
388                 393                 398                 403

gac aag gat cca gat aaa gat gac ttt ctg ggc aga atg aag ctg gat     1362
Asp Lys Asp Pro Asp Lys Asp Asp Phe Leu Gly Arg Met Lys Leu Asp
404                 409                 414                 419

gta ggg aag gtg tta cag gct agc gtt ctg gat gat tgg ttc cct cta     1410
Val Gly Lys Val Leu Gln Ala Ser Val Leu Asp Asp Trp Phe Pro Leu
420                 425                 430                 435

caa ggt ggg caa ggc caa gtt cac ttg agg cta gaa tgg ctg tca ctt     1458
Gln Gly Gly Gln Gly Gln Val His Leu Arg Leu Glu Trp Leu Ser Leu
436                 441                 446                 451

ttg tca gat gca gag aaa ctg gag cag gtt cta cag tgg aat tgg gga     1506
Leu Ser Asp Ala Glu Lys Leu Glu Gln Val Leu Gln Trp Asn Trp Gly
452                 457                 462                 467

gtc tcc tct cga cca gat ccc ccg tca gct gcc atc tta gtt gtc tac     1554
Val Ser Ser Arg Pro Asp Pro Pro Ser Ala Ala Ile Leu Val Val Tyr
468                 473                 478                 483

ctg gat cgg gcc cag gat ctt cct ctg aag aag ggg aac aag gaa ccc     1602
Leu Asp Arg Ala Gln Asp Leu Pro Leu Lys Lys Gly Asn Lys Glu Pro
484                 489                 494                 499
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aac cct atg gta caa ctg tca att cag gat gtg act cag gag agc aag     1650
Asn Pro Met Val Gln Leu Ser Ile Gln Asp Val Thr Gln Glu Ser Lys
500                 505                 510                 515

gct gtc tac agt acc aac tgc cca gtg tgg gag gaa gcg ttc cgg ttc     1698
Ala Val Tyr Ser Thr Asn Cys Pro Val Trp Glu Glu Ala Phe Arg Phe
516                 521                 526                 531

ttc cta caa gac cct caa agc cag gag ctc gat gtg caa gtg aag gat     1746
Phe Leu Gln Asp Pro Gln Ser Gln Glu Leu Asp Val Gln Val Lys Asp
532                 537                 542                 547

gat tcc agg gcc ctg act tta gga gca ctg acg ctg cct ctg gcc cgc     1794
Asp Ser Arg Ala Leu Thr Leu Gly Ala Leu Thr Leu Pro Leu Ala Arg
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ctg ctg act gcc cca gaa ctc atc ctg gac cag tgg ttc cag ctc agc     1842
Leu Leu Thr Ala Pro Glu Leu Ile Leu Asp Gln Trp Phe Gln Leu Ser
564                 569                 574                 579

agc tct ggt cca aac tcc aga ctc tat atg aaa cta gtc atg agg atc     1890
Ser Ser Gly Pro Asn Ser Arg Leu Tyr Met Lys Leu Val Met Arg Ile
580                 585                 590                 595

ctg tac ttg gat tca tca gaa ata tgc ttc ccc acg gtg cct ggt tgt     1938
Leu Tyr Leu Asp Ser Ser Glu Ile Cys Phe Pro Thr Val Pro Gly Cys
596                 601                 606                 611

cct ggt gct tgg gac gtg gac agt gag aat ccc cag aga ggc agc agt     1986
Pro Gly Ala Trp Asp Val Asp Ser Glu Asn Pro Gln Arg Gly Ser Ser
612                 617                 622                 627

gtg gat gcc cca cct cga ccc tgt cac acg act cct gat agc cag ttt     2034
Val Asp Ala Pro Pro Arg Pro Cys His Thr Thr Pro Asp Ser Gln Phe
628                 633                 638                 643

ggg act gag cat gtg ctt cgg atc cat gta tta gag gcc cag gac ctg     2082
Gly Thr Glu His Val Leu Arg Ile His Val Leu Glu Ala Gln Asp Leu
644                 649                 654                 659

att gcc aaa gac cgt ttc ttg ggg gga ctg gtg aag ggc aag tca gac     2130
Ile Ala Lys Asp Arg Phe Leu Gly Gly Leu Val Lys Gly Lys Ser Asp
660                 665                 670                 675

ccc tat gtc aaa cta aag ttg gca gga cga agc ttc cgg agc cat gtt     2178
Pro Tyr Val Lys Leu Lys Leu Ala Gly Arg Ser Phe Arg Ser His Val
676                 681                 686                 691

gtt cgg gaa gat ctc aat ccc cgc tgg aat gag gtt ttt gag gtg atc     2226
Val Arg Glu Asp Leu Asn Pro Arg Trp Asn Glu Val Phe Glu Val Ile
692                 697                 702                 707

gtc aca tca gtt cca ggc caa gag cta gag gtt gaa gtc ttt gac aag     2274
Val Thr Ser Val Pro Gly Gln Glu Leu Glu Val Glu Val Phe Asp Lys
708                 713                 718                 723
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gac ttg gac aag gat gat ttt ctg ggc agg tgt aaa gtg cgt ctc acc     2322
Asp Leu Asp Lys Asp Asp Phe Leu Gly Arg Cys Lys Val Arg Leu Thr
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aca gtc tta aac agt ggc ttc ctt gat gag tgg ctg acc ctg gag gat     2370
Thr Val Leu Asn Ser Gly Phe Leu Asp Glu Trp Leu Thr Leu Glu Asp
740                 745                 750                 755

gtc cca tct ggc cgc ctg cac ttg cgc ctg gag cgt ctc acc ccc cgt     2418
Val Pro Ser Gly Arg Leu His Leu Arg Leu Glu Arg Leu Thr Pro Arg
756                 761                 766                 771

ccc act gct gct gag tta gag gag gtg ctg cag gtg aat agt ttg atc     2466
Pro Thr Ala Ala Glu Leu Glu Glu Val Leu Gln Val Asn Ser Leu Ile
772                 777                 782                 787

cag act cag aag agt gcg gag ctg gct gcg gcc ctg cta tcc atc tat     2514
Gln Thr Gln Lys Ser Ala Glu Leu Ala Ala Ala Leu Leu Ser Ile Tyr
788                 793                 798                 803

atg gag cgg gca gag gac ctc ccg ctg cga aaa ggc acc aag cac ctc     2562
Met Glu Arg Ala Glu Asp Leu Pro Leu Arg Lys Gly Thr Lys His Leu
804                 809                 814                 819

agc cct tat gct act ctc act gtg gga gat agt tct cat aaa acc aag     2610
Ser Pro Tyr Ala Thr Leu Thr Val Gly Asp Ser Ser His Lys Thr Lys
820                 825                 830                 835

act att tcg caa act tca gcc cct gtc tgg gat gag agt gcc tcc ttt     2658
Thr Ile Ser Gln Thr Ser Ala Pro Val Trp Asp Glu Ser Ala Ser Phe
836                 841                 846                 851

ctc atc agg aaa cca cac act gag agc cta gag ttg cag gtt cgg ggt     2706
Leu Ile Arg Lys Pro His Thr Glu Ser Leu Glu Leu Gln Val Arg Gly
852                 857                 862                 867

gag ggc act ggc gtg ctg ggc tca tta tcc ctg ccc ctc tca gag ctc     2754
Glu Gly Thr Gly Val Leu Gly Ser Leu Ser Leu Pro Leu Ser Glu Leu
868                 873                 878                 883

ctc gtg gct gac cag ctc tgc ttg gac cgc tgg ttt aca ctc agc agt     2802
Leu Val Ala Asp Gln Leu Cys Leu Asp Arg Trp Phe Thr Leu Ser Ser
884                 889                 894                 899

ggt cag ggg cag gtg cta ctg aga gca cag cta ggg atc ctg gtg tcc     2850
Gly Gln Gly Gln Val Leu Leu Arg Ala Gln Leu Gly Ile Leu Val Ser
900                 905                 910                 915

cag cac tcg gga gtg gaa gct cat agc cac agc tac agc cac agc tcc     2898
Gln His Ser Gly Val Glu Ala His Ser His Ser Tyr Ser His Ser Ser
916                 921                 926                 931

tca tcg ctg agt gaa gaa cca gag ctc tcg ggg gga ccc cct cac atc     2946
Ser Ser Leu Ser Glu Glu Pro Glu Leu Ser Gly Gly Pro Pro His Ile
932                 937                 942                 947

acc tcc tca gcc cca gag ctc cgg cag cgc cta aca cat gtt gac agt     2994
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Thr Ser Ser Ala Pro Glu Leu Arg Gln Arg Leu Thr His Val Asp Ser
948                 953                 958                 963

ccc ctt gag gct cca gcc ggg cct ctg ggc cag gtg aaa ctg act ctg     3042
Pro Leu Glu Ala Pro Ala Gly Pro Leu Gly Gln Val Lys Leu Thr Leu
964                 969                 974                 979

tgg tac tac agt gaa gaa cga aag ctg gtc agc att gtt cat ggt tgc     3090
Trp Tyr Tyr Ser Glu Glu Arg Lys Leu Val Ser Ile Val His Gly Cys
980                 985                 990                 995

cgg tcc ctt cga cag aat gga cgt gat cct cct gat ccc tat gtg tca     3138
Arg Ser Leu Arg Gln Asn Gly Arg Asp Pro Pro Asp Pro Tyr Val Ser
996                1001                1006                1011

ctg ttg cta ctg cca gac aag aac cga ggc acc aag agg agg acc tca     3186
Leu Leu Leu Leu Pro Asp Lys Asn Arg Gly Thr Lys Arg Arg Thr Ser
1012                1017                1022                1027

cag aag aag agg acc ctg agt cct gaa ttt aat gaa cgg ttt gag tgg     3234
Gln Lys Lys Arg Thr Leu Ser Pro Glu Phe Asn Glu Arg Phe Glu Trp
1028                1033                1038                1043

gaa ctc ccc ctg gat gag gcc cag aga cga aag ctg gat gtc tct gtc     3282
Glu Leu Pro Leu Asp Glu Ala Gln Arg Arg Lys Leu Asp Val Ser Val
1044                1049                1054                1059

aag tct aat tcc tcc ttc atg tca aga gag cgt gag ctg ctg ggg aag     3330
Lys Ser Asn Ser Ser Phe Met Ser Arg Glu Arg Glu Leu Leu Gly Lys
1060                1065                1070                1075

gtg cag ctg gac cta gct gag aca gac ctt tcc cag ggt gta gcc cgg     3378
Val Gln Leu Asp Leu Ala Glu Thr Asp Leu Ser Gln Gly Val Ala Arg
1076                1081                1086                1091

tgg tat gac ctg atg gac aac aag gac aag ggc agc tcc tag gagctgg     3427
Trp Tyr Asp Leu Met Asp Asn Lys Asp Lys Gly Ser Ser  *
1092                1097                1102

cgagtcccag cctgactgct ctgtcttcct gccttcgtct cgctccatca ccgcctcaat   3487

gtgatgagcc taaagctagg gtccaagggc agagcctgtg cccttcagcc ctttcaccta   3547

acaggcccat attcgggcct ttgcctgacc aaagagaaga accgtatgtt ccctttactg   3607

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tttctttaac tagatggtca ccttcttccc taccacacat gggtgggaag gtggacaggc   3847

taacctctcc agctgtgagc ctcttagact actgcatgta gcaaatgttc agcagctcag   3907

gcccccatgt ccagttctgt ccccactgtc ctcaaccctg tcctgaaaat tctactgctt   3967
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tgatggctgg ggccagtctc ttgtcacttt ggaaactgag gacgcgtgga ttctactcaa   4027

gcctccaagt agtggcatat cagtcttgga gctcctagct ggtgatacgg agagggcttt   4087

ggaggacttg ggacagcagg gccaattttt ttgcccaagt gcctaggctg ctaactcact   4147

gactagaact taatctggta ctttacagtt ttgcaccaac tctgccaagc cactggatct   4207

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cagttgcagc ggccggggaa g  atg gtg gag gac ggc gcg gag gag ctg gag      171
                          Met Val Glu Asp Gly Ala Glu Glu Leu Glu
                            1               5

gat ctg gtg cac ttc tcc gtg tct gag ttg cct agt cgc ggc tac ggc      219
Asp Leu Val His Phe Ser Val Ser Glu Leu Pro Ser Arg Gly Tyr Gly
 11                  16                  21                  26

gtc atg gag gag atc cgg cgg cag ggc aag ctg tgc gac gtg acc ctc      267
Val Met Glu Glu Ile Arg Arg Gln Gly Lys Leu Cys Asp Val Thr Leu
 27                  32                  37                  42

aag att ggg gac cac aaa ttc agt gcc cac cgg att gtc tta gca gcc      315
Lys Ile Gly Asp His Lys Phe Ser Ala His Arg Ile Val Leu Ala Ala
 43                  48                  53                  58

tcg atc ccg tat ttc cat gct atg ttt aca aat gac atg atg gag tgc      363
Ser Ile Pro Tyr Phe His Ala Met Phe Thr Asn Asp Met Met Glu Cys
 59                  64                  69                  74

aag cag gat gag att gta atg caa gga atg gac cca agt gcc ctg gag      411
Lys Gln Asp Glu Ile Val Met Gln Gly Met Asp Pro Ser Ala Leu Glu
 75                  80                  85                  90

gct ctg atc aac ttt gcc tac aac ggc aac ctt gcc att gac cag caa      459
Ala Leu Ile Asn Phe Ala Tyr Asn Gly Asn Leu Ala Ile Asp Gln Gln
 91                  96                 101                 106

aat gtc cag tca ttg ctg atg ggg gcg agc ttc ctg cag ctg cag agc      507
Asn Val Gln Ser Leu Leu Met Gly Ala Ser Phe Leu Gln Leu Gln Ser
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107                 112                 117                 122

atc aaa gac gcc tgc tgc aca ttc ctt cga gaa cgg ctt cac cca aaa      555
Ile Lys Asp Ala Cys Cys Thr Phe Leu Arg Glu Arg Leu His Pro Lys
123                 128                 133                 138

aac tgc ctg ggt gtg cgc cag ttt gct gag aca atg atg tgt gct gtg      603
Asn Cys Leu Gly Val Arg Gln Phe Ala Glu Thr Met Met Cys Ala Val
139                 144                 149                 154

ctg tac gac gct gcc aac agc ttc atc cac cag cac ttt gtg gag gtg      651
Leu Tyr Asp Ala Ala Asn Ser Phe Ile His Gln His Phe Val Glu Val
155                 160                 165                 170

tcc atg tca gaa gag ttc ctg gcc ctg ccc ttg gaa gac gtg ctt gag      699
Ser Met Ser Glu Glu Phe Leu Ala Leu Pro Leu Glu Asp Val Leu Glu
171                 176                 181                 186

ctg gtg tct cgg gat gag ctg aat gtc aaa tct gag gag cag gtc ttt      747
Leu Val Ser Arg Asp Glu Leu Asn Val Lys Ser Glu Glu Gln Val Phe
187                 192                 197                 202

gaa gct gca ttg gcc tgg gtc aga tac gac cgg gag cag agg ggt ccc      795
Glu Ala Ala Leu Ala Trp Val Arg Tyr Asp Arg Glu Gln Arg Gly Pro
203                 208                 213                 218

tac ctg cct gag ctg ctg tcc aat atc cgc ctg ccc ctc tgt cgg ccc      843
Tyr Leu Pro Glu Leu Leu Ser Asn Ile Arg Leu Pro Leu Cys Arg Pro
219                 224                 229                 234

cag ttc ctt tca gac aga gta cag cag gat gac ctg gtg cgt tgc tgc      891
Gln Phe Leu Ser Asp Arg Val Gln Gln Asp Asp Leu Val Arg Cys Cys
235                 240                 245                 250

cac aaa tgc agg gac ctg gta gac gaa gca aag gac tac cac ctc atg      939
His Lys Cys Arg Asp Leu Val Asp Glu Ala Lys Asp Tyr His Leu Met
251                 256                 261                 266

cca gag cgc cgg ccc cac ctg cca gct ttc aga acc cgg cca cgc tgc      987
Pro Glu Arg Arg Pro His Leu Pro Ala Phe Arg Thr Arg Pro Arg Cys
267                 272                 277                 282

tgc aca tcc atc gct gga ctt atc tac gct gta ggg ggc ctc aac tca     1035
Cys Thr Ser Ile Ala Gly Leu Ile Tyr Ala Val Gly Gly Leu Asn Ser
283                 288                 293                 298

gca ggt gat tcc ctg aat gtg gtg gaa gtg ttc gac ccc att gcc aat     1083
Ala Gly Asp Ser Leu Asn Val Val Glu Val Phe Asp Pro Ile Ala Asn
299                 304                 309                 314

tgc tgg gag aga tgc cgt ccc atg aca aca gcc cgc agc cgc gtt ggc     1131
Cys Trp Glu Arg Cys Arg Pro Met Thr Thr Ala Arg Ser Arg Val Gly
315                 320                 325                 330

gtg gct gtg gtg aac ggg ctt ctc tat gcc atc gga gga tat gac ggc     1179
Val Ala Val Val Asn Gly Leu Leu Tyr Ala Ile Gly Gly Tyr Asp Gly
331                 336                 341                 346
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cag cta cgg ctg agc act gtg gag gcc tac aac ccg gag aca gac aca     1227
Gln Leu Arg Leu Ser Thr Val Glu Ala Tyr Asn Pro Glu Thr Asp Thr
347                 352                 357                 362

tgg acc aga gtg ggg agc atg aat agc aag aga agt gcc atg ggg aca     1275
Trp Thr Arg Val Gly Ser Met Asn Ser Lys Arg Ser Ala Met Gly Thr
363                 368                 373                 378

gtc gtg ctg gat ggg cag atc tac gtc tgt ggg ggc tac gat ggc aac     1323
Val Val Leu Asp Gly Gln Ile Tyr Val Cys Gly Gly Tyr Asp Gly Asn
379                 384                 389                 394

tct tcc ctc agc tcc gtg gag acc tac tca cct gag acg gac aaa tgg     1371
Ser Ser Leu Ser Ser Val Glu Thr Tyr Ser Pro Glu Thr Asp Lys Trp
395                 400                 405                 410

aca gtg gtg acc tcg atg agc tcg aat cgc agt gct gct ggg gtt aca     1419
Thr Val Val Thr Ser Met Ser Ser Asn Arg Ser Ala Ala Gly Val Thr
411                 416                 421                 426

gtc ttt gag ggc agg ata tat gtg tca ggc ggc cat gat ggt ttg cag     1467
Val Phe Glu Gly Arg Ile Tyr Val Ser Gly Gly His Asp Gly Leu Gln
427                 432                 437                 442

atc ttc agc agt gtg gaa cac tac aac cac cac aca gcc acc tgg cac     1515
Ile Phe Ser Ser Val Glu His Tyr Asn His His Thr Ala Thr Trp His
443                 448                 453                 458

cct gca gct ggc atg ctc aac aag cgc tgc cgg cac gga gcc gcc tcc     1563
Pro Ala Ala Gly Met Leu Asn Lys Arg Cys Arg His Gly Ala Ala Ser
459                 464                 469                 474

ctg ggg agc aag atg ttt gtc tgc ggg ggc tac gat ggc tct ggc ttc     1611
Leu Gly Ser Lys Met Phe Val Cys Gly Gly Tyr Asp Gly Ser Gly Phe
475                 480                 485                 490

ctc agc att gcc gag atg tac agc tct gtg gca gac cag tgg tgc ctg     1659
Leu Ser Ile Ala Glu Met Tyr Ser Ser Val Ala Asp Gln Trp Cys Leu
491                 496                 501                 506

att gtc ccc atg cac acg cgc agg agc cgg gtc tcc ctg gtg gcc agc     1707
Ile Val Pro Met His Thr Arg Arg Ser Arg Val Ser Leu Val Ala Ser
507                 512                 517                 522

tgt ggg cgc ctc tac gct gtt ggg ggc tac gac gga cag tca aac cta     1755
Cys Gly Arg Leu Tyr Ala Val Gly Gly Tyr Asp Gly Gln Ser Asn Leu
523                 528                 533                 538

agc tca gtg gag atg tat gac cca gag aca gac tgc tgg aca ttc atg     1803
Ser Ser Val Glu Met Tyr Asp Pro Glu Thr Asp Cys Trp Thr Phe Met
539                 544                 549                 554

gcc ccc atg gcg tgc cat gag gga ggg gtc ggt gtg ggc tgc atc cct     1851
Ala Pro Met Ala Cys His Glu Gly Gly Val Gly Val Gly Cys Ile Pro
555                 560                 565                 570
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ctc ctc acc atc taa ggcagaggat gggatgtggt ggggcaggga tctggtacag 1906
Leu Leu Thr Ile *
571

acataggcgc ttccttccag gaacagtccc tcaggagagg cagtggacca gaagagatgg 1966

cgaaacgtga gctcgccgga ggtacagttt ttccaggtgc ttaagccctc ccccactgtg 2026

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ggaaagattt catattgctt cctcctccct ggataggacc taatgtagca cagcgggact 3466

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gatcttgttc agatcatcat catcgtggtg gtg atg atg gtg atg gtg gtg gtg     174
                                    Met Met Val Met Val Val Val
                                      1               5

atc acg tgc ctg ctg agc cac tac aag ctg tct gca cgg tcc ttc atc      222
Ile Thr Cys Leu Leu Ser His Tyr Lys Leu Ser Ala Arg Ser Phe Ile
  8                  13                  18                  23

agc cgg cac agc cag ggg cgg agg aga gaa gat gcc ctg tcc tca gaa      270
Ser Arg His Ser Gln Gly Arg Arg Arg Glu Asp Ala Leu Ser Ser Glu
 24                  29                  34                  39

gga tgc ctg tgg ccc tcg gag agc aca gtg tca ggc aac gga atc cca      318
Gly Cys Leu Trp Pro Ser Glu Ser Thr Val Ser Gly Asn Gly Ile Pro
 40                  45                  50                  55

gag ccg cag gtc tac gcc ccg cct cgg ccc acc gac cgc ctg gcc gtg      366
Glu Pro Gln Val Tyr Ala Pro Pro Arg Pro Thr Asp Arg Leu Ala Val
 56                  61                  66                  71

ccg ccc ttc gcc cag cgg gag cgc ttc cac cgc ttc cag ccc acc tat      414
Pro Pro Phe Ala Gln Arg Glu Arg Phe His Arg Phe Gln Pro Thr Tyr
 72                  77                  82                  87

ccg tac ctg cag cac gag atc gac ctg cca ccc acc atc tcg ctg tca      462
Pro Tyr Leu Gln His Glu Ile Asp Leu Pro Pro Thr Ile Ser Leu Ser
 88                  93                  98                 103

gac ggg gag gag ccc cca ccc tac cag ggc ccc tgc acc ctc cag ctt      510
Asp Gly Glu Glu Pro Pro Pro Tyr Gln Gly Pro Cys Thr Leu Gln Leu
104                 109                 114                 119

cgg gac ccc gag cag cag ctg gaa ctg aac cgg gag tcg gtg cgc gca      558
Arg Asp Pro Glu Gln Gln Leu Glu Leu Asn Arg Glu Ser Val Arg Ala
120                 125                 130                 135

ccc cca aac aga acc atc ttc gac agt gac ctg atg gat agt gcc agg      606
Pro Pro Asn Arg Thr Ile Phe Asp Ser Asp Leu Met Asp Ser Ala Arg
136                 141                 146                 151

ctg ggc ggc ccc tgc ccc ccc agc agt aac tcg ggc atc agc gcc acg      654
Leu Gly Gly Pro Cys Pro Pro Ser Ser Asn Ser Gly Ile Ser Ala Thr
152                 157                 162                 167

tgc tac ggc agc ggc ggg cgc atg gag ggg ccg ccg ccc acc tac agc      702
Cys Tyr Gly Ser Gly Gly Arg Met Glu Gly Pro Pro Pro Thr Tyr Ser
168                 173                 178                 183

gag gtc atc ggc cac tac ccg ggg tcc tcc ttc cag cac cag cag agc      750
Glu Val Ile Gly His Tyr Pro Gly Ser Ser Phe Gln His Gln Gln Ser
184                 189                 194                 199

agt ggg ccg ccc tcc ttg ctg gag ggg acc cgg ctc cac cac aca cac      798
Ser Gly Pro Pro Ser Leu Leu Glu Gly Thr Arg Leu His His Thr His
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200                 205                 210                 215

atc gcg ccc cta gag agc gca gcc atc tgg agc aaa gag aag gat aaa      846
Ile Ala Pro Leu Glu Ser Ala Ala Ile Trp Ser Lys Glu Lys Asp Lys
216                 221                 226                 231

cag aaa gga cac cct ctc tag gg tccccagggg ggccgggctg gggctgcgta      899
Gln Lys Gly His Pro Leu  *
232                 237

ggtgaaaagg cagaacactc cgcgcttctt agaagaggag tgagaggaag gcgggggcg     959

cagcaacgca tcgtgtggcc ctcccctccc acctccctgt gtataaatat ttacatgtga   1019

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gggaagttgt ggctgtcgag a  atg ggg gtc tgt ggg tac ctg ttc ctg ccc     171
                         Met Gly Val Cys Gly Tyr Leu Phe Leu Pro
                           1               5

tgg aag tgc ctc gtg gtc gtg tct ctc agg ctg ctg ttc ctt gta ccc      219
Trp Lys Cys Leu Val Val Val Ser Leu Arg Leu Leu Phe Leu Val Pro
 11                  16                  21                  26

aca gga gtg ccc gtg cgc agc gga gat gcc acc ttc ccc aaa gct atg      267
Thr Gly Val Pro Val Arg Ser Gly Asp Ala Thr Phe Pro Lys Ala Met
 27                  32                  37                  42

gac aac gtg acg gtc cgg cag ggg gag agc gcc acc ctc agg tgc act      315
Asp Asn Val Thr Val Arg Gln Gly Glu Ser Ala Thr Leu Arg Cys Thr
 43                  48                  53                  58

att gac aac cgg gtc acc cgg gtg gcc tgg cta aac cgc agc acc atc      363
Ile Asp Asn Arg Val Thr Arg Val Ala Trp Leu Asn Arg Ser Thr Ile
 59                  64                  69                  74

ctc tat gct ggg aat gac aag tgg tgc ctg gat cct cgc gtg gtc ctt      411
Leu Tyr Ala Gly Asn Asp Lys Trp Cys Leu Asp Pro Arg Val Val Leu
 75                  80                  85                  90
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ctg agc aac acc caa acg cag tac agc atc gag atc cag aac gtg gat      459
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 91                  96                  101                 106

gtg tat gac gag ggc cct tac acc tgc tcg gtg cag aca gac aac cac      507
Val Tyr Asp Glu Gly Pro Tyr Thr Cys Ser Val Gln Thr Asp Asn His
107                 112                 117                 122

cca aag acc tct agg gtc cac ctc att gtg caa gta tct ccc aaa att      555
Pro Lys Thr Ser Arg Val His Leu Ile Val Gln Val Ser Pro Lys Ile
123                 128                 133                 138

gta gag att tct tca gat atc tcc att aat gaa ggg aac aat att agc      603
Val Glu Ile Ser Ser Asp Ile Ser Ile Asn Glu Gly Asn Asn Ile Ser
139                 144                 149                 154

ctc acc tgc ata gca act ggt aga cca gag cct acg gtt act tgg aga      651
Leu Thr Cys Ile Ala Thr Gly Arg Pro Glu Pro Thr Val Thr Trp Arg
155                 160                 165                 170

cac atc tct ccc aaa gcg gtt ggc ttt gtg agt gaa gac gaa tac ttg      699
His Ile Ser Pro Lys Ala Val Gly Phe Val Ser Glu Asp Glu Tyr Leu
171                 176                 181                 186

gaa att cag ggc atc acc cgg gag cag tca ggg gac tac gag tgc agt      747
Glu Ile Gln Gly Ile Thr Arg Glu Gln Ser Gly Asp Tyr Glu Cys Ser
187                 192                 197                 202

gcc tcc aat gac gtg gcc gcg ccc gtg gta cgg aga gta aag gtc acc      795
Ala Ser Asn Asp Val Ala Ala Pro Val Val Arg Arg Val Lys Val Thr
203                 208                 213                 218

gtg aac tat cca cca tac att tca gaa gcc aag ggt aca ggt gtc ccc      843
Val Asn Tyr Pro Pro Tyr Ile Ser Glu Ala Lys Gly Thr Gly Val Pro
219                 224                 229                 234

gtg gga caa aag ggg aca ctg cag tgt gaa gcc tca gca gtc ccc tca      891
Val Gly Gln Lys Gly Thr Leu Gln Cys Glu Ala Ser Ala Val Pro Ser
235                 240                 245                 250

gca gaa ttc cag tgg tac aag gat gac aaa aga ctg att gaa gga aag      939
Ala Glu Phe Gln Trp Tyr Lys Asp Asp Lys Arg Leu Ile Glu Gly Lys
251                 256                 261                 266

aaa ggg gtg aaa gtg gaa aac aga cct ttc ctc tca aaa ctc atc ttc      987
Lys Gly Val Lys Val Glu Asn Arg Pro Phe Leu Ser Lys Leu Ile Phe
267                 272                 277                 282

ttc aat gtc tct gaa cat gac tat ggg aac tac act tgc gtg gcc tcc     1035
Phe Asn Val Ser Glu His Asp Tyr Gly Asn Tyr Thr Cys Val Ala Ser
283                 288                 293                 298

aac aag ctg ggc cac acc aat gcc agc atc atg cta ttt ggt cca ggc     1083
Asn Lys Leu Gly His Thr Asn Ala Ser Ile Met Leu Phe Gly Pro Gly
299                 304                 309                 314

gcc gtc agc gag gtg agc aac ggc acg tcg agg agg gca ggc tgc gtc     1131
```

```
Ala Val Ser Glu Val Ser Asn Gly Thr Ser Arg Arg Ala Gly Cys Val
315                 320                 325                 330

tgg ctg ctg cct ctt ctg gtc ttg cac ctg ctt ctc aaa ttt tga tgt     1179
Trp Leu Leu Pro Leu Leu Val Leu His Leu Leu Leu Lys Phe  *
331                 336                 341

gagtgccact tccccacccg ggaaaggctg ccgccaccac caccaccaac acaacagcaa   1239

tggcaacacc gacagcaacc aatcagatat atacaaatga aattagaaga aacacagcct   1299

catgggacag aaatttgagg gaggggaaca aagaatactt tgggggggaaa agagttttaa   1359

aaaagaaatt gaaaattgcc ttgcagatat ttaggtacaa tggagttttc ttttcccaaa   1419

cgggaagaac acagcacacc cggcttggac ccactgcaag ctgcatcgtg caacctcttt   1479

ggtgccagtg tgggcaaggg ctcagcctct ctgcccacag agtgccccca cgtggaacat   1539

tctggagctg gccatcccaa attcaatcag tccatagaga cgaacagaat gagaccttcc   1599

ggcccaagcg tggcgctgcg ggcactttgg tagactgtgc caccacggcg tgtgttgtga   1659

aacgtgaaat aaaaagagc                                               1678
```

<210> 73
<211> 1586
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (101)..(1303)

<400> 73

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gcggccgcag ccccgggctc gcgtaggcgc cgaccgctcc cggcccgccc cctatgggcc     60

ccggctagag gcgccgccgc cgccggcccg cggagccccg  atg ctg gcc cgg agg     115
                                              Met Leu Ala Arg Arg
                                                1

aag ccg gtg ctg ccg gcg ctc acc atc aac cct acc atc gcc gag ggc      163
Lys Pro Val Leu Pro Ala Leu Thr Ile Asn Pro Thr Ile Ala Glu Gly
  6                  11                  16                  21

cca tcc cct acc agc gag ggc gcc tcc gag gca aac ctg gtg gac ctg      211
Pro Ser Pro Thr Ser Glu Gly Ala Ser Glu Ala Asn Leu Val Asp Leu
 22                  27                  32                  37

cag aag aag ctg gag gag ctg gaa ctt gac gag cag cag aag aag cgg      259
Gln Lys Lys Leu Glu Glu Leu Glu Leu Asp Glu Gln Gln Lys Lys Arg
 38                  43                  48                  53

ctg gaa gcc ttt ctc acc cag aaa gcc aag gtc ggc gaa ctc aaa gac      307
```

```
Leu Glu Ala Phe Leu Thr Gln Lys Ala Lys Val Gly Glu Leu Lys Asp
 54                  59                  64                  69

gat gac ttc gaa agg atc tca gag ctg ggc gcg ggc aac ggg cgg gtg      355
Asp Asp Phe Glu Arg Ile Ser Glu Leu Gly Ala Gly Asn Gly Arg Val
 70                  75                  80                  85

gtc acc aaa gtc cag cac aga ccc tcg ggc ctc atc atg gcc agg aag      403
Val Thr Lys Val Gln His Arg Pro Ser Gly Leu Ile Met Ala Arg Lys
 86                  91                  96                 101

ctg atc cac ctt gag atc aag ccg gcc atc cgg aac cag atc atc cgc      451
Leu Ile His Leu Glu Ile Lys Pro Ala Ile Arg Asn Gln Ile Ile Arg
102                 107                 112                 117

gag ctg cag gtc ctg cac gaa tgc aac tcg ccg tac atc gtg ggc ttc      499
Glu Leu Gln Val Leu His Glu Cys Asn Ser Pro Tyr Ile Val Gly Phe
118                 123                 128                 133

tac ggg gcc ttc tac agt gac ggg gag atc agc att tgc atg gaa cac      547
Tyr Gly Ala Phe Tyr Ser Asp Gly Glu Ile Ser Ile Cys Met Glu His
134                 139                 144                 149

atg gac ggc ggc tcc ctg gac cag gtg ctg aaa gag gcc aag agg att      595
Met Asp Gly Gly Ser Leu Asp Gln Val Leu Lys Glu Ala Lys Arg Ile
150                 155                 160                 165

ccc gag gag atc ctg ggg aaa gtc agc atc gcg gtt ctc cgg ggc ttg      643
Pro Glu Glu Ile Leu Gly Lys Val Ser Ile Ala Val Leu Arg Gly Leu
166                 171                 176                 181

gcg tac ctc cga gag aag cac cag atc atg cac cga gat gtg aag ccc      691
Ala Tyr Leu Arg Glu Lys His Gln Ile Met His Arg Asp Val Lys Pro
182                 187                 192                 197

tcc aac atc ctc gtg aac tct aga ggg gag atc aag ctg tgt gac ttc      739
Ser Asn Ile Leu Val Asn Ser Arg Gly Glu Ile Lys Leu Cys Asp Phe
198                 203                 208                 213

ggg gtg agc ggc cag ctc ata gac tcc atg gcc aac tcc ttc gtg ggc      787
Gly Val Ser Gly Gln Leu Ile Asp Ser Met Ala Asn Ser Phe Val Gly
214                 219                 224                 229

acg cgc tcc tac atg gct ccg gag cgg ttg cag ggc aca cat tac tcg      835
Thr Arg Ser Tyr Met Ala Pro Glu Arg Leu Gln Gly Thr His Tyr Ser
230                 235                 240                 245

gtg cag tcg gac atc tgg agc atg ggc ctg tcc ctg gtg gag ctg gcc      883
Val Gln Ser Asp Ile Trp Ser Met Gly Leu Ser Leu Val Glu Leu Ala
246                 251                 256                 261

gtc gga agg tac ccc atc ccc ccg ccc gac gcc aaa gag ctg gag gcc      931
Val Gly Arg Tyr Pro Ile Pro Pro Pro Asp Ala Lys Glu Leu Glu Ala
262                 267                 272                 277

atc ttt ggc cgg ccc gtg gtc gac ggg gaa gaa gga gag cct cac agc      979
Ile Phe Gly Arg Pro Val Val Asp Gly Glu Glu Gly Glu Pro His Ser
```

```
278                 283                 288                 293

atc tcg cct cgg ccg agg ccc ccc ggg cgc ccc gtc agc ggt cac ggg     1027
Ile Ser Pro Arg Pro Arg Pro Pro Gly Arg Pro Val Ser Gly His Gly
294                 299                 304                 309

atg gat agc cgg cct gcc atg gcc atc ttt gaa ctc ctg gac tat att     1075
Met Asp Ser Arg Pro Ala Met Ala Ile Phe Glu Leu Leu Asp Tyr Ile
310                 315                 320                 325

gtg aac gag cca cct cct aag ctg ccc aac ggt gtg ttc acc ccc gac     1123
Val Asn Glu Pro Pro Pro Lys Leu Pro Asn Gly Val Phe Thr Pro Asp
326                 331                 336                 341

ttc cag gag ttt gtc aat aaa tgc ctc atc aag aac cca gcg gag cgg     1171
Phe Gln Glu Phe Val Asn Lys Cys Leu Ile Lys Asn Pro Ala Glu Arg
342                 347                 352                 357

gcg gac ctg aag atg ctc aca aac cac acc ttc atc aag cgg tcc gag     1219
Ala Asp Leu Lys Met Leu Thr Asn His Thr Phe Ile Lys Arg Ser Glu
358                 363                 368                 373

gtg gaa gaa gtg gat ttt gcc ggc tgg ttg tgt aaa acc ctg cgg ctg     1267
Val Glu Glu Val Asp Phe Ala Gly Trp Leu Cys Lys Thr Leu Arg Leu
374                 379                 384                 389

aac cag ccc ggc aca ccc acg cgc acc gcc gtg tga cagt ggccgggctc     1317
Asn Gln Pro Gly Thr Pro Thr Arg Thr Ala Val  *
390                 395                 400

cctgcgtccc gctggtgacc tgcccaccgt ccctgtccat gccccgccct tccagctgag   1377

gacacgtggc gcctccaccc accctcctgc ctcacccctg cggagagcac cgtggcgggg   1437

cgacagcgca tgcaggaacg ggggtctcct ctcctgccag tcctggccgg ggtgcctctg   1497

gggacgggcg acgctgctgt gtgtggtctc agaggctctg cttccttagg ttacaaaaca   1557

aaacagggag agaaaaagca aaaaaaaaa                                     1586
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Sequence Listing

<210> 74
<211> 1284
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (101)..(991)

<400> 74

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ccggctagag gcgccgccgc cgccggcccg cggagccccg  atg ctg gcc cgg agg     115
                                             Met Leu Ala Arg Arg
```

```
aag ccg gtg ctg ccg gcg ctc acc atc aac cct acc atc gcc gag ggc      163
Lys Pro Val Leu Pro Ala Leu Thr Ile Asn Pro Thr Ile Ala Glu Gly
  6                  11                  16                  21

cca tcc cct acc agc gag ggc gcc tcc gag gca aac ctg gtg gac ctg      211
Pro Ser Pro Thr Ser Glu Gly Ala Ser Glu Ala Asn Leu Val Asp Leu
 22                  27                  32                  37

cag aag aag ctg gag gag ctg gaa ctt gac gag cag cag aag aag cgg      259
Gln Lys Lys Leu Glu Glu Leu Glu Leu Asp Glu Gln Gln Lys Lys Arg
 38                  43                  48                  53

ctg gaa gcc ttt ctc acc cag aaa gcc aag gtc ggc gaa ctc aaa gtc      307
Leu Glu Ala Phe Leu Thr Gln Lys Ala Lys Val Gly Glu Leu Lys Val
 54                  59                  64                  69

agc atc gcg gtt ctc cgg ggc ttg gcg tac ctc cga gag aag cac cag      355
Ser Ile Ala Val Leu Arg Gly Leu Ala Tyr Leu Arg Glu Lys His Gln
 70                  75                  80                  85

atc atg cac cga gat gtg aag ccc tcc aac atc ctc gtg aac tct aga      403
Ile Met His Arg Asp Val Lys Pro Ser Asn Ile Leu Val Asn Ser Arg
 86                  91                  96                 101

ggg gag atc aag ctg tgt gac ttc ggg gtg agc ggc cag ctc atc gac      451
Gly Glu Ile Lys Leu Cys Asp Phe Gly Val Ser Gly Gln Leu Ile Asp
102                 107                 112                 117

tcc atg gcc aac tcc ttc gtg ggc acg cgc tcc tac atg gct ccg gag      499
Ser Met Ala Asn Ser Phe Val Gly Thr Arg Ser Tyr Met Ala Pro Glu
118                 123                 128                 133

cgg ttg cag ggc aca cat tac tcg gtg cag tcg gac atc tgg agc atg      547
Arg Leu Gln Gly Thr His Tyr Ser Val Gln Ser Asp Ile Trp Ser Met
134                 139                 144                 149

ggc ctg tcc ctg gtg gag ctg gcc gtc gga agg tac ccc atc ccc ccg      595
Gly Leu Ser Leu Val Glu Leu Ala Val Gly Arg Tyr Pro Ile Pro Pro
150                 155                 160                 165

ccc gac gcc aaa gag ctg gag gcc atc ttt ggc cgg ccc gtg gtc gac      643
Pro Asp Ala Lys Glu Leu Glu Ala Ile Phe Gly Arg Pro Val Val Asp
166                 171                 176                 181

ggg gaa gaa gga gag cct cac agc atc tcg cct cgg ccg agg ccc ccc      691
Gly Glu Glu Gly Glu Pro His Ser Ile Ser Pro Arg Pro Arg Pro Pro
182                 187                 192                 197

ggg cgc ccc gtc agc ggt cac ggg atg gat agc cgg cct gcc atg gcc      739
Gly Arg Pro Val Ser Gly His Gly Met Asp Ser Arg Pro Ala Met Ala
198                 203                 208                 213

atc ttt gaa ctc ctg gac tat att gtg aac gag cca cct cct aag ctg      787
Ile Phe Glu Leu Leu Asp Tyr Ile Val Asn Glu Pro Pro Pro Lys Leu
214                 219                 224                 229
```

```
ccc aac ggt gtg ttc acc ccc gac ttc cag gag ttt gtc aat aaa tgc      835
Pro Asn Gly Val Phe Thr Pro Asp Phe Gln Glu Phe Val Asn Lys Cys
230                 235                 240                 245

ctc atc aag aac cca gcg gag cgg gcg gac ctg aag atg ctc aca aac      883
Leu Ile Lys Asn Pro Ala Glu Arg Ala Asp Leu Lys Met Leu Thr Asn
246                 251                 256                 261

cac acc ttc atc aag cgg tcc gag gtg gaa gaa gtg gat ttt gcc ggc      931
His Thr Phe Ile Lys Arg Ser Glu Val Glu Glu Val Asp Phe Ala Gly
262                 267                 272                 277

tgg ttg tgt aaa acc ctg cgg ctg aac cag ccc ggc aca ccc acg cgc      979
Trp Leu Cys Lys Thr Leu Arg Leu Asn Gln Pro Gly Thr Pro Thr Arg
278                 283                 288                 293

acc gcc gtg tga cag tggccgggct ccctgcgtcc cgctggtgac ctgcccaccg     1034
Thr Ala Val  *
294

tccctgtcca tgccccgccc ttccagctga ggacaggctg gcgcctccac ccaccctcct   1094

gcctcacccc tgcggagagc accgtggcgg ggcgacagcg catgcaggaa cgggggtctc   1154

ctctcctgcc cgtcctggcc ggggtgcctc tggggacggg cgacgctgct gtgtgtggtc   1214

tcagaggctc tgcttcctta ggttacaaaa caaaacaggg agagaaaaag caaaaaaaaa   1274

aaaaaaaaaa                                                         1284
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<210> 75
<211> 3139
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (816)..(2291)

<400> 75

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catggtaacg ccaggttttc cacacatcac acccttaaa acgccgcccc agtcccaaac     60

taaattcacc cttcactaaa gggaataagc ttcgcccctt aattaaacat cttcacataa    120

ccacacaccc accgttttat ttctcgcgga catggcaccc gagcgcggcc ttggccatcg    180

ggctacctct gcggggaagg gcaagcccgc aggctggagc ggggtgcgga ggctggcggg    240

gagcggcccc cggaggcttt cctggtagaa gttgatgcga ggaagggcgg cggggaccag    300

gtttgcgagt cctaggcgag ggtcatggga gttgggggta tttctggcag tagaatggcc    360

tgcgtcgtga ctaaactagc cctgtgacct tgggcaagtt cctgaaatcc atgggagctt    420
```

```
ttgtttcatt gtcagtaaac tgaagataac accaacttgg cagcgggagt ttgtgtcttc    480

tgtatgaaat ctccctgcct ctgtacctgg ttgagttgct gtcattattt taggggacgg    540

tattcagaat tcgagcgcag gagctccgct tctccacctg ctcccgggga gctattgggc    600

ctcctcttcc agcagcctct atctttattc tacaggatcc agagaatcac ccgctgatgg    660

tttttgccca ggcctgaaac aaccagagag ctacgggaaa ggaagggctt ggcttgccag    720

aggaattttc caagtgctca aacgccaggc ttacggcgcc tgtgatccgt ccaggaggac    780

aaagtgggat ttgaagatcc actccacctc tgctc   atg gcg ggc cag ggc ctg     833
                                          Met Ala Gly Gln Gly Leu
                                            1

ccc ctg cac gtg gcc aca ctg ctg act ggg ctg ctg gaa tgc ctg ggc      881
Pro Leu His Val Ala Thr Leu Leu Thr Gly Leu Leu Glu Cys Leu Gly
  7                  12                  17                  22

ttt gct ggc gtc ctc ttt ggc tgg cct tca cta gtg ttt gtc ttc aag      929
Phe Ala Gly Val Leu Phe Gly Trp Pro Ser Leu Val Phe Val Phe Lys
 23                  28                  33                  38

aat gaa gat tac ttt aag gat ctg tgt gga cca gat gct ggg ccg att      977
Asn Glu Asp Tyr Phe Lys Asp Leu Cys Gly Pro Asp Ala Gly Pro Ile
 39                  44                  49                  54

ggc aat gcc aca ggg cag gct gac tgc aaa gcc cag gat gag agg ttc     1025
Gly Asn Ala Thr Gly Gln Ala Asp Cys Lys Ala Gln Asp Glu Arg Phe
 55                  60                  65                  70

tca ctc atc ttc acc ctg ggg tcc ttc atg aac aac ttc atg aca ttc     1073
Ser Leu Ile Phe Thr Leu Gly Ser Phe Met Asn Asn Phe Met Thr Phe
 71                  76                  81                  86

ccc act ggc tac atc ttt gac cgg ttc aag acc acc gtg gca cgc ctc     1121
Pro Thr Gly Tyr Ile Phe Asp Arg Phe Lys Thr Thr Val Ala Arg Leu
 87                  92                  97                 102

ata gcc ata ttt ttc tac acc acc gcc aca ctc atc ata gcc ttc acc     1169
Ile Ala Ile Phe Phe Tyr Thr Thr Ala Thr Leu Ile Ile Ala Phe Thr
103                 108                 113                 118

tct gca ggc tca gcc gtg ctg ctc ttc ctg gcc atg cca atg ctc acc     1217
Ser Ala Gly Ser Ala Val Leu Leu Phe Leu Ala Met Pro Met Leu Thr
119                 124                 129                 134

att ggg gga atc ctg ttt ctc atc acc aac ctg cag att ggg aac cta     1265
Ile Gly Gly Ile Leu Phe Leu Ile Thr Asn Leu Gln Ile Gly Asn Leu
135                 140                 145                 150

ttt ggc caa cac cgt tcg acc atc atc act ctg tac aat gga gca ttt     1313
Phe Gly Gln His Arg Ser Thr Ile Ile Thr Leu Tyr Asn Gly Ala Phe
151                 156                 161                 166
```

```
gac tct tcc tcg gca gtc ttc ctt att att aag ctt ctt tat gaa aaa     1361
Asp Ser Ser Ser Ala Val Phe Leu Ile Ile Lys Leu Leu Tyr Glu Lys
167                 172                 177                 182

ggc atc agc ctc agg gcc tcc ttc atc ttc atc tct gtc tgc agt acc     1409
Gly Ile Ser Leu Arg Ala Ser Phe Ile Phe Ile Ser Val Cys Ser Thr
183                 188                 193                 198

tgg cat gta gca cgc act ttc ctc ctg atg ccc cgg ggg cac atc cca     1457
Trp His Val Ala Arg Thr Phe Leu Leu Met Pro Arg Gly His Ile Pro
199                 204                 209                 214

tac cca ctg ccc ccc aac tac agc tat ggc ctg tgc cct ggg aat ggc     1505
Tyr Pro Leu Pro Pro Asn Tyr Ser Tyr Gly Leu Cys Pro Gly Asn Gly
215                 220                 225                 230

acc aca aag gaa gag aag gaa aca gct gag cat gaa aac agg gag cta     1553
Thr Thr Lys Glu Glu Lys Glu Thr Ala Glu His Glu Asn Arg Glu Leu
231                 236                 241                 246

cag tca aag gag ttc ctt tca gcg aag gaa gag acc cca ggg gca ggg     1601
Gln Ser Lys Glu Phe Leu Ser Ala Lys Glu Glu Thr Pro Gly Ala Gly
247                 252                 257                 262

cag aag cag gaa ctc cgc tcc ttc tgg agc tac gct ttc tct cgg cgc     1649
Gln Lys Gln Glu Leu Arg Ser Phe Trp Ser Tyr Ala Phe Ser Arg Arg
263                 268                 273                 278

ttt gcc tgg cac ctg gtg tgg ctg tct gtg ata cag ttg tgg cac tac     1697
Phe Ala Trp His Leu Val Trp Leu Ser Val Ile Gln Leu Trp His Tyr
279                 284                 289                 294

ctc ttc att ggc act ctc aac tcc ttg ctg acc aac atg gcc ggt ggg     1745
Leu Phe Ile Gly Thr Leu Asn Ser Leu Leu Thr Asn Met Ala Gly Gly
295                 300                 305                 310

gac atg gca cga gtc agc acc tac aca aat gcc ttt gcc ttc act cag     1793
Asp Met Ala Arg Val Ser Thr Tyr Thr Asn Ala Phe Ala Phe Thr Gln
311                 316                 321                 326

ttc gga gtg ctg tgt gcc ccc tgg aat ggc ctg ctc atg gac cgg ctt     1841
Phe Gly Val Leu Cys Ala Pro Trp Asn Gly Leu Leu Met Asp Arg Leu
327                 332                 337                 342

aaa cag aag tac cag aag gaa gca aga aag aca ggt tcc tcc act ttg     1889
Lys Gln Lys Tyr Gln Lys Glu Ala Arg Lys Thr Gly Ser Ser Thr Leu
343                 348                 353                 358

gcg gtg gcc ctc tgc tcg acg gtg cct tcg ctg gcc ctg aca tcc ctg     1937
Ala Val Ala Leu Cys Ser Thr Val Pro Ser Leu Ala Leu Thr Ser Leu
359                 364                 369                 374

ctg tgc ctg ggc ttc gcc ctc tgt gcc tca gtc ccc atc ctc cct ctc     1985
Leu Cys Leu Gly Phe Ala Leu Cys Ala Ser Val Pro Ile Leu Pro Leu
375                 380                 385                 390

cag tac ctc acc ttc atc ctg caa gtg atc agc cgc tcc ttc ctc tat     2033
```

```
Gln Tyr Leu Thr Phe Ile Leu Gln Val Ile Ser Arg Ser Phe Leu Tyr
391                 396                 401                 406

ggg agc aac gcg gcc ttc ctc acc ctt gct ttc cct tca gag cac ttt     2081
Gly Ser Asn Ala Ala Phe Leu Thr Leu Ala Phe Pro Ser Glu His Phe
407                 412                 417                 422

ggc aag ctc ttt ggg ctg gtg atg gcc ttg tcg gct gtg gtg tct ctg     2129
Gly Lys Leu Phe Gly Leu Val Met Ala Leu Ser Ala Val Val Ser Leu
423                 428                 433                 438

ctc cag ttc ccc atc ttc acc ctc atc aaa ggc tcc ctt cag aat gac     2177
Leu Gln Phe Pro Ile Phe Thr Leu Ile Lys Gly Ser Leu Gln Asn Asp
439                 444                 449                 454

cca ttt tac gtg aat gtg atg ttc atg ctt gcc att ctt ctg aca ttc     2225
Pro Phe Tyr Val Asn Val Met Phe Met Leu Ala Ile Leu Leu Thr Phe
455                 460                 465                 470

ttc cac ccc ttt ctg gta tat cgg gaa tgc cgt act tgg aaa gaa agt     2273
Phe His Pro Phe Leu Val Tyr Arg Glu Cys Arg Thr Trp Lys Glu Ser
471                 476                 481                 486

ccc tct gca att gca tag ttcaga agccctcact tttcagcccc gaggatggtt     2327
Pro Ser Ala Ile Ala  *
487                 492

ttgttcatct tccaccacct ttgaggacct cgtgtcccaa aagactttgc ctatcccagc   2387

aaaacacaca cacacacaca cacacacaca aaataaagac acacaaggac gtctgcgcag   2447

caagaaaaga atctcagttg ccaagcagat tgatatcaca cagactcaaa gcaaaggcat   2507

gtggaacttc tttatttcaa aacagaagtg tctccttgca cttagccttg gcagaccctt   2567

gactccaggg gagatgacct gggggaggaa gtgtgtcaac tatttcttta ggcctgtttg   2627

gctccgaagc ctatatgtgc ctggatcctc tgccacgggt taaattttca ggtgaagagt   2687

gaggttgtca tggcctcagc tatgcttcct ggctctccct caagagtgca gccttggcta   2747

gagaactcac agctctggga aaaagaggag cagacagggt tccctgggcc cagtctcagc   2807

ccagccactg atgctggatg accttggcct gaccctggtc tggtctcaga atcacttttc   2867

ccatctgtaa aattgagatg aattttggtg ttgaaagttc ttcctggagc agatgtccta   2927

gaaggtttta ggaatagtga cagagtcagg ccaccccaag ggccatggga gccagctgac   2987

ctgcttgacc gaaggatttc tgacagacta tctttgggga tgttttcaag aagggatata   3047

agttatttac tttgggcatt taaaagaaaa tttctctcgg gaataatttt atagaaaaat   3107

aaagcttctg tgtctaaggc aaaaaaaaaa aa                                 3139
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<210> 76
<211> 709
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (144)..(653)

<400> 76
gcaatattcc cgggctgcga aaatgcgtac cagcaaatgg aagaattact ctttgaagtg 60

aatgaaggta tgctgcatta atcatttctt taattcagca taagttgtta tggcgaaatc 120

agcactgttc acggtgcgta ata atg agt cct gcc caa agt gcg ggg ctg 170
Met Ser Pro Ala Gln Ser Ala Gly Leu
1 5

aac tgg tta ttc gga tcc ggg aaa cac ggt ccg ttt ctt gga tgc tca 218
Asn Trp Leu Phe Gly Ser Gly Lys His Gly Pro Phe Leu Gly Cys Ser
10 15 20 25

cag tat ccg gcg tgt gac tac gtc cgt cct ctg aaa tct tca gcg gat 266
Gln Tyr Pro Ala Cys Asp Tyr Val Arg Pro Leu Lys Ser Ser Ala Asp
26 31 36 41

gga cat atc gtc aaa gtt ctg gag ggg cag gtt tgc cct gca tgt ggc 314
Gly His Ile Val Lys Val Leu Glu Gly Gln Val Cys Pro Ala Cys Gly
42 47 52 57

gca aat ctg gta tta cgc cag gga cgc ttt ggt atg ttt att ggt tgc 362
Ala Asn Leu Val Leu Arg Gln Gly Arg Phe Gly Met Phe Ile Gly Cys
58 63 68 73

att aac tac cct gaa tgc gaa cat acc gaa ctt atc gat aaa ccg gac 410
Ile Asn Tyr Pro Glu Cys Glu His Thr Glu Leu Ile Asp Lys Pro Asp
74 79 84 89

gaa aca gca att aca tgc ccc caa tgt cgg acg ggc cat ctg gtc cag 458
Glu Thr Ala Ile Thr Cys Pro Gln Cys Arg Thr Gly His Leu Val Gln
90 95 100 105

cgc cgc tcc cgt tat ggc aaa aca ttt cac tct tgt gat cgc tac ccg 506
Arg Arg Ser Arg Tyr Gly Lys Thr Phe His Ser Cys Asp Arg Tyr Pro
106 111 116 121

gag tgt caa ttt gcc att aac ttc aaa ccc ata gct gga gaa tgc cct 554
Glu Cys Gln Phe Ala Ile Asn Phe Lys Pro Ile Ala Gly Glu Cys Pro
122 127 132 137

gag tgt cat tat ccg cta ctc atc gaa aag aaa acc gcg cag ggt gta 602
Glu Cys His Tyr Pro Leu Leu Ile Glu Lys Lys Thr Ala Gln Gly Val
138 143 148 153

aaa cac ttt tgt gcc agt aaa caa tgt gga aag ccg gtt tcg gcg gaa 650
Lys His Phe Cys Ala Ser Lys Gln Cys Gly Lys Pro Val Ser Ala Glu

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                               Met Ser Asn Ala Lys Glu Arg Lys His
                                 1               5

gcc aag aaa atg aga aac cag cct acc aat gtg act ctg tcc tct ggc      161
Ala Lys Lys Met Arg Asn Gln Pro Thr Asn Val Thr Leu Ser Ser Gly
 10                  15                  20                  25

ttt gtg gct gac aga ggt gta aag cac cac agt gga ggt gaa aaa cct      209
Phe Val Ala Asp Arg Gly Val Lys His His Ser Gly Gly Glu Lys Pro
 26                  31                  36                  41

ttc caa gct caa aaa caa gag cct cat cct gga act tca cga cag cgg      257
Phe Gln Ala Gln Lys Gln Glu Pro His Pro Gly Thr Ser Arg Gln Arg
 42                  47                  52                  57

caa acc aga gtc aac ccc cat tct ctg cct gac cct gaa gtg aat gag      305
Gln Thr Arg Val Asn Pro His Ser Leu Pro Asp Pro Glu Val Asn Glu
 58                  63                  68                  73

cag tct tcc tcc aaa ggg atg ttt aga aaa aag gga gga tgg aaa gca      353
Gln Ser Ser Ser Lys Gly Met Phe Arg Lys Lys Gly Gly Trp Lys Ala
 74                  79                  84                  89

ggt ccc gag ggc acg tct cag gag atc ccc aag tat ata act gct tct      401
Gly Pro Glu Gly Thr Ser Gln Glu Ile Pro Lys Tyr Ile Thr Ala Ser
 90                  95                 100                 105

act ttt gct caa gca cga gct gct gaa atc agt gct atg tta aaa gct      449
Thr Phe Ala Gln Ala Arg Ala Ala Glu Ile Ser Ala Met Leu Lys Ala
106                 111                 116                 121

gtg acc cag aag tct tcg aat tca ctg gtt ttt cag act ctg cca cgg      497
Val Thr Gln Lys Ser Ser Asn Ser Leu Val Phe Gln Thr Leu Pro Arg
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122                 127                 132                 137

cac atg cga cga aga gcc atg agc cac aac gtc aaa cgc ctt ccc aga      545
His Met Arg Arg Arg Ala Met Ser His Asn Val Lys Arg Leu Pro Arg
138                 143                 148                 153

cgg tta cag gag att gcc cag aaa gag gcg gag aaa gcc gta cat cag      593
Arg Leu Gln Glu Ile Ala Gln Lys Glu Ala Glu Lys Ala Val His Gln
154                 159                 164                 169

aaa aaa gaa cat tca aaa aat aaa tgc cat aaa gct cga aga tgt cac      641
Lys Lys Glu His Ser Lys Asn Lys Cys His Lys Ala Arg Arg Cys His
170                 175                 180                 185

atg aac cgg acg cta gaa ttt aac cgt aga caa aag aag aac att tgg      689
Met Asn Arg Thr Leu Glu Phe Asn Arg Arg Gln Lys Lys Asn Ile Trp
186                 191                 196                 201

tta gaa act cac atc tgg cac gcc aag cgg ttt cat atg gtc aag aag      737
Leu Glu Thr His Ile Trp His Ala Lys Arg Phe His Met Val Lys Lys
202                 207                 212                 217

tgg ggc tac tgc ctt ggg gag agg cca aca gtc aag agc cac aga gcc      785
Trp Gly Tyr Cys Leu Gly Glu Arg Pro Thr Val Lys Ser His Arg Ala
218                 223                 228                 233

tgc tat cga gcc atg acg aac cgg tgc ctc ctg cag gat tta tcc tat      833
Cys Tyr Arg Ala Met Thr Asn Arg Cys Leu Leu Gln Asp Leu Ser Tyr
234                 239                 244                 249

tac tgt tgt ttg gag ttg aaa ggc aaa gag gaa gaa ata cta aag gcg      881
Tyr Cys Cys Leu Glu Leu Lys Gly Lys Glu Glu Glu Ile Leu Lys Ala
250                 255                 260                 265

ctt tct gga atg tgt aac ata gac aca ggg ctg acg ttt gca gca gtt      929
Leu Ser Gly Met Cys Asn Ile Asp Thr Gly Leu Thr Phe Ala Ala Val
266                 271                 276                 281

cac tgc ttg tct gga aag cgc caa ggg agc ctt gtg ctt tat cgg gtg      977
His Cys Leu Ser Gly Lys Arg Gln Gly Ser Leu Val Leu Tyr Arg Val
282                 287                 292                 297

aat aaa tat ccc aga gaa atg ctt ggg cct gtt acg ttt atc tgg aag     1025
Asn Lys Tyr Pro Arg Glu Met Leu Gly Pro Val Thr Phe Ile Trp Lys
298                 303                 308                 313

tcc cag agg acc ccg ggt gac cct tct gag agc agg cag ctg tgg atc     1073
Ser Gln Arg Thr Pro Gly Asp Pro Ser Glu Ser Arg Gln Leu Trp Ile
314                 319                 324                 329

tgg ctg cat cca acc ctt aaa cag gat atc tta gag gaa ata aaa gca     1121
Trp Leu His Pro Thr Leu Lys Gln Asp Ile Leu Glu Glu Ile Lys Ala
330                 335                 340                 345

gcg tgc cag tgt gtg gaa ccc atc aaa tca gct gtc tgc atc gct gac     1169
Ala Cys Gln Cys Val Glu Pro Ile Lys Ser Ala Val Cys Ile Ala Asp
346                 351                 356                 361
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cca ctt cca aca cca tcc caa gaa aaa agc caa act gaa ttg cct gac     1217
Pro Leu Pro Thr Pro Ser Gln Glu Lys Ser Gln Thr Glu Leu Pro Asp
362                 367                 372                 377

gag aaa att ggc aag aaa aga aaa agg aaa gat gat gga gaa aat gct     1265
Glu Lys Ile Gly Lys Lys Arg Lys Arg Lys Asp Asp Gly Glu Asn Ala
378                 383                 388                 393

aaa cca att aaa aaa att atc ggt gat gga act aga gat cca tgt cta     1313
Lys Pro Ile Lys Lys Ile Ile Gly Asp Gly Thr Arg Asp Pro Cys Leu
394                 399                 404                 409

cca tac tct tgg atc tct cca acc aca ggc att ata atc agc gat ttg     1361
Pro Tyr Ser Trp Ile Ser Pro Thr Thr Gly Ile Ile Ile Ser Asp Leu
410                 415                 420                 425

acg atg gag atg aac aga ttc cgg ctg att ggg cca ctt tcc cac tcc     1409
Thr Met Glu Met Asn Arg Phe Arg Leu Ile Gly Pro Leu Ser His Ser
426                 431                 436                 441

atc cta act gaa gca ata aaa gct gct tct gtc cac act gtg gga gag     1457
Ile Leu Thr Glu Ala Ile Lys Ala Ala Ser Val His Thr Val Gly Glu
442                 447                 452                 457

gac aca gag gag aca cct cac cgc tgg tgg ata gaa acc tgt aag aaa     1505
Asp Thr Glu Glu Thr Pro His Arg Trp Trp Ile Glu Thr Cys Lys Lys
458                 463                 468                 473

cct gac agc gtt tcc ctt cat tgc aga caa gaa gcc att ttc gag ttg     1553
Pro Asp Ser Val Ser Leu His Cys Arg Gln Glu Ala Ile Phe Glu Leu
474                 479                 484                 489

ttg gga gga ata aca tca cca gca gaa att ccg gca ggt act att ctg     1601
Leu Gly Gly Ile Thr Ser Pro Ala Glu Ile Pro Ala Gly Thr Ile Leu
490                 495                 500                 505

gga ctg aca gtt ggg gat cct cga ata aat ttg ccc caa aag aag tcc     1649
Gly Leu Thr Val Gly Asp Pro Arg Ile Asn Leu Pro Gln Lys Lys Ser
506                 511                 516                 521

aaa gct ttg ccc aat cca gaa aaa tgc caa gat aat gag aaa gtt aga     1697
Lys Ala Leu Pro Asn Pro Glu Lys Cys Gln Asp Asn Glu Lys Val Arg
522                 527                 532                 537

cag ctg ctt ctg gag ggt gtg cct gtg gaa tgt acg cat agc ttt atc     1745
Gln Leu Leu Leu Glu Gly Val Pro Val Glu Cys Thr His Ser Phe Ile
538                 543                 548                 553

tgg aac caa gat atc tgt aag agt gtc aca gag aat aaa atc tcg gat     1793
Trp Asn Gln Asp Ile Cys Lys Ser Val Thr Glu Asn Lys Ile Ser Asp
554                 559                 564                 569

cag gat tta aac cgg atg agg agt gaa ttg ctg gtg cct ggg tca cag     1841
Gln Asp Leu Asn Arg Met Arg Ser Glu Leu Leu Val Pro Gly Ser Gln
570                 575                 580                 585
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ctt att tta ggt ccc cat gaa tcc aag ata cct ata ctt ttg att cag     1889
Leu Ile Leu Gly Pro His Glu Ser Lys Ile Pro Ile Leu Leu Ile Gln
586                 591                 596                 601

cag cca gga aaa gtg act ggt gaa gat cga cta ggc tgg gga agt ggc     1937
Gln Pro Gly Lys Val Thr Gly Glu Asp Arg Leu Gly Trp Gly Ser Gly
602                 607                 612                 617

tgg gat gtc cta ctc cca aag ggc tgg ggc atg gct ttc tgg att cca     1985
Trp Asp Val Leu Leu Pro Lys Gly Trp Gly Met Ala Phe Trp Ile Pro
618                 623                 628                 633

ttt att tat cga ggt gtg aga gtc gga ggg ttg aaa gag tct gca gtg     2033
Phe Ile Tyr Arg Gly Val Arg Val Gly Gly Leu Lys Glu Ser Ala Val
634                 639                 644                 649

cat tct cag tat aag agg tcg cct aat gtc cca ggc gat ttt cca gac     2081
His Ser Gln Tyr Lys Arg Ser Pro Asn Val Pro Gly Asp Phe Pro Asp
650                 655                 660                 665

tgc cct gcc ggg atg ctg ttt gcg gaa gag caa gct aag aat ctt ctt     2129
Cys Pro Ala Gly Met Leu Phe Ala Glu Glu Gln Ala Lys Asn Leu Leu
666                 671                 676                 681

gaa aag tac aaa aga cgc cct cct gca aaa cgg ccc aac tac gtt aag     2177
Glu Lys Tyr Lys Arg Arg Pro Pro Ala Lys Arg Pro Asn Tyr Val Lys
682                 687                 692                 697

ctt ggc act ctg gca cct ttc tgc tgt ccc tgg gag cag tta act caa     2225
Leu Gly Thr Leu Ala Pro Phe Cys Cys Pro Trp Glu Gln Leu Thr Gln
698                 703                 708                 713

gac tgg gag tca aga gtc cag gct tac gaa gaa cct tct gta gct tca     2273
Asp Trp Glu Ser Arg Val Gln Ala Tyr Glu Glu Pro Ser Val Ala Ser
714                 719                 724                 729

tct cca aat ggt aag gag agt gac cta aga aga tct gag gtg cct tgt     2321
Ser Pro Asn Gly Lys Glu Ser Asp Leu Arg Arg Ser Glu Val Pro Cys
730                 735                 740                 745

gct ccc atg cct aaa aaa act cat cag cca tct gat gaa gtg ggc aca     2369
Ala Pro Met Pro Lys Lys Thr His Gln Pro Ser Asp Glu Val Gly Thr
746                 751                 756                 761

tcc ata gag cac ccc agg gag gca gag gag gta atg gat gca ggg tgt     2417
Ser Ile Glu His Pro Arg Glu Ala Glu Glu Val Met Asp Ala Gly Cys
762                 767                 772                 777

caa gaa tcg gca ggg cct gag agg atc aca gac cag gag gcc agt gaa     2465
Gln Glu Ser Ala Gly Pro Glu Arg Ile Thr Asp Gln Glu Ala Ser Glu
778                 783                 788                 793

aac cat gtt gct gcc aca ggg agt cac ctc tgc gtt ctc agg agt aga     2513
Asn His Val Ala Ala Thr Gly Ser His Leu Cys Val Leu Arg Ser Arg
794                 799                 804                 809

aaa tta ctg aag caa ctg tca gcc tgg tgt ggg ccc agt tct gag gat     2561
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Lys Leu Leu Lys Gln Leu Ser Ala Trp Cys Gly Pro Ser Ser Glu Asp
810                 815                 820                 825

agt cgg gga ggc cgg cga gct ccc ggc aga ggc cag caa gga ttg acc     2609
Ser Arg Gly Gly Arg Arg Ala Pro Gly Arg Gly Gln Gln Gly Leu Thr
826                 831                 836                 841

aga gag gct tgc ctg tcc atc ttg ggc cac ttc ccc agg gcc ctg gtt     2657
Arg Glu Ala Cys Leu Ser Ile Leu Gly His Phe Pro Arg Ala Leu Val
842                 847                 852                 857

tgg gtc agc ctg tcc ctg ctc agc aag ggc agc ccc gag cct cac acc     2705
Trp Val Ser Leu Ser Leu Leu Ser Lys Gly Ser Pro Glu Pro His Thr
858                 863                 868                 873

atg atc tgt gtc cca gcc aag gag gac ttc ctc cag ctc cat gag gac     2753
Met Ile Cys Val Pro Ala Lys Glu Asp Phe Leu Gln Leu His Glu Asp
874                 879                 884                 889

tgg cat tac tgt ggg ccc cag gaa tcc aaa cac agt gac cca ttc agg     2801
Trp His Tyr Cys Gly Pro Gln Glu Ser Lys His Ser Asp Pro Phe Arg
890                 895                 900                 905

agc aag atc ctg aaa cag aaa gag aag aag aaa agg gag aag agg cag     2849
Ser Lys Ile Leu Lys Gln Lys Glu Lys Lys Lys Arg Glu Lys Arg Gln
906                 911                 916                 921

aag cca gga cgt gcc tct tct gat ggc ccg gcg ggg gaa gag ccc gtg     2897
Lys Pro Gly Arg Ala Ser Ser Asp Gly Pro Ala Gly Glu Glu Pro Val
922                 927                 932                 937

gct ggg cag gaa gct ctg act cta ggg ctg tgg tca ggc cct ctg ccg     2945
Ala Gly Gln Glu Ala Leu Thr Leu Gly Leu Trp Ser Gly Pro Leu Pro
938                 943                 948                 953

cgt gtg acg ttg cac tgc tcc aga act ctc cta ggc ttt gtg act cag     2993
Arg Val Thr Leu His Cys Ser Arg Thr Leu Leu Gly Phe Val Thr Gln
954                 959                 964                 969

gga gat ttt tcc atg gct gtt ggc tgt gga gaa gcc ctg ggg ttt gtt     3041
Gly Asp Phe Ser Met Ala Val Gly Cys Gly Glu Ala Leu Gly Phe Val
970                 975                 980                 985

agc ttg aca ggc ttg ctg gat atg ctg tcc agc cag cct gca gcg cag     3089
Ser Leu Thr Gly Leu Leu Asp Met Leu Ser Ser Gln Pro Ala Ala Gln
986                 991                 996                1001

agg ggc tta gtg cta ctg agg cct ccc gcc tct ctg cag tat cga ttt     3137
Arg Gly Leu Val Leu Leu Arg Pro Pro Ala Ser Leu Gln Tyr Arg Phe
1002                1007                1012                1017

gcg agg att gct att gag gtg tga atgcgtgctt gtatcccagc agggcataga    3191
Ala Arg Ile Ala Ile Glu Val  *
1018                1023

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gtttacatca ttccagtaat gtcattgatt ttcatctttc cctgtccttg ctgtaatact 3371

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aaatgtaaat atgcagttag gcattatttt atgtaaatgc attgggtttt tactgtagca 4511

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agtcaggaag tacctgccac caatgagatg tctgatgctt tgcctcttac catgcctctg 4631

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Met Pro Leu Val Val Phe Cys Gly Leu
1 5

ccg tac agc ggc aag agc cgg cgt gct gaa gag ttg cgc gtg gcg ctg 159
Pro Tyr Ser Gly Lys Ser Arg Arg Ala Glu Glu Leu Arg Val Ala Leu
10 15 20 25

gct gcc gag ggc cgc gcg gtg tac gtg gtg gac gac gca gct gtc ctg 207
Ala Ala Glu Gly Arg Ala Val Tyr Val Val Asp Asp Ala Ala Val Leu
26 31 36 41

ggc gca gag gac cca gcg gtg tac ggc gat tct gcc cgt gag aag gca 255
Gly Ala Glu Asp Pro Ala Val Tyr Gly Asp Ser Ala Arg Glu Lys Ala
42 47 52 57

ttg cgt gga gct ctg cga gcc tcc gtg gaa cgg cgc ctg agt cgc cac 303
Leu Arg Gly Ala Leu Arg Ala Ser Val Glu Arg Arg Leu Ser Arg His
58 63 68 73

gac gtg gtc atc ctg gac tcg ctt aac tac atc aaa ggt ttc cgt tac 351
Asp Val Val Ile Leu Asp Ser Leu Asn Tyr Ile Lys Gly Phe Arg Tyr
74 79 84 89

gag ctc tac tgc ctg gca cgg gcg gcg cgc acc ccg ctc tgc ctg gtc 399
Glu Leu Tyr Cys Leu Ala Arg Ala Ala Arg Thr Pro Leu Cys Leu Val
90 95 100 105

tac tgc gta cgg ccc ggc ggc ccg atc gcg gga cct cag gtg gcg ggc 447
Tyr Cys Val Arg Pro Gly Gly Pro Ile Ala Gly Pro Gln Val Ala Gly
106 111 116 121

gcg aac gag aac cct ggc cgg aac gtc agt gtg agt tgg cgg cca cgc 495
Ala Asn Glu Asn Pro Gly Arg Asn Val Ser Val Ser Trp Arg Pro Arg
122 127 132 137

gct gag gag gac ggg aga gcc cag gcg gcg ggc agc agc gtc ctc agg 543
Ala Glu Glu Asp Gly Arg Ala Gln Ala Ala Gly Ser Ser Val Leu Arg
138 143 148 153

gaa ctg cat act gcg gac tct gta gta aat gga agt gcc cag gcc gac 591
Glu Leu His Thr Ala Asp Ser Val Val Asn Gly Ser Ala Gln Ala Asp
154 159 164 169

gta ccc aag gaa ctg gag cga gaa gaa tcc ggg gct gcg gag tct cca 639
Val Pro Lys Glu Leu Glu Arg Glu Glu Ser Gly Ala Ala Glu Ser Pro
170 175 180 185

gct ctt gtg act ccg gat tca gag aaa tct gca aag cat ggg tcc ggt 687

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Ala Leu Val Thr Pro Asp Ser Glu Lys Ser Ala Lys His Gly Ser Gly
186                 191                 196                 201

gcc ttt tac tct ccc gaa ctc ctg gag gcc cta acg ctg cgc ttt gag      735
Ala Phe Tyr Ser Pro Glu Leu Leu Glu Ala Leu Thr Leu Arg Phe Glu
202                 207                 212                 217

gct ccc gat tct cgg aat cgc tgg gac cgg cct tta ttc act ttg gtg      783
Ala Pro Asp Ser Arg Asn Arg Trp Asp Arg Pro Leu Phe Thr Leu Val
218                 223                 228                 233

ggc cta gag gag ccg ttg ccc ctg gcg ggg atc cgc tct gcc ctg ttt      831
Gly Leu Glu Glu Pro Leu Pro Leu Ala Gly Ile Arg Ser Ala Leu Phe
234                 239                 244                 249

gag aac cgg gcc cca cca ccc cat cag tct acg cag tcc cag ccc ctc      879
Glu Asn Arg Ala Pro Pro Pro His Gln Ser Thr Gln Ser Gln Pro Leu
250                 255                 260                 265

gcc tcc ggc agc ttt ctg cac cag ttg gac cag gtc acg agt caa gta      927
Ala Ser Gly Ser Phe Leu His Gln Leu Asp Gln Val Thr Ser Gln Val
266                 271                 276                 281

ctg gcc gga ttg atg gaa gcg cag aag agc gct gtc ccc ggg gac ttg      975
Leu Ala Gly Leu Met Glu Ala Gln Lys Ser Ala Val Pro Gly Asp Leu
282                 287                 292                 297

ctc acg ctt cct ggt acc aca gag cac ttg cgg ttt acc cgg ccc ttg     1023
Leu Thr Leu Pro Gly Thr Thr Glu His Leu Arg Phe Thr Arg Pro Leu
298                 303                 308                 313

acc atg gca gaa ctg agt cgc ctt cgt cgc cag ttt att tcg tac act     1071
Thr Met Ala Glu Leu Ser Arg Leu Arg Arg Gln Phe Ile Ser Tyr Thr
314                 319                 324                 329

aaa atg cat ccc aac aat gag aac ttg ccg caa ctg gcc aac atg ttt     1119
Lys Met His Pro Asn Asn Glu Asn Leu Pro Gln Leu Ala Asn Met Phe
330                 335                 340                 345

ctt cag tat ttg agc cag agc ctg cac tga c cagaggaggt agggggaag      1170
Leu Gln Tyr Leu Ser Gln Ser Leu His  *
346                 351

ccatggcttc tgatctccac tccactttat ttctctggga aaaataggct gcaggtctcc   1230

agagcatatc gatgcagtac tgtactagag ctgttgtgac tgattcactc aaactttcct   1290

gcataccccct gtgccaggcc ttgggtttac agcataagtt cagactaaag agaatggaga   1350

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tcctgagagt ctgagtagtg ccaggaagca gcctcagaat ttgggggccc attacacacc 780

ccagcc atg ttc ctg cga cgg ctt ggt ggc tgg cta cct cgc cct tgg 828
Met Phe Leu Arg Arg Leu Gly Gly Trp Leu Pro Arg Pro Trp
1 5 10

ggc cgc cgg aaa cca atg agg cct gac ccg cct tac cca gaa ccc aga 876
Gly Arg Arg Lys Pro Met Arg Pro Asp Pro Pro Tyr Pro Glu Pro Arg
15 20 25 30

cgg gtg gac agc tcc tcg gag aat tca gga agt gac tgg gat agt gcc 924
Arg Val Asp Ser Ser Ser Glu Asn Ser Gly Ser Asp Trp Asp Ser Ala
31 36 41 46

cca gaa acc atg gaa gat gtg ggg cat ccc aag act aag gac tcg ggg 972
Pro Glu Thr Met Glu Asp Val Gly His Pro Lys Thr Lys Asp Ser Gly
47 52 57 62

gca ttg agg gtt tct ggg gct gct tcc gaa cca agc aag gag gag ccc 1020
Ala Leu Arg Val Ser Gly Ala Ala Ser Glu Pro Ser Lys Glu Glu Pro
63 68 73 78

caa gtt gag cag cta ggg agc aaa aga atg gat tcc ctc aag tgg gac 1068
Gln Val Glu Gln Leu Gly Ser Lys Arg Met Asp Ser Leu Lys Trp Asp

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 79                  84                  89                  94

cag cct atc tct agc act caa gag tct ggg aga ctg gag gct gga ggg     1116
Gln Pro Ile Ser Ser Thr Gln Glu Ser Gly Arg Leu Glu Ala Gly Gly
 95                 100                 105                 110

gcc agt ccc aaa ctc aga tgg gat cat gtg gat tca ggt ggc acc agg     1164
Ala Ser Pro Lys Leu Arg Trp Asp His Val Asp Ser Gly Gly Thr Arg
111                 116                 121                 126

aga cca ggg gtg tcc cct gaa ggg gga ctg agc gtc cct ggg cca gga     1212
Arg Pro Gly Val Ser Pro Glu Gly Gly Leu Ser Val Pro Gly Pro Gly
127                 132                 137                 142

gcc cca ttg gag aaa cct ggt agg cgt gag aag ctg ttg ggc tgg ctg     1260
Ala Pro Leu Glu Lys Pro Gly Arg Arg Glu Lys Leu Leu Gly Trp Leu
143                 148                 153                 158

cgg ggg gaa cca gga gct ccc tcc cgg tac ttg ggg ggc cca gaa gag     1308
Arg Gly Glu Pro Gly Ala Pro Ser Arg Tyr Leu Gly Gly Pro Glu Glu
159                 164                 169                 174

tgt ctg cag atc tcc acc aac ctg acc ctg cat ctt ctg gag ctg ctg     1356
Cys Leu Gln Ile Ser Thr Asn Leu Thr Leu His Leu Leu Glu Leu Leu
175                 180                 185                 190

gcc tct gcc ctg ctg gcc ctg tgc tca cga cca ctg cgg gca gcc ttg     1404
Ala Ser Ala Leu Leu Ala Leu Cys Ser Arg Pro Leu Arg Ala Ala Leu
191                 196                 201                 206

gac aca ctg ggc ctg cgt gga ccg ctg ggc ctc tgg cta cat ggc cta     1452
Asp Thr Leu Gly Leu Arg Gly Pro Leu Gly Leu Trp Leu His Gly Leu
207                 212                 217                 222

ctg tcc ttc ctg gct gcc ctg cat ggg ctc cat gct gtt ctg agc cta     1500
Leu Ser Phe Leu Ala Ala Leu His Gly Leu His Ala Val Leu Ser Leu
223                 228                 233                 238

ctt act gcc cac cct ttg cac ttc gcc tgc ctc ttt ggt ctc ctg cag     1548
Leu Thr Ala His Pro Leu His Phe Ala Cys Leu Phe Gly Leu Leu Gln
239                 244                 249                 254

gcc ttg gtg ctg gct gtc agc ctc cgg gag ccc aat ggg gat gag gcg     1596
Ala Leu Val Leu Ala Val Ser Leu Arg Glu Pro Asn Gly Asp Glu Ala
255                 260                 265                 270

gcc act gac tgg gag agt gag ggg ttg gag agg gaa ggt gag gag cag     1644
Ala Thr Asp Trp Glu Ser Glu Gly Leu Glu Arg Glu Gly Glu Glu Gln
271                 276                 281                 286

agg gga gac ccg gga aag ggg ctg tga ccgtg gggtgggggc aaagggtgaa     1696
Arg Gly Asp Pro Gly Lys Gly Leu  *
287                 292

gagagtgtgg gctttaggag aaaagtgtga ggcatgaccc aaattgtaag catagggacc   1756

tcagggatgg ggaagaaacc cgagtacgag ggtgcagggc ccccccttcat acacaggaga  1816
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gaacagaact atttagggtg tttgtgttta tggacagtga gggcactgct cttggattca   1876

ccagctgtta tttttgcttt tacttttctc ccaccttcag ttttttttt tttttccacc   1936

tccacttttt aaaagcaaaa aaaaaaaaa                                    1965
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<210> 80
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<213> Homo sapiens

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<222> (483)..(1610)

<400> 80

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ggtcgcaggt gggctctccc agctgtgacg acgcggcccc ggcctgagga gccccgcgga    180

caaggttgag cgagtcgtgg gctttttttc cgtccccacg tgggcacggc ccgggctgcg    240

tgagctcact tcctccacat cttatctcct gccgggcgcg gccctgaccc tctattctgc    300

accctgtgag ccaccgagac tgaaccaaac ccaggaagcg gcgccaccaa ccagcctcgc    360

agaggcagag gccctggagc agtgacagca caggagatct gctggctcgg gggaagggga    420

ggaaagagga aaacaaaggg agtgatcgag tgagcctcgc cccgccctcc ctgcgccggc    480

cc   atg atg tgt cag tca gag gcg cgg caa gga cca gag ctc cgc gcg      527
     Met Met Cys Gln Ser Glu Ala Arg Gln Gly Pro Glu Leu Arg Ala
       1               5                  10

gcg aaa tgg ttg cac ttc ccc cag ctg gcc ctg agg cgg agg ctg ggg      575
Ala Lys Trp Leu His Phe Pro Gln Leu Ala Leu Arg Arg Arg Leu Gly
 16                  21                  26                  31

cag ctg agc tgc atg tcc aga ccc gct ctg aaa ctg cgc tcc tgg ccc      623
Gln Leu Ser Cys Met Ser Arg Pro Ala Leu Lys Leu Arg Ser Trp Pro
 32                  37                  42                  47

ttg acc gtc ctc tac tac ctc ctg ccc ttc ggc gcc ctc aga ccg ctc      671
Leu Thr Val Leu Tyr Tyr Leu Leu Pro Phe Gly Ala Leu Arg Pro Leu
 48                  53                  58                  63

agc cgg gtg gga tgg agg ccc gta agc agg gtg gct ttg tac aag tca      719
Ser Arg Val Gly Trp Arg Pro Val Ser Arg Val Ala Leu Tyr Lys Ser
 64                  69                  74                  79

gtg cca acg cgc ttg ctg tca cgg gcc tgg ggt cgc ctc aat cag gtg      767
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Val Pro Thr Arg Leu Leu Ser Arg Ala Trp Gly Arg Leu Asn Gln Val
 80                  85                  90                  95

gag ctg cca cac tgg ctg cgc agg ccc gtc tac agc ctg tac atc tgg      815
Glu Leu Pro His Trp Leu Arg Arg Pro Val Tyr Ser Leu Tyr Ile Trp
 96                 101                 106                 111

acg ttt ggg gtg aac atg aaa gag gcc gct gtg gag gac ctg cat cac      863
Thr Phe Gly Val Asn Met Lys Glu Ala Ala Val Glu Asp Leu His His
112                 117                 122                 127

tac cgc aac ctc agc gag ttc ttc cgg cgc aag ctg aag ccg cag gcc      911
Tyr Arg Asn Leu Ser Glu Phe Phe Arg Arg Lys Leu Lys Pro Gln Ala
128                 133                 138                 143

cgg cct gtc tgt ggc ctg cac agc gtg att agc cca tcg gat gga agg      959
Arg Pro Val Cys Gly Leu His Ser Val Ile Ser Pro Ser Asp Gly Arg
144                 149                 154                 159

atc ctc aac ttt ggg cag gtg aag aac tgt gag gtg gag cag gta aag     1007
Ile Leu Asn Phe Gly Gln Val Lys Asn Cys Glu Val Glu Gln Val Lys
160                 165                 170                 175

ggg gtc acc tac tcc ctg gag tcg ttc ctg ggc ccg cgt atg tgc aca     1055
Gly Val Thr Tyr Ser Leu Glu Ser Phe Leu Gly Pro Arg Met Cys Thr
176                 181                 186                 191

gag gac ctg ccc ttc cca cca gcc gcg tcg tgt gac tcc ttc aag aac     1103
Glu Asp Leu Pro Phe Pro Pro Ala Ala Ser Cys Asp Ser Phe Lys Asn
192                 197                 202                 207

cag ctg gtc acc cgg gaa ggg aat gag ctc tat cac tgt gtc atc tac     1151
Gln Leu Val Thr Arg Glu Gly Asn Glu Leu Tyr His Cys Val Ile Tyr
208                 213                 218                 223

ctg gcc cct ggg gac tac cac tgc ttc cac tcc ccc acc gac tgg act     1199
Leu Ala Pro Gly Asp Tyr His Cys Phe His Ser Pro Thr Asp Trp Thr
224                 229                 234                 239

gtg tcc cac cgg cgc cac ttc cca ggc tcc ctg atg tca gtg aac cct     1247
Val Ser His Arg Arg His Phe Pro Gly Ser Leu Met Ser Val Asn Pro
240                 245                 250                 255

ggc atg gct cgc tgg atc aaa gag ctc ttc tgc cat aac gag cgg gtg     1295
Gly Met Ala Arg Trp Ile Lys Glu Leu Phe Cys His Asn Glu Arg Val
256                 261                 266                 271

gtc ctg acg ggg gac tgg aaa cat ggc ttc ttc tca ctg aca gct gtg     1343
Val Leu Thr Gly Asp Trp Lys His Gly Phe Phe Ser Leu Thr Ala Val
272                 277                 282                 287

ggg gcc acc aac gtg ggc tcc att cgc atc tac ttt gac cgg gac ctg     1391
Gly Ala Thr Asn Val Gly Ser Ile Arg Ile Tyr Phe Asp Arg Asp Leu
288                 293                 298                 303

cac aca aac agc cca agg cac agc aag ggc tcc tac aat gac ttc agc     1439
His Thr Asn Ser Pro Arg His Ser Lys Gly Ser Tyr Asn Asp Phe Ser
```

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304                 309                 314                 319

ttc gtg acg cac acc aat aga gag ggc gtc ccc atg cgt aag ggc gag     1487
Phe Val Thr His Thr Asn Arg Glu Gly Val Pro Met Arg Lys Gly Glu
320                 325                 330                 335

cac ctg ggc gag ttc aac ctg ggc tcc acc atc gtg ctc atc ttc gag     1535
His Leu Gly Glu Phe Asn Leu Gly Ser Thr Ile Val Leu Ile Phe Glu
336                 341                 346                 351

gcc ccc aag gac ttc aat ttc cag ctg aaa aca gga cag aaa atc cgc     1583
Ala Pro Lys Asp Phe Asn Phe Gln Leu Lys Thr Gly Gln Lys Ile Arg
352                 357                 362                 367

ttt ggg gaa gcc ctg ggc tcg ctc tag agtct ctttcctgat tatggctgct     1635
Phe Gly Glu Ala Leu Gly Ser Leu  *
368                 373

aagggatctt ttccaaacag agtgagggtc ttttcaagag ggaggcccat gaggccatcc   1695

aggtaagggc ctgcctcagc gtggttggga gtctgaccag gtaggacttg aatgattcgg   1755

ctaccacctg ttccagaggt gcagacaaga ggtggcgaga gcccccatca tgcccctcaa   1815

cctatcccgt tccttctgcc tacaaataaa aagtgcaggc tggaatgatc tcagtcacat   1875

ttggatcttt ttaaacactg tatagacgga agagcctgca ttcctgaccg aaccttcagt   1935

tggtctcggt tgtcgttttt tcttgctgct cctcccccca tcacctgagc tgttttctgt   1995

tggccccttt tgttttttgg ccttaacgct cctgctgcac agggtgaggt gcctccttgg   2055

cacagactgt ggatgcctct cccccagcag agccacacag ccttcgtgac aactgctttc   2115

cgttcccaca ttcacctcat cctgctcttt agaaaaagca gtctttgtgc ttgtggctga   2175

acgcatcacc ctggactctg ctagtgtctt ctgaggacac tgatgacact gattaatgat   2235

acagaccttt gcaggacctg atgagtgacc cttctggagc tggccaggtc ctctgcagca   2295

ggcaagacca atcaatcact gaacctgcct catggcacca gagtgaacag ggcaggcagg   2355

tagtaggccc agctggggaa atgggagagt tcctgtcccc ctccacatat ccctacatga   2415

aatatgggaa agttgctgct attgattcag ggtctgtctt ggaggcagag gacccttggt   2475

ggatagttgg tcagtgcctg gaaaacctgt cccagtttat caggaacgca ggcctgggga   2535

gcccccagtg gcggggacag ggccagattt catgttgacc ctggggatgc tgtgaatttc   2595

tcctgcagga gagacatcat tgaatttttt caactgtatc agtagcacag tatttttgta   2655

tgaaaagtgg gagacttctg aacagtaatt catttaattg caaagcattt tgaaataaaa   2715

aaaatcaaac ttaaaaaaaa aaaa                                          2739
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Case 5:20-cv-00526-JD Document 1-2 Filed 01/28/20 Page 322 of 350

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<212> DNA
<213> Homo sapiens

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<221> CDS
<222> (483)..(1787)

<400> 81
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ggtcgcaggt gggctctccc agctgtgacg acgcggcccc ggcctgagga gccccgcgga 180

caaggttgag cgagtcgtgg gctttttttc cgtccccacg tgggcacggc ccgggctgcg 240

tgagctcact tcctccacat cttatctcct gccgggcgcg gccctgaccc tctattctgc 300

accctgtgag ccaccgagac tgaaccaaac ccaggaagcg gcgccaccaa ccagcctcgc 360

agaggcagag gccctggagc agtgacagca caggagatct gctggctcgg gggaagggga 420

ggaaagagga aaacaaaggg agtgatcgag tgagcctcgc cccgccctcc ctgcgccggc 480

cc atg atg tgt cag tca gag gcg cgg caa gga cca gag ctc cgc gcg 527
Met Met Cys Gln Ser Glu Ala Arg Gln Gly Pro Glu Leu Arg Ala
1 5 10

gcg aaa tgg ttg cac ttc ccc cag ctg gcc ctg agg cgg agg ctg ggg 575
Ala Lys Trp Leu His Phe Pro Gln Leu Ala Leu Arg Arg Arg Leu Gly
16 21 26 31

cag ctg agc tgc atg tcc aga ccc gct ctg aaa ctg cgc tcc tgg ccc 623
Gln Leu Ser Cys Met Ser Arg Pro Ala Leu Lys Leu Arg Ser Trp Pro
32 37 42 47

ttg acc gtc ctc tac tac ctc ctg ccc ttc ggc gcc ctc aga ccg ctc 671
Leu Thr Val Leu Tyr Tyr Leu Leu Pro Phe Gly Ala Leu Arg Pro Leu
48 53 58 63

agc cgg gtg gga tgg agg ccc gta agc agg gtg gct ttg tac aag tca 719
Ser Arg Val Gly Trp Arg Pro Val Ser Arg Val Ala Leu Tyr Lys Ser
64 69 74 79

gtg cca acg cgc ttg ctg tca cgg gcc tgg ggt cgc ctc aat cag gtg 767
Val Pro Thr Arg Leu Leu Ser Arg Ala Trp Gly Arg Leu Asn Gln Val
80 85 90 95

gag ctg cca cac tgg ctg cgc agg ccc gtc tac agc ctg tac atc tgg 815
Glu Leu Pro His Trp Leu Arg Arg Pro Val Tyr Ser Leu Tyr Ile Trp
96 101 106 111

acg ttt ggg gtg aac atg aaa gag gcc gct gtg gag gac ctg cat cac 863

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Thr Phe Gly Val Asn Met Lys Glu Ala Ala Val Glu Asp Leu His His
112                 117                 122                 127

tac cgc aac ctc agc gag ttc ttc cgg cgc aag ctg aag ccg cag gcc      911
Tyr Arg Asn Leu Ser Glu Phe Phe Arg Arg Lys Leu Lys Pro Gln Ala
128                 133                 138                 143

cgg cct gtc tgt ggc ctg cac agc gtg gtg agg cct gac cct ttc ctc      959
Arg Pro Val Cys Gly Leu His Ser Val Val Arg Pro Asp Pro Phe Leu
144                 149                 154                 159

ctg cag gaa aca gga ctt ttt cct gcc tcc cca gca cag ccc ccc tgg     1007
Leu Gln Glu Thr Gly Leu Phe Pro Ala Ser Pro Ala Gln Pro Pro Trp
160                 165                 170                 175

tct cca gcg tat ctg gaa ggg gca gga atg aca agg gga ggt ggg ggc     1055
Ser Pro Ala Tyr Leu Glu Gly Ala Gly Met Thr Arg Gly Gly Gly Gly
176                 181                 186                 191

tgt ctc ctg ggg gga gga gac cct gct ctc cct ggc agc aag cct ctc     1103
Cys Leu Leu Gly Gly Gly Asp Pro Ala Leu Pro Gly Ser Lys Pro Leu
192                 197                 202                 207

ctg ccc ttc cag att agc cca tcg gat gga agg atc ctc aac ttt ggg     1151
Leu Pro Phe Gln Ile Ser Pro Ser Asp Gly Arg Ile Leu Asn Phe Gly
208                 213                 218                 223

cag gtg aag aac tgt gag gtg gag cag gta aag ggg gtc acc tac tcc     1199
Gln Val Lys Asn Cys Glu Val Glu Gln Val Lys Gly Val Thr Tyr Ser
224                 229                 234                 239

ctg gag tcg ttc ctg ggc ccg cgt atg tgc aca gag gac ctg ccc ttc     1247
Leu Glu Ser Phe Leu Gly Pro Arg Met Cys Thr Glu Asp Leu Pro Phe
240                 245                 250                 255

cca cca gcc gcg tcg tgt gac tcc ttc aag aac cag ctg gtc acc cgg     1295
Pro Pro Ala Ala Ser Cys Asp Ser Phe Lys Asn Gln Leu Val Thr Arg
256                 261                 266                 271

gaa ggg aat gag ctc tat cac tgt gtc atc tac ctg gcc cct ggg gac     1343
Glu Gly Asn Glu Leu Tyr His Cys Val Ile Tyr Leu Ala Pro Gly Asp
272                 277                 282                 287

tac cac tgc ttc cac tcc ccc acc gac tgg act gtg tcc cac cgg cgc     1391
Tyr His Cys Phe His Ser Pro Thr Asp Trp Thr Val Ser His Arg Arg
288                 293                 298                 303

cac ttc cca ggc tcc ctg atg tca gtg aac cct ggc atg gct cgc tgg     1439
His Phe Pro Gly Ser Leu Met Ser Val Asn Pro Gly Met Ala Arg Trp
304                 309                 314                 319

atc aaa gag ctc ttc tgc cat aac gag cgg gtg gtc ctg acg ggg gac     1487
Ile Lys Glu Leu Phe Cys His Asn Glu Arg Val Val Leu Thr Gly Asp
320                 325                 330                 335

tgg aaa cat ggc ttc ttc tca ctg aca gct gtg ggg gcc acc aac gtg     1535
Trp Lys His Gly Phe Phe Ser Leu Thr Ala Val Gly Ala Thr Asn Val
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336                 341                 346                 351

ggc tcc att cgc atc tac ttt gac cgg gac ctg cac aca aac agc cca     1583
Gly Ser Ile Arg Ile Tyr Phe Asp Arg Asp Leu His Thr Asn Ser Pro
352                 357                 362                 367

agg cac agc aag ggc tcc tac aat gac ttc agc ttc gtg acg cac acc     1631
Arg His Ser Lys Gly Ser Tyr Asn Asp Phe Ser Phe Val Thr His Thr
368                 373                 378                 383

aat aga gag ggc gtc ccc atg cgt aag ggc gag cac ctg ggc gag ttc     1679
Asn Arg Glu Gly Val Pro Met Arg Lys Gly Glu His Leu Gly Glu Phe
384                 389                 394                 399

aac ctg ggc tcc acc atc gtg ctc atc ttc gag gcc ccc aag gac ttc     1727
Asn Leu Gly Ser Thr Ile Val Leu Ile Phe Glu Ala Pro Lys Asp Phe
400                 405                 410                 415

aat ttc cag ctg aaa aca gga cag aaa atc cgc ttt ggg gaa gcc ctg     1775
Asn Phe Gln Leu Lys Thr Gly Gln Lys Ile Arg Phe Gly Glu Ala Leu
416                 421                 426                 431

ggc tcg ctc tag agt ctctttcctg attatggctg ctaagggatc ttttccaaac     1830
Gly Ser Leu  *
432

agagtgaggg tcttttcaag agggaggccc atgaggccat ccaggtaagg gcctgcctca   1890

gcgtggttgg gagtctgacc aggtaggact tgaatgattc ggctaccacc tgttccagag   1950

gtgcagacaa gaggtggcga gagcccccat catgcccctc aacctatccc gttccttctg   2010

cctacaaata aaaagtgcag gctggaatga tctcagtcac atttggatct ttttaaacac   2070

tgtatagacg gaagagcctg cattcctgac cgaaccttca gttggtctcg gttgtcgttt   2130

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tgctagtgtc ttctgaggac actgatgaca ctgattaatg atacagacct ttgcaggacc   2430

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tggaaaacct gtcccagttt atcaggaacg caggcctggg gagcccccag tggcggggac   2730

agggccagat ttcatgttga ccctggggat gctgtgaatt tctcctgcag gagagacatc   2790
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attgaatttt ttcaactgta tcagtagcac agtatttttg tatgaaaagt gggagacttc   2850

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aaaaaa                                                             2916
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<213> Homo sapiens

<220>
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taatttgatc ctcaggaatt tgttctgccc tcatctggcc ctggccagct ctgcatttga    180

caaatgccag gaagaggaaa ctgttgagaa aacggaacta ctggggaaag ggagggctca    240

ctgagaacca tcccggtaac ccgaccgccg ctggtcacc   atg aac cac att gtg     294
                                              Met Asn His Ile Val
                                                1

caa acc ttc tct cct gtc aac agc ggc cag cct ccc aac tac gag atg      342
Gln Thr Phe Ser Pro Val Asn Ser Gly Gln Pro Pro Asn Tyr Glu Met
  6                  11                  16                  21

ctc aag gag gag cag gaa gtg gct atg ctg ggg gcg ccc cac aac cct      390
Leu Lys Glu Glu Gln Glu Val Ala Met Leu Gly Ala Pro His Asn Pro
 22                  27                  32                  37

gct ccc ccg acg tcc acc gtg atc cac atc cgc agc gag acc tcc gtg      438
Ala Pro Pro Thr Ser Thr Val Ile His Ile Arg Ser Glu Thr Ser Val
 38                  43                  48                  53

cct gac cat gtc gtc tgg tcc ctg ttc aac acc ctc ttc atg aac acc      486
Pro Asp His Val Val Trp Ser Leu Phe Asn Thr Leu Phe Met Asn Thr
 54                  59                  64                  69

tgc tgc ctg ggc ttc ata gca ttc gcc tac tcc gtg aag tct agg gac      534
Cys Cys Leu Gly Phe Ile Ala Phe Ala Tyr Ser Val Lys Ser Arg Asp
 70                  75                  80                  85

agg aag atg gtt ggc gac gtg acc ggg gcc cag gcc tat gcc tcc acc      582
Arg Lys Met Val Gly Asp Val Thr Gly Ala Gln Ala Tyr Ala Ser Thr
 86                  91                  96                 101

gcc aag tgc ctg acc atc tgg gcc ctg att ttg ggc atc ttc atg acc      630
```

```
Ala Lys Cys Leu Thr Ile Trp Ala Leu Ile Leu Gly Ile Phe Met Thr
102                 107                 112                 117

att ctg ctc gtc atc atc cca gtg ttg gtc gtc cag gcc cag cga tag      678
Ile Leu Leu Val Ile Ile Pro Val Leu Val Val Gln Ala Gln Arg  *
118                 123                 128                 133

atcaggaggc atcattgagg ccaggagctc tgcccgtgac ctgtatccca cgtactctat    738

cttccattcc tcgccctgcc cccagaggcc aggagctctg cccttgacct gtattccact    798

tactccacct tccattcctc gccctgtccc cacagccgag tcctgcatca gccctttatc    858

ctcacacgct tttctacaat ggcattcaat aaagtgtata tgtttctggt gctggtcgac    918

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atg ctg gat cat ttc cag gcc acg ccc cac cat ggg gtc tac tct cgg      168
Met Leu Asp His Phe Gln Ala Thr Pro His His Gly Val Tyr Ser Arg
  1               5                  10                  15

gag gag gag ctg ctg agg gag cgg aaa cgc ctg ggg gtc ttc ggc atc      216
Glu Glu Glu Leu Leu Arg Glu Arg Lys Arg Leu Gly Val Phe Gly Ile
 17                  22                  27                  32

acc tcc tac gac ttc cac agc gag agt ggc ctc ttc ctc ttc cag gcc      264
Thr Ser Tyr Asp Phe His Ser Glu Ser Gly Leu Phe Leu Phe Gln Ala
 33                  38                  43                  48

agc aac agc ctc ttc cgc tgc cgc gac ggc ggc aag aac ggc ttc atg      312
Ser Asn Ser Leu Phe Arg Cys Arg Asp Gly Gly Lys Asn Gly Phe Met
 49                  54                  59                  64

gtg tcc cct atg aaa ccg ctg gaa atc aag acc cag tgc tca ggg ccc      360
Val Ser Pro Met Lys Pro Leu Glu Ile Lys Thr Gln Cys Ser Gly Pro
 65                  70                  75                  80

cgg atg gac ccc aaa atc tgc cct gcc gac cct gcc ttc ttc tcc ttc      408
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Arg Met Asp Pro Lys Ile Cys Pro Ala Asp Pro Ala Phe Phe Ser Phe
 81                  86                  91                  96

atc aat aac agc gac ctg tgg gtg gcc aac atc gag aca ggc gag gag      456
Ile Asn Asn Ser Asp Leu Trp Val Ala Asn Ile Glu Thr Gly Glu Glu
 97                 102                 107                 112

cgg cgg ctg acc ttc tgc cac caa ggt tta tcc aat gtc ctg gat gac      504
Arg Arg Leu Thr Phe Cys His Gln Gly Leu Ser Asn Val Leu Asp Asp
113                 118                 123                 128

ccc aag tct gcg ggt gtg gcc acc ttc gtc ata cag gaa gag ttc gac      552
Pro Lys Ser Ala Gly Val Ala Thr Phe Val Ile Gln Glu Glu Phe Asp
129                 134                 139                 144

cgc ttc act ggg tac tgg tgg tgc ccc aca gcc tcc tgg gaa ggt tca      600
Arg Phe Thr Gly Tyr Trp Trp Cys Pro Thr Ala Ser Trp Glu Gly Ser
145                 150                 155                 160

gag ggc ctc aag acg ctg cga atc ctg tat gag gaa gtc gat gag tcc      648
Glu Gly Leu Lys Thr Leu Arg Ile Leu Tyr Glu Glu Val Asp Glu Ser
161                 166                 171                 176

gag gtg gag gtc att cac gtc ccc tct cct gcg cta gaa gaa agg aag      696
Glu Val Glu Val Ile His Val Pro Ser Pro Ala Leu Glu Glu Arg Lys
177                 182                 187                 192

acg gac tcg tat cgg tac ccc agg aca ggc agc aag aat ccc aag att      744
Thr Asp Ser Tyr Arg Tyr Pro Arg Thr Gly Ser Lys Asn Pro Lys Ile
193                 198                 203                 208

gcc ttg aaa ctg gct gag ttc cag act gac agc cag ggc aag atc gtc      792
Ala Leu Lys Leu Ala Glu Phe Gln Thr Asp Ser Gln Gly Lys Ile Val
209                 214                 219                 224

tcg acc cag gag aag gag ctg gtg cag ccc ttc agc tcg ctg ttc ccg      840
Ser Thr Gln Glu Lys Glu Leu Val Gln Pro Phe Ser Ser Leu Phe Pro
225                 230                 235                 240

aag gtg gag tac atc gcc agg gcc ggg tgg acc cgg gat ggc aaa tac      888
Lys Val Glu Tyr Ile Ala Arg Ala Gly Trp Thr Arg Asp Gly Lys Tyr
241                 246                 251                 256

gcc tgg gcc atg ttc ctg gac cgg ccc cag cag tgg ctc cag ctc gtc      936
Ala Trp Ala Met Phe Leu Asp Arg Pro Gln Gln Trp Leu Gln Leu Val
257                 262                 267                 272

ctc ctc ccc ccg gcc ctg ttc atc ccg agc aca gag aat gag gag cag      984
Leu Leu Pro Pro Ala Leu Phe Ile Pro Ser Thr Glu Asn Glu Glu Gln
273                 278                 283                 288

cgg cta gcc tct gcc aga gct gtc ccc agg aat gtc cag ccg tat gtg     1032
Arg Leu Ala Ser Ala Arg Ala Val Pro Arg Asn Val Gln Pro Tyr Val
289                 294                 299                 304

gtg tac gag gag gtc acc aac gtc tgg atc aat gtt cat gac atc ttc     1080
Val Tyr Glu Glu Val Thr Asn Val Trp Ile Asn Val His Asp Ile Phe
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305                 310                 315                 320

tat ccc ttc ccc caa tca gag gga gag gac gag ctc tgc ttt ctc cgc     1128
Tyr Pro Phe Pro Gln Ser Glu Gly Glu Asp Glu Leu Cys Phe Leu Arg
321                 326                 331                 336

gcc aat gaa tgc aag acc ggc ttc tgc cat ttg tac aaa gtc acc gcc     1176
Ala Asn Glu Cys Lys Thr Gly Phe Cys His Leu Tyr Lys Val Thr Ala
337                 342                 347                 352

gtt tta aaa tcc cag ggc tac gat tgg agt gag ccc ttc agc ccc ggg     1224
Val Leu Lys Ser Gln Gly Tyr Asp Trp Ser Glu Pro Phe Ser Pro Gly
353                 358                 363                 368

gaa ggt gag cag agc ctg acg aat gct atc tgg gtc aat gag gag acc     1272
Glu Gly Glu Gln Ser Leu Thr Asn Ala Ile Trp Val Asn Glu Glu Thr
369                 374                 379                 384

aag ctg gtg tac ttc cag ggc acc aag gac acg ccg ctg gag cac cac     1320
Lys Leu Val Tyr Phe Gln Gly Thr Lys Asp Thr Pro Leu Glu His His
385                 390                 395                 400

ctc tac gtg gtc agc tat gag gcg gcc ggc gag atc gta cgc ctc acc     1368
Leu Tyr Val Val Ser Tyr Glu Ala Ala Gly Glu Ile Val Arg Leu Thr
401                 406                 411                 416

acg ccc ggc ttc tcc cat agc tgc tcc atg agc cag aac ttc gac atg     1416
Thr Pro Gly Phe Ser His Ser Cys Ser Met Ser Gln Asn Phe Asp Met
417                 422                 427                 432

ttc gtc agc cac tac agc agc gtg agc acg ccg ccc tgc gtg cac gtc     1464
Phe Val Ser His Tyr Ser Ser Val Ser Thr Pro Pro Cys Val His Val
433                 438                 443                 448

tac aag ctg agc ggc ccc gac gac gac ccc ctg cac aag cag ccc cgc     1512
Tyr Lys Leu Ser Gly Pro Asp Asp Asp Pro Leu His Lys Gln Pro Arg
449                 454                 459                 464

ttc tgg gct agc atg atg gag gca gcc aag atc ttc cat ttc cac acg     1560
Phe Trp Ala Ser Met Met Glu Ala Ala Lys Ile Phe His Phe His Thr
465                 470                 475                 480

cgc tcg gat gtg cgg ctc tac ggc atg atc tac aag ccc cac gcc ttg     1608
Arg Ser Asp Val Arg Leu Tyr Gly Met Ile Tyr Lys Pro His Ala Leu
481                 486                 491                 496

cag cca ggg aag aag cac ccc acc gtc ctc ttt gta tat gga ggc ccc     1656
Gln Pro Gly Lys Lys His Pro Thr Val Leu Phe Val Tyr Gly Gly Pro
497                 502                 507                 512

cag gtg cag ctg gtg aat aac tcc ttc aaa ggc atc aag tac ttg cgg     1704
Gln Val Gln Leu Val Asn Asn Ser Phe Lys Gly Ile Lys Tyr Leu Arg
513                 518                 523                 528

ctc aac aca ctg gcc tcc ctg ggc tac gcc gtg gtt gtg att gac ggc     1752
Leu Asn Thr Leu Ala Ser Leu Gly Tyr Ala Val Val Val Ile Asp Gly
529                 534                 539                 544
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agg ggc tcc tgt cag cga ggg ctt cgg ttc gaa ggg gcc ctg aaa aac     1800
Arg Gly Ser Cys Gln Arg Gly Leu Arg Phe Glu Gly Ala Leu Lys Asn
545                 550                 555                 560

caa atg ggc cag gtg gag atc gag gac cag gtg gag ggc ctg cag ttc     1848
Gln Met Gly Gln Val Glu Ile Glu Asp Gln Val Glu Gly Leu Gln Phe
561                 566                 571                 576

gtg gcc gag aag tat ggc ttc atc gac ctg agc cga gtt gcc atc cat     1896
Val Ala Glu Lys Tyr Gly Phe Ile Asp Leu Ser Arg Val Ala Ile His
577                 582                 587                 592

ggc tgg tcc tac ggg ggc ttc ctc tcg ctc atg ggg cta atc cac aag     1944
Gly Trp Ser Tyr Gly Gly Phe Leu Ser Leu Met Gly Leu Ile His Lys
593                 598                 603                 608

ccc cag gtg ttc aag gtg gcc atc gcg ggt gcc ccg gtc acc gtc tgg     1992
Pro Gln Val Phe Lys Val Ala Ile Ala Gly Ala Pro Val Thr Val Trp
609                 614                 619                 624

atg gcc tac gac aca ggg tac act gag cgc tac atg gac gtc cct gag     2040
Met Ala Tyr Asp Thr Gly Tyr Thr Glu Arg Tyr Met Asp Val Pro Glu
625                 630                 635                 640

aac aac cag cac ggc tat gag gcg ggt tcc gtg gcc ctg cac gtg gag     2088
Asn Asn Gln His Gly Tyr Glu Ala Gly Ser Val Ala Leu His Val Glu
641                 646                 651                 656

aag ctg ccc aat gag ccc aac cgc ttg ctt atc ctc cac ggc ttc ctg     2136
Lys Leu Pro Asn Glu Pro Asn Arg Leu Leu Ile Leu His Gly Phe Leu
657                 662                 667                 672

gac gaa aac gtg cac ttt ttc cac aca aac ttc ctc gtc tcc caa ctg     2184
Asp Glu Asn Val His Phe Phe His Thr Asn Phe Leu Val Ser Gln Leu
673                 678                 683                 688

atc cga gca ggg aaa cct tac cag ctc cag gtg gcc ctg cct cct gtc     2232
Ile Arg Ala Gly Lys Pro Tyr Gln Leu Gln Val Ala Leu Pro Pro Val
689                 694                 699                 704

tcc ccg cag atc tac ccc aac gag aga cac agt att cgc tgc ccc gag     2280
Ser Pro Gln Ile Tyr Pro Asn Glu Arg His Ser Ile Arg Cys Pro Glu
705                 710                 715                 720

tcg ggc gag cac tat gaa gtc acg ttg ctg cac ttt cta cag gaa tac     2328
Ser Gly Glu His Tyr Glu Val Thr Leu Leu His Phe Leu Gln Glu Tyr
721                 726                 731                 736

ctc tga gcctgcccac cgggagccgc cacatcacag cacaagtggc tgcagcctcc      2384
Leu  *
737

gcggggaacc aggcgggagg gactgagtgg cccgcgggcc ccagtgaggc actttgtccc   2444

gcccagcgct ggccagcccc gaggagccgc tgccttcacc gccccgacgc cttttatcct   2504
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tttttaaacg ctcttgggtt ttatgtccgc tgcttcttgg ttgccgagac agagagatgg   2564

tggtctcggg ccagcccctc ctctccccgc cttctgggag gaggaggtca cacgctgatg   2624

ggcactggag aggccagaag agactcagag gagcgggctg ccttccgcct ggggctccct   2684

gtgacctctc agtcccctgg cccggccagc caccgtcccc agcacccaag catgcaattg   2744

cctgtccccc ccggccagcc tccccaactt gatgtttgtg ttttgtttgg ggggatattt   2804

ttcataatta tttaaaagac aggccgggcg cggtggctca cgtctgtaat cccagcactt   2864

tgggaggctg aggcgggcgg atcacctgag gttgggagtt caagaccagc ctggccaaca   2924

tggggaaacc ccgtctctac taaaaataca aaaaattagc cgggtgtggt ggcgcgtgcc   2984

tataatccca gctactcggg aggctgaggc aggagaatcg cttgaacccg ggaggtggag   3044

gttgcggtga gccaagatcg caccattgca ctccagcctg ggcaacaaga gcgaaactct   3104

gtctcaaaat aaataaaaaa taaaagacag aaagcaaggg gtgcctaaat ctagacttgg   3164

ggtccacacc gggcagcggg gttgcaaccc agcacctggt aggctccatt tcttcccaag   3224

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                                                     Met Pro Glu
                                                       1

gca aaa cca gcg gcc aaa aag gcc ccc aaa ggc aaa gat gcc ccc aaa      104
Ala Lys Pro Ala Ala Lys Lys Ala Pro Lys Gly Lys Asp Ala Pro Lys
  4                   9                  14                  19

gga gcc ccc aag gag gct ccc cct aag gag gct cct gca gag gcc ccc      152
Gly Ala Pro Lys Glu Ala Pro Pro Lys Glu Ala Pro Ala Glu Ala Pro
 20                  25                  30                  35

aaa gaa gcc cca ccc gag gac cag tcc ccg act gca gag gag ccc acc      200
Lys Glu Ala Pro Pro Glu Asp Gln Ser Pro Thr Ala Glu Glu Pro Thr
 36                  41                  46                  51

ggc gtt ttc ctg aag aag ccg gac tcc gtc tca gtg gag act ggg aag      248
Gly Val Phe Leu Lys Lys Pro Asp Ser Val Ser Val Glu Thr Gly Lys
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 52                  57                  62                  67

gac gca gtg gtc gtg gcc aag gtg aac ggg aag gag ctc cca gac aaa      296
Asp Ala Val Val Val Ala Lys Val Asn Gly Lys Glu Leu Pro Asp Lys
 68                  73                  78                  83

ccg acc atc aag tgg ttc aag ggg aag tgg ctg gag ctg ggc agc aag      344
Pro Thr Ile Lys Trp Phe Lys Gly Lys Trp Leu Glu Leu Gly Ser Lys
 84                  89                  94                  99

agt ggc gcc cgc ttc tcc ttc aag gag tcc cac aac tcc gcc agc aat      392
Ser Gly Ala Arg Phe Ser Phe Lys Glu Ser His Asn Ser Ala Ser Asn
100                 105                 110                 115

gtg tac acc gtg gag ctg cac att ggg aag gtg gta ctg ggg gac cgt      440
Val Tyr Thr Val Glu Leu His Ile Gly Lys Val Val Leu Gly Asp Arg
116                 121                 126                 131

ggg tat tac cgc ctc gag gtc aaa gcc aag gac acc tgt gac agc tgt      488
Gly Tyr Tyr Arg Leu Glu Val Lys Ala Lys Asp Thr Cys Asp Ser Cys
132                 137                 142                 147

ggc ttc aac atc gat gtg gag gca ccc cgt cag gat gcc tct ggg cag      536
Gly Phe Asn Ile Asp Val Glu Ala Pro Arg Gln Asp Ala Ser Gly Gln
148                 153                 158                 163

agt cta gaa agc ttc aag cgt acg agt gaa aag aag tcg gat act gca      584
Ser Leu Glu Ser Phe Lys Arg Thr Ser Glu Lys Lys Ser Asp Thr Ala
164                 169                 174                 179

ggt gag ctg gat ttc agt ggc ctg ttg aag aag agg gag gtg gtg gag      632
Gly Glu Leu Asp Phe Ser Gly Leu Leu Lys Lys Arg Glu Val Val Glu
180                 185                 190                 195

gag gag aag aag aag aaa aag aaa gat gac gat gac cta ggc atc ccc      680
Glu Glu Lys Lys Lys Lys Lys Lys Asp Asp Asp Asp Leu Gly Ile Pro
196                 201                 206                 211

ccg gag att tgg gag ctc ctg aaa ggg gca aag aag agc gag tac gag      728
Pro Glu Ile Trp Glu Leu Leu Lys Gly Ala Lys Lys Ser Glu Tyr Glu
212                 217                 222                 227

aaa atc gcc ttc cag tat ggc atc acc gac ctc cgg ggc atg ctg aag      776
Lys Ile Ala Phe Gln Tyr Gly Ile Thr Asp Leu Arg Gly Met Leu Lys
228                 233                 238                 243

cgg ctg aaa aag gct aag gtc gag gtc aag aag agt gca gca ttc aca      824
Arg Leu Lys Lys Ala Lys Val Glu Val Lys Lys Ser Ala Ala Phe Thr
244                 249                 254                 259

aag aag ctg gat cca gcc tac caa gtg gac aga ggc aac aag atc aag      872
Lys Lys Leu Asp Pro Ala Tyr Gln Val Asp Arg Gly Asn Lys Ile Lys
260                 265                 270                 275

ttg atg gta gag atc agc gac cca gac ctg acc ctc aag tgg ttc aag      920
Leu Met Val Glu Ile Ser Asp Pro Asp Leu Thr Leu Lys Trp Phe Lys
276                 281                 286                 291
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aac ggc cag gag atc aaa cca agc agc aag tac gtg ttt gag aac gtt      968
Asn Gly Gln Glu Ile Lys Pro Ser Ser Lys Tyr Val Phe Glu Asn Val
292                 297                 302                 307

ggt aag aag cga att ctt acc atc aac aag tgc acg ctg gcg gat gac     1016
Gly Lys Lys Arg Ile Leu Thr Ile Asn Lys Cys Thr Leu Ala Asp Asp
308                 313                 318                 323

gct gcc tat gaa gta gct gtc aag gat gag aag tgt ttc acc gag ctc     1064
Ala Ala Tyr Glu Val Ala Val Lys Asp Glu Lys Cys Phe Thr Glu Leu
324                 329                 334                 339

ttc gtc aaa gaa cct cca gtc cta att gtc aca cct ctt gag gac cag     1112
Phe Val Lys Glu Pro Pro Val Leu Ile Val Thr Pro Leu Glu Asp Gln
340                 345                 350                 355

cag gtg ttt gtg ggt gac cgg gtg gaa atg gca gtg gag gtg tca gaa     1160
Gln Val Phe Val Gly Asp Arg Val Glu Met Ala Val Glu Val Ser Glu
356                 361                 366                 371

gag ggt gcc cag gtg atg tgg atg aaa gat ggt gtg gaa ctg act cgg     1208
Glu Gly Ala Gln Val Met Trp Met Lys Asp Gly Val Glu Leu Thr Arg
372                 377                 382                 387

gag gat tcc ttc aag gcc cgg tac cgc ttc aag aag gac ggg aag cgc     1256
Glu Asp Ser Phe Lys Ala Arg Tyr Arg Phe Lys Lys Asp Gly Lys Arg
388                 393                 398                 403

cac atc ctc atc ttc tca gac gtg gtc cag gag gac agg ggt cgc tat     1304
His Ile Leu Ile Phe Ser Asp Val Val Gln Glu Asp Arg Gly Arg Tyr
404                 409                 414                 419

cag gtc ata acc aat ggc ggc cag tgt gag gcc gag ctg att gtg gaa     1352
Gln Val Ile Thr Asn Gly Gly Gln Cys Glu Ala Glu Leu Ile Val Glu
420                 425                 430                 435

gag aaa cag ctg gag gtc ctg cag gac atc gcg gat ctg acg gtg aag     1400
Glu Lys Gln Leu Glu Val Leu Gln Asp Ile Ala Asp Leu Thr Val Lys
436                 441                 446                 451

gcc tca gaa caa gct gtg ttc aag tgc gag gtg tct gat gag aaa gtg     1448
Ala Ser Glu Gln Ala Val Phe Lys Cys Glu Val Ser Asp Glu Lys Val
452                 457                 462                 467

acg ggc aag tgg tat aag aat ggg gtc gag gtg cgg ccc agc aag agg     1496
Thr Gly Lys Trp Tyr Lys Asn Gly Val Glu Val Arg Pro Ser Lys Arg
468                 473                 478                 483

atc acc att tcc cat gta ggc agg ttc cac aag ctg gtg atc gat gac     1544
Ile Thr Ile Ser His Val Gly Arg Phe His Lys Leu Val Ile Asp Asp
484                 489                 494                 499

gtc cgc ccc gag gat gag gga gac tac acg ttt gtg cct gac ggc tac     1592
Val Arg Pro Glu Asp Glu Gly Asp Tyr Thr Phe Val Pro Asp Gly Tyr
500                 505                 510                 515
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gcc ctt ggt tcg ctc tcg gcc aag ctc aac ttc ctg gaa atc aag gtg     1640
Ala Leu Gly Ser Leu Ser Ala Lys Leu Asn Phe Leu Glu Ile Lys Val
516                 521                 526                 531

gag tac gtt ccc aag caa gag cca cca aag atc cac ttg gat tgc tcg     1688
Glu Tyr Val Pro Lys Gln Glu Pro Pro Lys Ile His Leu Asp Cys Ser
532                 537                 542                 547

ggg aag acc tca gag aat gcg att gtg gtt gtg gct gga aac aag ctg     1736
Gly Lys Thr Ser Glu Asn Ala Ile Val Val Val Ala Gly Asn Lys Leu
548                 553                 558                 563

agg ctt gac gtg tcc atc aca ggg gag ccc cct ccc gtc gct acc tgg     1784
Arg Leu Asp Val Ser Ile Thr Gly Glu Pro Pro Pro Val Ala Thr Trp
564                 569                 574                 579

ctg aag gga gat gag gta ttc acg acc acc gag ggc agg acc cgc atc     1832
Leu Lys Gly Asp Glu Val Phe Thr Thr Thr Glu Gly Arg Thr Arg Ile
580                 585                 590                 595

gag aag cgg gtg gac tgc agc agc ttt gtg att gag agt gcg cag cgg     1880
Glu Lys Arg Val Asp Cys Ser Ser Phe Val Ile Glu Ser Ala Gln Arg
596                 601                 606                 611

gaa gac gag ggc cgc tac acc atc aag gtc acc aac ccc gtc ggc gag     1928
Glu Asp Glu Gly Arg Tyr Thr Ile Lys Val Thr Asn Pro Val Gly Glu
612                 617                 622                 627

gac gtg gct tcc atc ttc ctg caa gtt gta gat gtc cca gac ccc ccg     1976
Asp Val Ala Ser Ile Phe Leu Gln Val Val Asp Val Pro Asp Pro Pro
628                 633                 638                 643

gag gct gtg cgc atc acc tcg gtt gga gag gat tgg gcc atc ctt gtc     2024
Glu Ala Val Arg Ile Thr Ser Val Gly Glu Asp Trp Ala Ile Leu Val
644                 649                 654                 659

tgg gag cca cca atg tac gat ggg ggg aag cca gtc acc ggg tac ctc     2072
Trp Glu Pro Pro Met Tyr Asp Gly Gly Lys Pro Val Thr Gly Tyr Leu
660                 665                 670                 675

gta gag cgg aag aag aag ggc tct cag cgc tgg atg aag ctg aac ttt     2120
Val Glu Arg Lys Lys Lys Gly Ser Gln Arg Trp Met Lys Leu Asn Phe
676                 681                 686                 691

gag gtc ttc aca gag acc acc tat gag tcc acc aag atg atc gag ggc     2168
Glu Val Phe Thr Glu Thr Thr Tyr Glu Ser Thr Lys Met Ile Glu Gly
692                 697                 702                 707

atc ctc tat gag atg cgt gtc ttc gcc gtc aat gct ata ggg gtc tcc     2216
Ile Leu Tyr Glu Met Arg Val Phe Ala Val Asn Ala Ile Gly Val Ser
708                 713                 718                 723

cag ccc agc atg aac acc aag cct ttt atg cct att gca ccc acg agt     2264
Gln Pro Ser Met Asn Thr Lys Pro Phe Met Pro Ile Ala Pro Thr Ser
724                 729                 734                 739

gaa ccc ctg cac ctg ata gtg gag gat gtg aca gac acc acc acc aca     2312
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Glu Pro Leu His Leu Ile Val Glu Asp Val Thr Asp Thr Thr Thr Thr
740                 745                 750                 755

ctc aag tgg agg cct ccg aac agg atc ggg gca ggt ggc atc gat ggg     2360
Leu Lys Trp Arg Pro Pro Asn Arg Ile Gly Ala Gly Gly Ile Asp Gly
756                 761                 766                 771

tac ctg gtg gag tac tgc ctg gaa ggc tcc gag gaa tgg gtc cct gcc     2408
Tyr Leu Val Glu Tyr Cys Leu Glu Gly Ser Glu Glu Trp Val Pro Ala
772                 777                 782                 787

aac acc gag ccc gtg gag cgc tgt ggc ttc acc gtc aag aat ctc ccg     2456
Asn Thr Glu Pro Val Glu Arg Cys Gly Phe Thr Val Lys Asn Leu Pro
788                 793                 798                 803

acc gga gcc aga atc ctc ttc cga gta gtt ggg gtc aac atc gcg ggg     2504
Thr Gly Ala Arg Ile Leu Phe Arg Val Val Gly Val Asn Ile Ala Gly
804                 809                 814                 819

cgc agc gag ccg gcc acc ctg gcc cag ccg gtc acc atc agg gag att     2552
Arg Ser Glu Pro Ala Thr Leu Ala Gln Pro Val Thr Ile Arg Glu Ile
820                 825                 830                 835

gcg gag cca ccc aag atc cgg ctt ccc cgc cat ctc cgc cag acc tac     2600
Ala Glu Pro Pro Lys Ile Arg Leu Pro Arg His Leu Arg Gln Thr Tyr
836                 841                 846                 851

atc cgc aaa gtg ggc gag cag ctc aac ctt gtc gtc ccc ttc cag gga     2648
Ile Arg Lys Val Gly Glu Gln Leu Asn Leu Val Val Pro Phe Gln Gly
852                 857                 862                 867

aag ccc cgg ccc cag gtg gtg tgg acc aag ggc ggg gcc ccg ctg gac     2696
Lys Pro Arg Pro Gln Val Val Trp Thr Lys Gly Gly Ala Pro Leu Asp
868                 873                 878                 883

acc tcc cgc gtg cac gtg cgg acc agc gac ttc gac acc gtg ttc ttc     2744
Thr Ser Arg Val His Val Arg Thr Ser Asp Phe Asp Thr Val Phe Phe
884                 889                 894                 899

gtg cgc cag gcg gcc cgc tcc gac tcc ggg gag tac gag ctg agc gtg     2792
Val Arg Gln Ala Ala Arg Ser Asp Ser Gly Glu Tyr Glu Leu Ser Val
900                 905                 910                 915

cag atc gag aac atg aag gac acc gcc acc atc cgc atc cgc gtt gtg     2840
Gln Ile Glu Asn Met Lys Asp Thr Ala Thr Ile Arg Ile Arg Val Val
916                 921                 926                 931

gaa aag gct ggg ccc ccc ata aac gtg atg gtg aag gag gtg tgg ggc     2888
Glu Lys Ala Gly Pro Pro Ile Asn Val Met Val Lys Glu Val Trp Gly
932                 937                 942                 947

acg aac gcg ctg gtg gag tgg cag gcc ccc aaa gat gat ggg aac agt     2936
Thr Asn Ala Leu Val Glu Trp Gln Ala Pro Lys Asp Asp Gly Asn Ser
948                 953                 958                 963

gag atc atg ggg tat ttc gtc cag aaa gca gac aaa aaa acc atg gag     2984
Glu Ile Met Gly Tyr Phe Val Gln Lys Ala Asp Lys Lys Thr Met Glu
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964                 969                 974                 979

tgg ttc aac gtc tat gaa cgt aac agg cac act agc tgt act gtg tcc     3032
Trp Phe Asn Val Tyr Glu Arg Asn Arg His Thr Ser Cys Thr Val Ser
980                 985                 990                 995

gac ctt atc gtg ggc aat gaa tac tat ttc cga gtt tac acc gag aac     3080
Asp Leu Ile Val Gly Asn Glu Tyr Tyr Phe Arg Val Tyr Thr Glu Asn
996                1001                1006                1011

atc tgt ggg ctc agt gac tca cct ggt gtc tcc aag aac acg gcc cgc     3128
Ile Cys Gly Leu Ser Asp Ser Pro Gly Val Ser Lys Asn Thr Ala Arg
1012                1017                1022                1027

atc ctc aag aca gga atc acc ttc aaa ccg ttc gag tat aag gag cat     3176
Ile Leu Lys Thr Gly Ile Thr Phe Lys Pro Phe Glu Tyr Lys Glu His
1028                1033                1038                1043

gac ttc cgg atg gct ccc aag ttc ctg aca cct ctc ata gac cgc gtg     3224
Asp Phe Arg Met Ala Pro Lys Phe Leu Thr Pro Leu Ile Asp Arg Val
1044                1049                1054                1059

gtc gtg gct ggg tac tcg gca gcc ctc aac tgt gct gtc aga ggc cac     3272
Val Val Ala Gly Tyr Ser Ala Ala Leu Asn Cys Ala Val Arg Gly His
1060                1065                1070                1075

ccg aag ccg aag gtg gtc tgg atg aag aac aag atg gaa atc cgt gaa     3320
Pro Lys Pro Lys Val Val Trp Met Lys Asn Lys Met Glu Ile Arg Glu
1076                1081                1086                1091

gat ccc aag ttc ctg ata acc aat tac caa gga gtc ctg acg ctg aac     3368
Asp Pro Lys Phe Leu Ile Thr Asn Tyr Gln Gly Val Leu Thr Leu Asn
1092                1097                1102                1107

atc cgt cgc ccc tcg ccc ttc gac gct ggg act tac acc tgc cgg gcc     3416
Ile Arg Arg Pro Ser Pro Phe Asp Ala Gly Thr Tyr Thr Cys Arg Ala
1108                1113                1118                1123

gtc aac gag ctg ggc gag gcg ctg gct gag tgc aag ctg gag gtc cga     3464
Val Asn Glu Leu Gly Glu Ala Leu Ala Glu Cys Lys Leu Glu Val Arg
1124                1129                1134                1139

gtg ccg cag tga gac ctgtccccta cctgccaaga caattggtgg tggagtcctg     3519
Val Pro Gln  *
1140

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<222> (2)..(925)

<400> 85

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a    ttt ggc cct cga ggc caa gaa ttc ggc acg aga agc cgt ggc cag      46
     Phe Gly Pro Arg Gly Gln Glu Phe Gly Thr Arg Ser Arg Gly Gln
       1               5                  10

ctc gac gcc gga cag tcc agc gag cag cac ggc ggg aac cgg cag ccg      94
Leu Asp Ala Gly Gln Ser Ser Glu Gln His Gly Gly Asn Arg Gln Pro
 16                  21                  26                  31

gag cag tcc cgg agc aga agc agc agc agc agc agc agc cct cgc cgt     142
Glu Gln Ser Arg Ser Arg Ser Ser Ser Ser Ser Ser Ser Pro Arg Arg
 32                  37                  42                  47

tcg cgg agc gca gcc gag ccg gcc atg gcg ttg tcg atg ccg ctg aat     190
Ser Arg Ser Ala Ala Glu Pro Ala Met Ala Leu Ser Met Pro Leu Asn
 48                  53                  58                  63

ggg ctg aag gag gag gac aaa gag ccc ctc atc gag ctc ttc gtc aag     238
Gly Leu Lys Glu Glu Asp Lys Glu Pro Leu Ile Glu Leu Phe Val Lys
 64                  69                  74                  79

gct ggc agt gat ggt gaa agc ata gga aac tgc ccc ttt tcc cag agg     286
Ala Gly Ser Asp Gly Glu Ser Ile Gly Asn Cys Pro Phe Ser Gln Arg
 80                  85                  90                  95

ctc ttc atg att ctt tgg ctc aaa gga gtt gta ttt agt gtg acg act     334
Leu Phe Met Ile Leu Trp Leu Lys Gly Val Val Phe Ser Val Thr Thr
 96                 101                 106                 111

gtt gac ctg aaa agg aag cca gca gac ctg cag aac ttg gct ccc ggg     382
Val Asp Leu Lys Arg Lys Pro Ala Asp Leu Gln Asn Leu Ala Pro Gly
112                 117                 122                 127

acc cac cca cca ttt ata act ttc aac agt gaa gtc aaa acg gat gta     430
Thr His Pro Pro Phe Ile Thr Phe Asn Ser Glu Val Lys Thr Asp Val
128                 133                 138                 143

aat aag att gag gaa ttt ctt gaa gaa gtc tta tgc cct ccc aag tac     478
Asn Lys Ile Glu Glu Phe Leu Glu Glu Val Leu Cys Pro Pro Lys Tyr
144                 149                 154                 159

tta aag ctt tca cca aaa cac cca gaa tca aat act gct gga atg gac     526
Leu Lys Leu Ser Pro Lys His Pro Glu Ser Asn Thr Ala Gly Met Asp
160                 165                 170                 175

atc ttt gcc aaa ttc tct gca tat atc aag aat tca agg cca gag gct     574
Ile Phe Ala Lys Phe Ser Ala Tyr Ile Lys Asn Ser Arg Pro Glu Ala
176                 181                 186                 191

aat gaa gca ctg gag agg ggt ctc ctg aaa acc ctg cag aaa ctg gat     622
Asn Glu Ala Leu Glu Arg Gly Leu Leu Lys Thr Leu Gln Lys Leu Asp
192                 197                 202                 207
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gaa tat ctg aat tct cct ctc cct gat gaa att gat gaa aat agt atg      670
Glu Tyr Leu Asn Ser Pro Leu Pro Asp Glu Ile Asp Glu Asn Ser Met
208                 213                 218                 223

gag gac ata aag ttt tct aca cgt aaa ttt ctg gat ggc aat gaa atg      718
Glu Asp Ile Lys Phe Ser Thr Arg Lys Phe Leu Asp Gly Asn Glu Met
224                 229                 234                 239

aca tta gct gat tgc aac ctg ctg ccc aaa ctg cat att gtc aag gtg      766
Thr Leu Ala Asp Cys Asn Leu Leu Pro Lys Leu His Ile Val Lys Val
240                 245                 250                 255

gtg gcc aaa aaa tat cgc aac ttt gat att cca aaa gaa atg act ggc      814
Val Ala Lys Lys Tyr Arg Asn Phe Asp Ile Pro Lys Glu Met Thr Gly
256                 261                 266                 271

atc tgg aga tac cta act aat gca tac agt agg gac gag ttc acc aat      862
Ile Trp Arg Tyr Leu Thr Asn Ala Tyr Ser Arg Asp Glu Phe Thr Asn
272                 277                 282                 287

acc tgt ccc agt gat aag gag gtt gaa ata gca tat agt gat gta gcc      910
Thr Cys Pro Ser Asp Lys Glu Val Glu Ile Ala Tyr Ser Asp Val Ala
288                 293                 298                 303

aaa aga ctc acc aag taaaatcgcg tttgtaaaag agatgtcttc atgtcttccc      965
Lys Arg Leu Thr Lys
304

ctaagaatac gcttttccta acaggctact ccttcctgta gagcagaaat tgtattttgc   1025

acgaacatgc agttattgaa gattaggatc aaggatagac aaggtatagt agttatctta   1085

aaatatacac tcctaagcag tattatttta aaatccttta ccctggctac ctcccctacc   1145

cgggttcccc tctctttaat ttggagacac tccaccacaa acttttcact ttagaggtag   1205

cttgccatct ctcaggagcc ctcaccattg tgtccattca ctgtgtatag atggcagaac   1265

ttttgaggtg caatgtttaa ttgttaaaaa tagtagccac gactttatca ggcagcccca   1325

aactggtgca taatgcatgg tacaagaaat atttatgtat tttttggaat tttgtaatat   1385

ttagtaagag tatatgaaag gattgctact gtatcagaaa tattgtttca atttagtcta   1445

tcctggatat gtactaacga atattaccac cagagaagag agctttctac aaaagtcact   1505

acagattttg ctatattgct ttgtagatag atttttactt ttgcctaaaa gcatttatcc   1565

ttcataccaa ttgtaacatc tgacaccatg tagaagctaa aagtttagag ggagtgagcg   1625

ttttctcaag accttcctca agcattttat ctttagaaga gaaactgatg ggcacctgat   1685

actctgtcta aatacgtttg ttatatgtgt tttgccctgt gccattcatt tggaacttta   1745

ttgcattctt tattttaaaa agcttgtttt tacgtaatca tagagcttgc tatttgtaca   1805
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tctgttgagc aacactacat aactgatttt tagttgactt agctatagca gtacaatgat 1865

tagtaatgta aaaattaaca cagaaattaa cctaaggaat gaagggtggg tttgtcaaaa 1925

tatcaagtaa atttttgttt ctaaagtaca tttaatgtag atgacctaaa gaatgcgtta 1985

tccatcctat ataaaagaaa gataaaacac aggtcaccaa ttttctcatt tcaccccatt 2045

taccttgtat agaggattgt tcattccttt gggactaagt tatagttatg gtgagtgtgt 2105

atttactgta gttttgcctg atctcactca ttgcacttcc tggagttaaa ttttccaaca 2165

gccatgttga ggaatagcac tctgcatgtt tttgttttgt ttttcggggt ttttttaat 2225

tgaagcccta aaccaggaat tatttgtgtt ctaacaggag gatgaacttg ctgaaaataa 2285

aactttgcta tgtatttact ctttttaaa agacaaaagc aaaaccagac tttctacgta 2345

ctactccaaa gactgtgatt gtgactataa tacatttttg gtaatttttt tatacctaat 2405

ttgtatagga agtgctattt ctcataggct gtttcttgaa attttaagtt tattgcttta 2465

aaatggcagt gtttctccca ctttgatatg ctaacattta gtaagcactg gctttatgaa 2525

agcggctttt tataagtata ctgcattttt tgagcctatc attaattagc ttagtatgaa 2585

agataagaaa atctccatgt tgtatccatt tggctcagga agattctttg ccttaccttt 2645

cttagaactc tttattgctt atcaaaagtt tgagtacccg cttggttttt ttttggtaat 2705

taaatattgt atgatttatc tggttcaagg aagatgcact attcagttat ctattgagaa 2765

attattttgc agtggtttta gtgggtgaaa atgtcccatc tgcaccagta cacaggcagg 2825

cattatcatt cttcacctac tttttaaata gtggcaactt gggattcatt ctggtgattc 2885

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tccagtgaat ggtggactga gtggtgcgag gtggagggct aacaagagga aagaactaca 3005

ttcttcagaa tacagtgatg aaaattcatt ttgaaactca aatattttca ttttggatat 3065

tctcctgttt ttattaaacc agtgattaca cctggccatc cctctaaatg ttctaggaag 3125

gcatgtctat tgtgattttg atgaagacag aattattttt ctctgtagaa acacagatac 3185

cactttatca gggaagttag tcaaatgaaa tggaaattgg taaatggaca aaagctagct 3245

agtaaaaagg acgacccagc aacatgcttt aaccccattg tatgtttgtg gaaagagcat 3305

agtttaacat cttgagaaat ttgggacata aagttttcat ggtagacagt tcatgcagta 3365

tatgaattga cataatggaa ataatctgat tttatttta caactaacat ccattcccct 3425

tcatttaaac acctttgtg ttttacttca gtgaggagat tggagtctga atggatctgt 3485

tttccaagag attctgagaa atttttgtat tcagcagttg gaaagctctc tattctagtt 3545

gataaaactt ccctttttg atgtagatgc agatattcta tacagttctg ttgtctttta 3605

ctaggactgt aaacttttgt gataaaattc aaataagatt ttatttcttg gtaattttgg 3665

ctttcacaat ttatctttaa atccttgagc aatctgtata caattaagag atttctgaca 3725

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gaaaataact acaaagtaaa aatgtagagg aaatagaaat gtatttttc atgaacattt 3905

tgatacaaat ttcatcattt aatgattcac caatttcttg cattaatttg aatttaagca 3965

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cctttataaa tagtcaaggt ttgggccaca caaagtatat ttttatcatg gaaaaatttc 4085

aactcctcaa gccgtaatgt tgaacagaat tggagtattt tctttataat ttcttgaaca 4145

ggcaaatgaa agcttattat agaatgcatg tattttcttt tatctttgga acatcagcac 4205

cagtatattg ctggcagcta ttgtattaaa aaataaagta tattttcact atcataaagg 4265

attctttttt ccccccctcat gaaaataaac aacaacttgg ggtaaaaaaa aaa 4318

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<213> Homo sapiens

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<222> (42)..(1064)

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Met Ala Lys Trp
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Leu Arg Asp Tyr Leu Ser Phe Gly Gly Arg Arg Pro Pro Pro Gln Pro
5 10 15 20

ccc acc ccg gac tac acc gag agc gac atc ctg agg gcc tac cgc gcg 149
Pro Thr Pro Asp Tyr Thr Glu Ser Asp Ile Leu Arg Ala Tyr Arg Ala
21 26 31 36

cag aaa aac ctg gac ttc gag gac ccc tat gag gac tcc gag agc cgc 197
Gln Lys Asn Leu Asp Phe Glu Asp Pro Tyr Glu Asp Ser Glu Ser Arg
37 42 47 52

ttg gag ccg gac ccc gcg ggc cct ggg gac tcc aag aac ccc gga gat 245

```
Leu Glu Pro Asp Pro Ala Gly Pro Gly Asp Ser Lys Asn Pro Gly Asp
 53                  58                  63                  68

gcc aag tat ggt tct ccc aag cac cgg ctc atc aag gtg gag gct gcg      293
Ala Lys Tyr Gly Ser Pro Lys His Arg Leu Ile Lys Val Glu Ala Ala
 69                  74                  79                  84

gat atg gcc aga gcc aag gcc ctt ctg ggc ggc ccc ggg gag gag ctg      341
Asp Met Ala Arg Ala Lys Ala Leu Leu Gly Gly Pro Gly Glu Glu Leu
 85                  90                  95                 100

gaa gcc gac act gag tat tta gac ccc ttt gat gct cag cct cat cct      389
Glu Ala Asp Thr Glu Tyr Leu Asp Pro Phe Asp Ala Gln Pro His Pro
101                 106                 111                 116

gca ccc ccg gat gat ggg tac atg gag ccc tac gat gcc caa tgg gtc      437
Ala Pro Pro Asp Asp Gly Tyr Met Glu Pro Tyr Asp Ala Gln Trp Val
117                 122                 127                 132

atg agt gaa ctt ccc ggc aga ggg gtg cag ctc tat gac acc cct tat      485
Met Ser Glu Leu Pro Gly Arg Gly Val Gln Leu Tyr Asp Thr Pro Tyr
133                 138                 143                 148

gag gaa cag gac cca gag aca gca gat gga ccc cct tct ggg cag aag      533
Glu Glu Gln Asp Pro Glu Thr Ala Asp Gly Pro Pro Ser Gly Gln Lys
149                 154                 159                 164

cct cgg cag agc cgg atg ccc cag gaa gat gaa cgg cca gca gat gag      581
Pro Arg Gln Ser Arg Met Pro Gln Glu Asp Glu Arg Pro Ala Asp Glu
165                 170                 175                 180

tat gat cag ccc tgg gag tgg aag aaa gac cac atc tcc agg gcg ttt      629
Tyr Asp Gln Pro Trp Glu Trp Lys Lys Asp His Ile Ser Arg Ala Phe
181                 186                 191                 196

gca gtg cag ttt gac agt cca gag tgg gag agg act cca ggc tca gcc      677
Ala Val Gln Phe Asp Ser Pro Glu Trp Glu Arg Thr Pro Gly Ser Ala
197                 202                 207                 212

aag gag ctc cgg aga cct ccg ccc aga agc ccc cag cct gcg gag cgt      725
Lys Glu Leu Arg Arg Pro Pro Pro Arg Ser Pro Gln Pro Ala Glu Arg
213                 218                 223                 228

gtg gac cca gcc ctg ccc ctg gag aaa cag ccg tgg ttt cat ggc ccc      773
Val Asp Pro Ala Leu Pro Leu Glu Lys Gln Pro Trp Phe His Gly Pro
229                 234                 239                 244

ctg aac agg gcg gat gca gag agc ctc ctg tcc ctc tgc aag gaa ggc      821
Leu Asn Arg Ala Asp Ala Glu Ser Leu Leu Ser Leu Cys Lys Glu Gly
245                 250                 255                 260

agc tac cta gtg cgg ctc agt gag acc aac ccc cag gac tgc tcc ttg      869
Ser Tyr Leu Val Arg Leu Ser Glu Thr Asn Pro Gln Asp Cys Ser Leu
261                 266                 271                 276

tct ctc agg agc agc cag ggc ttc ctg cat ctg aag ttc gcg cgg acc      917
Ser Leu Arg Ser Ser Gln Gly Phe Leu His Leu Lys Phe Ala Arg Thr
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277                 282                 287                 292

cgt gag aac cag gtg gtg ctg ggc caa cac agc ggg ccc ttc ccc agc      965
Arg Glu Asn Gln Val Val Leu Gly Gln His Ser Gly Pro Phe Pro Ser
293                 298                 303                 308

gtg ccc gag ctc gtc ctc cac tac agt tca cgc cca ctg ccg gtg cag     1013
Val Pro Glu Leu Val Leu His Tyr Ser Ser Arg Pro Leu Pro Val Gln
309                 314                 319                 324

ggt gcc gag cat ctg gct ctg ctg tac ccc gtg gtc acg cag acc ccc     1061
Gly Ala Glu His Leu Ala Leu Leu Tyr Pro Val Val Thr Gln Thr Pro
325                 330                 335                 340

tga cagt gaccctcggc ccccttttga gtcctcgggc ccagaatcgt atcccaaagc     1118
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341

cctcccatgg cctagaaaat aaataagtta ttgttaaaaa aaaaaaaaaa aaaaaaaaaa   1178

aaaattggcg gtcgcaagct tattcccttt a                                  1209
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<213> Homo sapiens

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<222> (177)..(1901)

<400> 87

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ctgtctgtcc gtggtggatc taagcctcat ctgtatcctc ttgtgatggc gtgaaggaaa    120

gccatggcag atttccagcc tggtgatgct gtacagaaca caggtggcct gcttcc   176

atg cct cct cag ctt caa gaa act aga atg aac cga agc att cct gtg      224
Met Pro Pro Gln Leu Gln Glu Thr Arg Met Asn Arg Ser Ile Pro Val
  1               5                  10                  15

gag gtt gat gaa tca gaa cca tac cca agt cag ttg ctg aaa cca atc      272
Glu Val Asp Glu Ser Glu Pro Tyr Pro Ser Gln Leu Leu Lys Pro Ile
 17                  22                  27                  32

cca gaa tat tcc ccg gaa gag gaa tca gaa cca cct gct cca aat ata      320
Pro Glu Tyr Ser Pro Glu Glu Glu Ser Glu Pro Pro Ala Pro Asn Ile
 33                  38                  43                  48

agg aac atg gca ccc aac agc ttg tct gca ccc aca atg ctt cac aat      368
Arg Asn Met Ala Pro Asn Ser Leu Ser Ala Pro Thr Met Leu His Asn
 49                  54                  59                  64
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tcc tcc gga gac ttt tct caa gct cac tca acc ctg aaa ctt gca aat      416
Ser Ser Gly Asp Phe Ser Gln Ala His Ser Thr Leu Lys Leu Ala Asn
 65                  70                  75                  80

cac cag cgg cct gta tcc cgg cag gtc acc tgc ctg cgc act caa gtt      464
His Gln Arg Pro Val Ser Arg Gln Val Thr Cys Leu Arg Thr Gln Val
 81                  86                  91                  96

ctg gag gac agt gaa gac agt ttc tgc agg aga cac cca ggc ctg ggc      512
Leu Glu Asp Ser Glu Asp Ser Phe Cys Arg Arg His Pro Gly Leu Gly
 97                 102                 107                 112

aaa gct ttc cct tct ggg tgc tct gca gtc agc gag cct gcg tct gag      560
Lys Ala Phe Pro Ser Gly Cys Ser Ala Val Ser Glu Pro Ala Ser Glu
113                 118                 123                 128

tct ggg gtt gga gcc ctc cct gca gag cat cag ttt tca ttt atg gaa      608
Ser Gly Val Gly Ala Leu Pro Ala Glu His Gln Phe Ser Phe Met Glu
129                 134                 139                 144

aaa cgt aat caa tgg ctg gta tct cag ctt tca gcg gct tct cct gac      656
Lys Arg Asn Gln Trp Leu Val Ser Gln Leu Ser Ala Ala Ser Pro Asp
145                 150                 155                 160

act ggc cat gac tca gac aaa tca gac caa agt tta cct aat gcc tca      704
Thr Gly His Asp Ser Asp Lys Ser Asp Gln Ser Leu Pro Asn Ala Ser
161                 166                 171                 176

gca gac tcc ttg ggc ggt agc cag gag atg gtg caa cgg ccc cag cct      752
Ala Asp Ser Leu Gly Gly Ser Gln Glu Met Val Gln Arg Pro Gln Pro
177                 182                 187                 192

cac agg aac cga gca ggc ctg gat ctg cca acc ata gac acg gga tat      800
His Arg Asn Arg Ala Gly Leu Asp Leu Pro Thr Ile Asp Thr Gly Tyr
193                 198                 203                 208

gat tcc cag ccc cag gat gtc ctg ggc atc agg cag ctg gaa agg ccc      848
Asp Ser Gln Pro Gln Asp Val Leu Gly Ile Arg Gln Leu Glu Arg Pro
209                 214                 219                 224

ctg ccc ctc acc tcc gtg tgt tac ccc cag gac ctc ccc aga cct ctc      896
Leu Pro Leu Thr Ser Val Cys Tyr Pro Gln Asp Leu Pro Arg Pro Leu
225                 230                 235                 240

agg tcc agg gag ttc cct cag ttt gaa cct cag agg tat cca gca tgt      944
Arg Ser Arg Glu Phe Pro Gln Phe Glu Pro Gln Arg Tyr Pro Ala Cys
241                 246                 251                 256

gca cag atg ctg cct ccc aat ctt tcc cca cat gct cca tgg aac tat      992
Ala Gln Met Leu Pro Pro Asn Leu Ser Pro His Ala Pro Trp Asn Tyr
257                 262                 267                 272

cat tac cat tgt cct gga agt ccc gat cac cag gtg cca tat ggc cat     1040
His Tyr His Cys Pro Gly Ser Pro Asp His Gln Val Pro Tyr Gly His
273                 278                 283                 288

gac tac cct cga gca gcc tac cag caa gtg atc cag ccg gct ctg cct     1088
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```
Asp Tyr Pro Arg Ala Ala Tyr Gln Gln Val Ile Gln Pro Ala Leu Pro
289                 294                 299                 304

ggg cag ccc ctg cct gga gcc agt gtg aga ggc ctg cac cct gtg cag     1136
Gly Gln Pro Leu Pro Gly Ala Ser Val Arg Gly Leu His Pro Val Gln
305                 310                 315                 320

aag gtt atc ctg aat tat ccc agc ccc tgg gac caa gaa gag agg ccc     1184
Lys Val Ile Leu Asn Tyr Pro Ser Pro Trp Asp Gln Glu Glu Arg Pro
321                 326                 331                 336

gca cag aga gac tgc tcc ttt ccg ggg ctt cca agg cac cag gac cag     1232
Ala Gln Arg Asp Cys Ser Phe Pro Gly Leu Pro Arg His Gln Asp Gln
337                 342                 347                 352

cca cat cac cag cca cct aat aga gct ggt gct cct ggg gag tcc ttg     1280
Pro His His Gln Pro Pro Asn Arg Ala Gly Ala Pro Gly Glu Ser Leu
353                 358                 363                 368

gag tgc cct gca gag ctg aga cca cag gtt ccc cag cct ccg tcc cca     1328
Glu Cys Pro Ala Glu Leu Arg Pro Gln Val Pro Gln Pro Pro Ser Pro
369                 374                 379                 384

gct gct gtg cct aga ccc cct agc aac cct cca gcc aga gga act cta     1376
Ala Ala Val Pro Arg Pro Pro Ser Asn Pro Pro Ala Arg Gly Thr Leu
385                 390                 395                 400

aaa aca agc aat ttg cca gaa gaa ttg cgg aaa gtc ttt atc act tat     1424
Lys Thr Ser Asn Leu Pro Glu Glu Leu Arg Lys Val Phe Ile Thr Tyr
401                 406                 411                 416

tcg atg gac aca gct atg gag gtg gtg aaa ttc gtg aac ttt ttg ttg     1472
Ser Met Asp Thr Ala Met Glu Val Val Lys Phe Val Asn Phe Leu Leu
417                 422                 427                 432

gta aat ggc ttc caa act gca att gac ata ttt gag gat aga atc cga     1520
Val Asn Gly Phe Gln Thr Ala Ile Asp Ile Phe Glu Asp Arg Ile Arg
433                 438                 443                 448

ggc att gat atc att aaa tgg atg gag cgc tac ctt agg gat aag acc     1568
Gly Ile Asp Ile Ile Lys Trp Met Glu Arg Tyr Leu Arg Asp Lys Thr
449                 454                 459                 464

gtg atg ata atc gta gca atc agc ccc aaa tac aaa cag gac gtg gaa     1616
Val Met Ile Ile Val Ala Ile Ser Pro Lys Tyr Lys Gln Asp Val Glu
465                 470                 475                 480

ggc gct gag tcg cag ctg gac gag gat gag cat ggc tta cat act aag     1664
Gly Ala Glu Ser Gln Leu Asp Glu Asp Glu His Gly Leu His Thr Lys
481                 486                 491                 496

tac att cat cga atg atg cag att gag ttc ata aaa caa gga agc atg     1712
Tyr Ile His Arg Met Met Gln Ile Glu Phe Ile Lys Gln Gly Ser Met
497                 502                 507                 512

aat ttc aga ttc atc cct gtg ctc ttc cca aat gct aag aag gag cat     1760
Asn Phe Arg Phe Ile Pro Val Leu Phe Pro Asn Ala Lys Lys Glu His
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513                 518                 523                 528

gtg ccc acc tgg ctt cag aac act cat gtc tac agc tgg ccc aag aat     1808
Val Pro Thr Trp Leu Gln Asn Thr His Val Tyr Ser Trp Pro Lys Asn
529                 534                 539                 544

aaa aaa aac atc ctg ctg cgg ctg ctg aga gag gaa gag tat gtg gct     1856
Lys Lys Asn Ile Leu Leu Arg Leu Leu Arg Glu Glu Glu Tyr Val Ala
545                 550                 555                 560

cct cca cgg ggg cct ctg ccc acc ctt cag gtg gtt ccc ttg tga cac     1904
Pro Pro Arg Gly Pro Leu Pro Thr Leu Gln Val Val Pro Leu  *
561                 566                 571

cgttcatccc cagatcactg aggccaggcc atgtttgggg ccttgttctg acagcattct   1964

ggctgaggct ggtcggtagc actcctggct ggtttttttc tgttcctccc cgagaggccc   2024

tctggccccc aggaaacctg ttgtgcagag ctcttccccg gagacctcca cacaccctgg   2084

ctttgaagtg gagtctgtga ctgctctgca ttctctgctt ttaaaaaaac cattgcaggt   2144

gccagtgtcc catatgttcc tcctgacagt ttgatgtgtc cattctgggc ctctcagtgc   2204

ttagcaagta gataatgtaa gggatgtggc agcaaatgga aatgactaca aacactctcc   2264

tatcaatcac ttcaggctac ttttatgagt tagccagatg cttgtgtatc ctcagaccaa   2324

actgattcat gtacaaataa taaaatgttt actcttttgt aa                     2366
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<222> (144)..(848)

<400> 88

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gtcgacgctg gtgcacagga agg    atg agg aag acc agg ctc tgg ggg ctg     170
                            Met Arg Lys Thr Arg Leu Trp Gly Leu
                              1               5

ctg tgg atg ctc ttt gtc tca gaa ctc cga gct gca act aaa tta act     218
Leu Trp Met Leu Phe Val Ser Glu Leu Arg Ala Ala Thr Lys Leu Thr
 10                  15                  20                  25

gag gaa aag tat gaa ctg aaa gag ggg cag acc ctg gat gtg aaa tgt     266
Glu Glu Lys Tyr Glu Leu Lys Glu Gly Gln Thr Leu Asp Val Lys Cys
```

```
 26                  31                  36                  41

gac tac acg cta gag aag ttt gcc agc agc cag aaa gct tgg cag ata      314
Asp Tyr Thr Leu Glu Lys Phe Ala Ser Ser Gln Lys Ala Trp Gln Ile
 42                  47                  52                  57

ata agg gac gga gag atg ccc aag acc ctg gca tgc aca gag agg cct      362
Ile Arg Asp Gly Glu Met Pro Lys Thr Leu Ala Cys Thr Glu Arg Pro
 58                  63                  68                  73

tca aag aat tcc cat cca gtc caa gtg ggg agg atc ata cta gaa gac      410
Ser Lys Asn Ser His Pro Val Gln Val Gly Arg Ile Ile Leu Glu Asp
 74                  79                  84                  89

tac cat gat cat ggt tta ctg cgc gtc cga atg gtc aac ctt caa gtg      458
Tyr His Asp His Gly Leu Leu Arg Val Arg Met Val Asn Leu Gln Val
 90                  95                 100                 105

gaa gat tct gga ctg tat cag tgt gtg atc tac cag cct ccc aag gag      506
Glu Asp Ser Gly Leu Tyr Gln Cys Val Ile Tyr Gln Pro Pro Lys Glu
106                 111                 116                 121

cct cac atg ctg ttc gat cgc atc cgc ttg gtg gtg acc aag ggt ttt      554
Pro His Met Leu Phe Asp Arg Ile Arg Leu Val Val Thr Lys Gly Phe
122                 127                 132                 137

tca ggg acc cct ggc tcc aat gag aat tct acc cag aat gtg tat aag      602
Ser Gly Thr Pro Gly Ser Asn Glu Asn Ser Thr Gln Asn Val Tyr Lys
138                 143                 148                 153

att cct cct acc acc act aag gcc ttg tgc cca ctc tat acc agc ccc      650
Ile Pro Pro Thr Thr Thr Lys Ala Leu Cys Pro Leu Tyr Thr Ser Pro
154                 159                 164                 169

aga act gtg acc caa gct cca ccc aag tca act gcc gat gtc tcc act      698
Arg Thr Val Thr Gln Ala Pro Pro Lys Ser Thr Ala Asp Val Ser Thr
170                 175                 180                 185

cct gac tct gaa atc aac ctt aca aat gtg aca gat atc atc agg gtt      746
Pro Asp Ser Glu Ile Asn Leu Thr Asn Val Thr Asp Ile Ile Arg Val
186                 191                 196                 201

ccg gtg ttc aac att gtc att ctc ctg gct ggt gga ttc ctg agt aag      794
Pro Val Phe Asn Ile Val Ile Leu Leu Ala Gly Gly Phe Leu Ser Lys
202                 207                 212                 217

agc ctg gtc ttc tct gtc ctg ttt gct gtc acg ctg agg tca ttt gta      842
Ser Leu Val Phe Ser Val Leu Phe Ala Val Thr Leu Arg Ser Phe Val
218                 223                 228                 233

ccc tag gcccacgaac ccacgagaat gtcctctgac ttccagccac atccatctgg       898
Pro  *
234

cagttgtgcc aagggaggag ggaggaggta aaaggcaggg agttaataac atgaattaaa    958

tctgtaatca ccagctattt ctaaagtcag cgtctcacct tcctgcccac tgccctcgtt   1018
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gctcgccttc ctttcacttc ctgttccttc agaaagcgct gtgccttgga ccaaccttac    180

ttcttactat tgacagctca gctaactcct attcatcctt caaaacccat ctctggtggt    240

ttggctttga   atg aca gca aga act ctg tct tta atg gct tca ttg gta      289
             Met Thr Ala Arg Thr Leu Ser Leu Met Ala Ser Leu Val
               1               5                  10

gcg tat gat gat tcg gac tcg gag gct gag aca gag cat gca gga agt      337
Ala Tyr Asp Asp Ser Asp Ser Glu Ala Glu Thr Glu His Ala Gly Ser
 14                  19                  24                  29

ttt aat gct acc ggc cag cag aaa gac act tct ggt gtg gcc aga cca      385
Phe Asn Ala Thr Gly Gln Gln Lys Asp Thr Ser Gly Val Ala Arg Pro
 30                  35                  40                  45

cct ggg cag gat ttt gca tct ggt aca ctg gat gtg ccc aga gca ggg      433
Pro Gly Gln Asp Phe Ala Ser Gly Thr Leu Asp Val Pro Arg Ala Gly
 46                  51                  56                  61

gca cag ccc aca aag cat ggc tcc tgt gaa gac cca ggg ggc tat cgc      481
Ala Gln Pro Thr Lys His Gly Ser Cys Glu Asp Pro Gly Gly Tyr Arg
 62                  67                  72                  77

ctt cca ttg gct cag ctt ggg aga agc gat cgg gga tct tgc ccc agc      529
Leu Pro Leu Ala Gln Leu Gly Arg Ser Asp Arg Gly Ser Cys Pro Ser
 78                  83                  88                  93

cag agg cta cag tgg ccc ggg aag gag cct caa gtc acc ttc ccc atc      577
Gln Arg Leu Gln Trp Pro Gly Lys Glu Pro Gln Val Thr Phe Pro Ile
 94                  99                 104                 109

aaa gag cct tct tgt tct tct ctg tgg acg agc cat gtt cca gcc agc      625
Lys Glu Pro Ser Cys Ser Ser Leu Trp Thr Ser His Val Pro Ala Ser
110                 115                 120                 125
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cac atg ccc ctg gca gct gcc cgc ttt aag caa gta aaa ctc tcc agg      673
His Met Pro Leu Ala Ala Ala Arg Phe Lys Gln Val Lys Leu Ser Arg
126                 131                 136                 141

aac ttt ccc aag tca tct ttc cat gct caa agt gag tct gaa acc gta      721
Asn Phe Pro Lys Ser Ser Phe His Ala Gln Ser Glu Ser Glu Thr Val
142                 147                 152                 157

ggt aaa aat ggc agc tct ttt cag aag aaa aaa tgt gag gac tgt gtg      769
Gly Lys Asn Gly Ser Ser Phe Gln Lys Lys Lys Cys Glu Asp Cys Val
158                 163                 168                 173

gta ccc tat act ccc aga aga cta aga cag cgg cag gca tta agc acg      817
Val Pro Tyr Thr Pro Arg Arg Leu Arg Gln Arg Gln Ala Leu Ser Thr
174                 179                 184                 189

gag aca ggc aag ggt aaa gac gtg gag cca cag ggg ccc cct gca ggg      865
Glu Thr Gly Lys Gly Lys Asp Val Glu Pro Gln Gly Pro Pro Ala Gly
190                 195                 200                 205

cgt gcc cca gcc cct ctc tac gtg ggc ccg gga gtg tct gag ttt att      913
Arg Ala Pro Ala Pro Leu Tyr Val Gly Pro Gly Val Ser Glu Phe Ile
206                 211                 216                 221

cag cca tat ttg aat agc cat tat aaa gaa acc aca gtt ccc cgg aaa      961
Gln Pro Tyr Leu Asn Ser His Tyr Lys Glu Thr Thr Val Pro Arg Lys
222                 227                 232                 237

gtg ctt ttc cac ctg aga ggc cac agg ggc cct gtc aac acc att cag     1009
Val Leu Phe His Leu Arg Gly His Arg Gly Pro Val Asn Thr Ile Gln
238                 243                 248                 253

tgg tgt ccg gtc ctt tct aag agc cac atg ctt ctc tcc act tct atg     1057
Trp Cys Pro Val Leu Ser Lys Ser His Met Leu Leu Ser Thr Ser Met
254                 259                 264                 269

gat aaa act ttc aag gta tgg aac gcc gtg gac tcc ggg cac tgc ctg     1105
Asp Lys Thr Phe Lys Val Trp Asn Ala Val Asp Ser Gly His Cys Leu
270                 275                 280                 285

cag acc tac tcc ctg cac aca gag gca gtg cgg gcc gcc cgg tgg gct     1153
Gln Thr Tyr Ser Leu His Thr Glu Ala Val Arg Ala Ala Arg Trp Ala
286                 291                 296                 301

ccc tgt ggc cgg cgc atc ctc agt ggt ggc ttt gac ttc gcg ctg cac     1201
Pro Cys Gly Arg Arg Ile Leu Ser Gly Gly Phe Asp Phe Ala Leu His
302                 307                 312                 317

cta aca gac ctt gaa aca gga acc cag cta ttt agt ggt cga agt gac     1249
Leu Thr Asp Leu Glu Thr Gly Thr Gln Leu Phe Ser Gly Arg Ser Asp
318                 323                 328                 333

ttt aga atc act acc ttg aaa ttc cat cca aaa gac cac aac atc ttt     1297
Phe Arg Ile Thr Thr Leu Lys Phe His Pro Lys Asp His Asn Ile Phe
334                 339                 344                 349
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tta tgt gga ggc ttc agc tct gaa atg aaa gct tgg gat ata agg act     1345
Leu Cys Gly Gly Phe Ser Ser Glu Met Lys Ala Trp Asp Ile Arg Thr
350                 355                 360                 365

ggc aag gtg atg aga agc tac aag gcg acc atc cag cag acc ttg gac     1393
Gly Lys Val Met Arg Ser Tyr Lys Ala Thr Ile Gln Gln Thr Leu Asp
366                 371                 376                 381

atc ctg ttc ctc cgg gaa ggc tcc gag ttc ctg agc agc aca gac gct     1441
Ile Leu Phe Leu Arg Glu Gly Ser Glu Phe Leu Ser Ser Thr Asp Ala
382                 387                 392                 397

tcc acc cgg gac tca gct gac cgc acc att att gcc tgg gat ttc cgg     1489
Ser Thr Arg Asp Ser Ala Asp Arg Thr Ile Ile Ala Trp Asp Phe Arg
398                 403                 408                 413

acc tct gcc aaa atc tcc aac cag att ttc cac gag agg ttc acc tgc     1537
Thr Ser Ala Lys Ile Ser Asn Gln Ile Phe His Glu Arg Phe Thr Cys
414                 419                 424                 429

ccc agc ctc gcc ttg cac ccg aga gag ccc gtg ttc ctg gca cag acc     1585
Pro Ser Leu Ala Leu His Pro Arg Glu Pro Val Phe Leu Ala Gln Thr
430                 435                 440                 445

aat ggc aac tac ctg gcc ctt ttc tcc act gtg tgg ccc tac cgg atg     1633
Asn Gly Asn Tyr Leu Ala Leu Phe Ser Thr Val Trp Pro Tyr Arg Met
446                 451                 456                 461

agc aga cgg cgg cgc tat gaa ggg cac aag gtg gag ggc tac tca gtg     1681
Ser Arg Arg Arg Arg Tyr Glu Gly His Lys Val Glu Gly Tyr Ser Val
462                 467                 472                 477

ggc tgc gag tgc tcc cca ggc ggt gac ttg ctg gtg acg ggc agc gcc     1729
Gly Cys Glu Cys Ser Pro Gly Gly Asp Leu Leu Val Thr Gly Ser Ala
478                 483                 488                 493

gat ggc cgg gtc ctg atg tac agc ttc cgc aca gcc agc cga gca tgc     1777
Asp Gly Arg Val Leu Met Tyr Ser Phe Arg Thr Ala Ser Arg Ala Cys
494                 499                 504                 509

aca ctg cag ggg cac aca cag gcc tgt gtc ggc acc acc tac cac ccc     1825
Thr Leu Gln Gly His Thr Gln Ala Cys Val Gly Thr Thr Tyr His Pro
510                 515                 520                 525

gtg ctg ccc tcc gtc ctc gcc acc tgc tcc tgg gga ggg gac atg aag     1873
Val Leu Pro Ser Val Leu Ala Thr Cys Ser Trp Gly Gly Asp Met Lys
526                 531                 536                 541

atc tgg cac tga gct ttttgtcact gaaccttccc gatgccagct gggctcttgg     1928
Ile Trp His  *
542

actcccctct tcctcaaggg tagatgagag gaacgagcac agaggttggc tgtgggtcct   1988

gggtaccacc ttctgagcct cagtttcctc atctgtaaag tggggagaaa agtctgtttg   2048

cctcaggagt gtgaggacta cactagtgaa agcgcctggc gggcagccgg cgatgcccaa   2108
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taaatgtgtg ttttgctgtt tgttaagtga tttcagcaaa aaaaaaaaa 2157

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<222> (194)..(1834)

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ctcagccgcc tcctagcggc gcggcgctcg ctcctacgcc taaaatgacc aatgtgtgat 180

ttcagtggaa taa atg gcg tcc aaa gtc aca gat gct ata gtc tgg tat 229
Met Ala Ser Lys Val Thr Asp Ala Ile Val Trp Tyr
1 5 10

caa aag aag att gga gca tat gat caa caa ata tgg gaa aaa tct gtt 277
Gln Lys Lys Ile Gly Ala Tyr Asp Gln Gln Ile Trp Glu Lys Ser Val
13 18 23 28

gaa cag aga gaa atc aag ggg cta agg aat aaa cca aag aaa aca gca 325
Glu Gln Arg Glu Ile Lys Gly Leu Arg Asn Lys Pro Lys Lys Thr Ala
29 34 39 44

cat gtg aaa cca gac ctc ata gat gtt gat ctt gta aga ggg tct gca 373
His Val Lys Pro Asp Leu Ile Asp Val Asp Leu Val Arg Gly Ser Ala
45 50 55 60

ttt gca aag gca aag cct gaa agt cct tgg act tct ctg acc aga aag 421
Phe Ala Lys Ala Lys Pro Glu Ser Pro Trp Thr Ser Leu Thr Arg Lys
61 66 71 76

gga att gtt cga gtt gta ttt ttc ccc ttt ttc ttc cgg tgg tgg tta 469
Gly Ile Val Arg Val Val Phe Phe Pro Phe Phe Phe Arg Trp Trp Leu
77 82 87 92

caa gta aca tca aag gtc atc ttt ttc tgg ctt ctt gtc ctt tat ctt 517
Gln Val Thr Ser Lys Val Ile Phe Phe Trp Leu Leu Val Leu Tyr Leu
93 98 103 108

ctt caa gtt gct gca ata gta tta ttc tgc tcc act tct agc cca cac 565
Leu Gln Val Ala Ala Ile Val Leu Phe Cys Ser Thr Ser Ser Pro His
109 114 119 124

agc ata cct ctg aca gag gtg att ggg ccg ata tgg ctg atg ctg ctc 613
Ser Ile Pro Leu Thr Glu Val Ile Gly Pro Ile Trp Leu Met Leu Leu
125 130 135 140

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ctg gga act gtg cat tgc cag att gtt tcc aca aga aca ccc aaa cct      661
Leu Gly Thr Val His Cys Gln Ile Val Ser Thr Arg Thr Pro Lys Pro
141                 146                 151                 156

cct cta agt aca ggg ggt aaa aga aga agg aaa tta aga aaa gca gcc      709
Pro Leu Ser Thr Gly Gly Lys Arg Arg Arg Lys Leu Arg Lys Ala Ala
157                 162                 167                 172

cat ttg gaa gta cat agg gaa gga gat ggt tct agt acc aca gat aac      757
His Leu Glu Val His Arg Glu Gly Asp Gly Ser Ser Thr Thr Asp Asn
173                 178                 183                 188

aca caa gag gga gca gtt cag aac cac ggt aca agc acc tct cac agc      805
Thr Gln Glu Gly Ala Val Gln Asn His Gly Thr Ser Thr Ser His Ser
189                 194                 199                 204

gtt ggc act gtc ttc aga gat ctc tgg cat gct gct ttc ttt tta tca      853
Val Gly Thr Val Phe Arg Asp Leu Trp His Ala Ala Phe Phe Leu Ser
205                 210                 215                 220

gga tca aag aaa gca aag aat tca att gat aaa tca act gaa act gac      901
Gly Ser Lys Lys Ala Lys Asn Ser Ile Asp Lys Ser Thr Glu Thr Asp
221                 226                 231                 236

aat ggc tat gta tcc ctt gat ggg aag aag act gtt aaa agc ggt gaa      949
Asn Gly Tyr Val Ser Leu Asp Gly Lys Lys Thr Val Lys Ser Gly Glu
237                 242                 247                 252

gat gga ata caa aac cat gaa cct cag tgt gaa act att cga cca gaa      997
Asp Gly Ile Gln Asn His Glu Pro Gln Cys Glu Thr Ile Arg Pro Glu
253                 258                 263                 268

gag aca gcc tgg aac aca gga aca ctg agg aat ggt cct agc aaa gat     1045
Glu Thr Ala Trp Asn Thr Gly Thr Leu Arg Asn Gly Pro Ser Lys Asp
269                 274                 279                 284

acc caa agg aca ata aca aat gtc tct gat gaa gtc tcc agt gag gaa     1093
Thr Gln Arg Thr Ile Thr Asn Val Ser Asp Glu Val Ser Ser Glu Glu
285                 290                 295                 300

ggt cct gaa aca gga tac tca tta cgt cgt cat gtg gac agg act tct     1141
Gly Pro Glu Thr Gly Tyr Ser Leu Arg Arg His Val Asp Arg Thr Ser
301                 306                 311                 316

gaa ggt gtt ctt cgg aat aga aag tca cac cat tat aag aaa cat tac     1189
Glu Gly Val Leu Arg Asn Arg Lys Ser His His Tyr Lys Lys His Tyr
317                 322                 327                 332

cct aat gag gac gcc cct aaa tcg ggt act agt tgc agc tct cgc tgt     1237
Pro Asn Glu Asp Ala Pro Lys Ser Gly Thr Ser Cys Ser Ser Arg Cys
333                 338                 343                 348

tca agt tcc aga cag gat tct gag agt gca agg cca gaa tct gaa aca     1285
Ser Ser Ser Arg Gln Asp Ser Glu Ser Ala Arg Pro Glu Ser Glu Thr
349                 354                 359                 364
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gaa gat gtg tta tgg gaa gac ttg tta cat tgt gca gaa tgc cat tca     1333
Glu Asp Val Leu Trp Glu Asp Leu Leu His Cys Ala Glu Cys His Ser
365                 370                 375                 380

tct tgt acc agt gag aca gat gtg gaa aat cat cag att aat cca tgt     1381
Ser Cys Thr Ser Glu Thr Asp Val Glu Asn His Gln Ile Asn Pro Cys
381                 386                 391                 396

gtg aaa aaa gaa tat aga gat gac cct ttt cat cag agt cat ttg ccc     1429
Val Lys Lys Glu Tyr Arg Asp Asp Pro Phe His Gln Ser His Leu Pro
397                 402                 407                 412

tgg ctc cat agt tcc cac cca gga tta gaa aaa ata agt gct ata gta     1477
Trp Leu His Ser Ser His Pro Gly Leu Glu Lys Ile Ser Ala Ile Val
413                 418                 423                 428

tgg gaa ggt aat gat tgt aag aaa gca gac atg tct gta ctt gaa atc     1525
Trp Glu Gly Asn Asp Cys Lys Lys Ala Asp Met Ser Val Leu Glu Ile
429                 434                 439                 444

agt gga atg ata atg aac aga gtg aac agc cat ata cca gga ata gga     1573
Ser Gly Met Ile Met Asn Arg Val Asn Ser His Ile Pro Gly Ile Gly
445                 450                 455                 460

tac cag att ttt gga aat gca gtc tct ctc ata ctg ggt tta act cca     1621
Tyr Gln Ile Phe Gly Asn Ala Val Ser Leu Ile Leu Gly Leu Thr Pro
461                 466                 471                 476

ttt gtt ttc cga ctt tct caa gct aca gac ttg gaa caa ctc aca gca     1669
Phe Val Phe Arg Leu Ser Gln Ala Thr Asp Leu Glu Gln Leu Thr Ala
477                 482                 487                 492

cat tct gct tca gaa ctt tat gtg att gca ttt ggt tct aat gaa gat     1717
His Ser Ala Ser Glu Leu Tyr Val Ile Ala Phe Gly Ser Asn Glu Asp
493                 498                 503                 508

gtc ata gtt ctt tct atg gtt ata ata agt ttt gtg gtt cgc gtg tct     1765
Val Ile Val Leu Ser Met Val Ile Ile Ser Phe Val Val Arg Val Ser
509                 514                 519                 524

ctt gtg tgg att ttc ttt ttt ttg ctc tgt gta gca gaa aga act tat     1813
Leu Val Trp Ile Phe Phe Phe Leu Leu Cys Val Ala Glu Arg Thr Tyr
525                 530                 535                 540

aaa cag gtg ggt ata atg tag ac ttccgaataa gaatatttta tcgttttcat     1866
Lys Gln Val Gly Ile Met  *
541                 546

aatattaaaa gtattcctga agtactttat tatttcatta tatcattttt acctaattat   1926

ttttttttttt tgcttttata gtacctaacc aaataaaatc ttaacaattc             1976
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ctcagccgcc tcctagcggc gcggcgctcg ctcctacgcc taaaatgacc aatgtgtgat     180

ttcagtggaa taa   atg gcg tcc aaa gtc aca gat gct ata gtc tgg tat       229
                Met Ala Ser Lys Val Thr Asp Ala Ile Val Trp Tyr
                  1               5                  10

caa aag aag att gga gca tat gat caa caa ata tgg gaa aaa tct gtt       277
Gln Lys Lys Ile Gly Ala Tyr Asp Gln Gln Ile Trp Glu Lys Ser Val
 13                  18                  23                  28

gaa cag aga gaa atc aag ggg cta agg aat aaa cca aag aaa aca gca       325
Glu Gln Arg Glu Ile Lys Gly Leu Arg Asn Lys Pro Lys Lys Thr Ala
 29                  34                  39                  44

cat gtg aaa cca gac ctc ata gat gtt gat ctt gta aga ggg tct gca       373
His Val Lys Pro Asp Leu Ile Asp Val Asp Leu Val Arg Gly Ser Ala
 45                  50                  55                  60

ttt gca aag gca aag cct gaa agt cct tgg act tct ctg acc aga aag       421
Phe Ala Lys Ala Lys Pro Glu Ser Pro Trp Thr Ser Leu Thr Arg Lys
 61                  66                  71                  76

gga att gtt cga gtt gta ttt ttc ccc ttt ttc ttc cgg tgg tgg tta       469
Gly Ile Val Arg Val Val Phe Phe Pro Phe Phe Phe Arg Trp Trp Leu
 77                  82                  87                  92

caa gta aca tca aag gtc atc ttt ttc tgg ctt ctt gtc ctt tat ctt       517
Gln Val Thr Ser Lys Val Ile Phe Phe Trp Leu Leu Val Leu Tyr Leu
 93                  98                 103                 108

ctt caa gtt gct gca ata gta tta ttc tgc tcc act tct agc cca cac       565
Leu Gln Val Ala Ala Ile Val Leu Phe Cys Ser Thr Ser Ser Pro His
109                 114                 119                 124

agc ata cct ctg aca gag gtg att ggg ccg ata tgg ctg atg ctg ctc       613
Ser Ile Pro Leu Thr Glu Val Ile Gly Pro Ile Trp Leu Met Leu Leu
125                 130                 135                 140

ctg gga act gtg cat tgc cag att gtt tcc aca aga aca ccc aaa cct       661
Leu Gly Thr Val His Cys Gln Ile Val Ser Thr Arg Thr Pro Lys Pro
141                 146                 151                 156

cct cta agt aca ggg ggt aaa aga aga agg tca aag aaa gca aag aat       709
Pro Leu Ser Thr Gly Gly Lys Arg Arg Arg Ser Lys Lys Ala Lys Asn
157                 162                 167                 172
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tca att gat aaa tca act gaa act gac aat ggc tat gta tcc ctt gat      757
Ser Ile Asp Lys Ser Thr Glu Thr Asp Asn Gly Tyr Val Ser Leu Asp
173                 178                 183                 188

ggg aag aag act gtt aaa agc ggt gaa gat gga ata caa aac cat gaa      805
Gly Lys Lys Thr Val Lys Ser Gly Glu Asp Gly Ile Gln Asn His Glu
189                 194                 199                 204

cct cag tgt gaa act att cga cca gaa gag aca gcc tgg aac aca gga      853
Pro Gln Cys Glu Thr Ile Arg Pro Glu Glu Thr Ala Trp Asn Thr Gly
205                 210                 215                 220

aca ctg agg aat ggt cct agc aaa gat acc caa agg aca ata aca aat      901
Thr Leu Arg Asn Gly Pro Ser Lys Asp Thr Gln Arg Thr Ile Thr Asn
221                 226                 231                 236

gtc tct gat gaa gtc tcc agt gag gaa ggt cct gaa aca gga tac tca      949
Val Ser Asp Glu Val Ser Ser Glu Glu Gly Pro Glu Thr Gly Tyr Ser
237                 242                 247                 252

tta cgt cgt cat gtg gac agg act tct gaa ggt gtt ctt cgg aat aga      997
Leu Arg Arg His Val Asp Arg Thr Ser Glu Gly Val Leu Arg Asn Arg
253                 258                 263                 268

aag tca cac cat tat aag aaa cat tac cct aat gag gac gcc cct aaa     1045
Lys Ser His His Tyr Lys Lys His Tyr Pro Asn Glu Asp Ala Pro Lys
269                 274                 279                 284

tcg ggt act agt tgc agc tct cgc tgt tca agt tcc aga cag gat tct     1093
Ser Gly Thr Ser Cys Ser Ser Arg Cys Ser Ser Ser Arg Gln Asp Ser
285                 290                 295                 300

gag agt gca agg cca gaa tct gaa aca gaa gat gtg tta tgg gaa gac     1141
Glu Ser Ala Arg Pro Glu Ser Glu Thr Glu Asp Val Leu Trp Glu Asp
301                 306                 311                 316

ttg tta cat tgt gca gaa tgc cat tca tct tgt acc agt gag aca gat     1189
Leu Leu His Cys Ala Glu Cys His Ser Ser Cys Thr Ser Glu Thr Asp
317                 322                 327                 332

gtg gaa aat cat cag att aat cca tgt gtg aaa aaa gaa tat aga gat     1237
Val Glu Asn His Gln Ile Asn Pro Cys Val Lys Lys Glu Tyr Arg Asp
333                 338                 343                 348

gac cct ttt cat cag agt cat ttg ccc tgg ctc cat agt tcc cac cca     1285
Asp Pro Phe His Gln Ser His Leu Pro Trp Leu His Ser Ser His Pro
349                 354                 359                 364

gga tta gaa aaa ata agt gct ata gta tgg gaa ggt aat gat tgt aag     1333
Gly Leu Glu Lys Ile Ser Ala Ile Val Trp Glu Gly Asn Asp Cys Lys
365                 370                 375                 380

aaa gca gac atg tct gta ctt gaa atc agt gga atg ata atg aac aga     1381
Lys Ala Asp Met Ser Val Leu Glu Ile Ser Gly Met Ile Met Asn Arg
381                 386                 391                 396
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gtg aac agc cat ata cca gga ata gga tac cag att ttt gga aat gca     1429
Val Asn Ser His Ile Pro Gly Ile Gly Tyr Gln Ile Phe Gly Asn Ala
397                 402                 407                 412

gtc tct ctc ata ctg ggt tta act cca ttt gtt ttc cga ctt tct caa     1477
Val Ser Leu Ile Leu Gly Leu Thr Pro Phe Val Phe Arg Leu Ser Gln
413                 418                 423                 428

gct aca gac ttg gaa caa ctc aca gca cat tct gct tca gaa ctt tat     1525
Ala Thr Asp Leu Glu Gln Leu Thr Ala His Ser Ala Ser Glu Leu Tyr
429                 434                 439                 444

gtg att gca ttt ggt tct aat gaa gat gtc ata gtt ctt tct atg gtt     1573
Val Ile Ala Phe Gly Ser Asn Glu Asp Val Ile Val Leu Ser Met Val
445                 450                 455                 460

ata ata agt ttt gtg gtt cgc gtg tct ctt gtg tgg att ttc ttt ttt     1621
Ile Ile Ser Phe Val Val Arg Val Ser Leu Val Trp Ile Phe Phe Phe
461                 466                 471                 476

ttg ctc tgt gta gca gaa aga act tat aaa cag gtg ggt ata atg tag     1669
Leu Leu Cys Val Ala Glu Arg Thr Tyr Lys Gln Val Gly Ile Met  *
477                 482                 487                 492

acttccgaat aagaatattt tatcgttttc ataatattaa aagtattcct gaagtacttt   1729

attatttcat tatatcattt ttacctaatt attttttttt tttgctttta tagtacctaa   1789

ccaaataaaa tcttaacaat tc                                           1811
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<400> 92

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taacagttga ttgatgaata tgaaatcaga gcaagagggg ctaattagag attttactag    180

ctagggctat ttacccaaac catctatcca gactgtagac atagaatcac cagatggcta    240

ggatcctggt gcagctggtt ccccttttttc cttaccctga atgtcattaa ggatgcattg    300

ccaaatgctg cccctctggc ctgatgacta cactccatat tggtcacctg ccttcttttt    360

cctacagtct tcctccagac aggcacgcca tacaaccgac tacacttggg ctcactgaat    420
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gaatcacatt cttctgctgt gcctcccaga gatttcatca aagcacccgc agtggccttc 480

tggaggctcc tcaaactctc cactcaatgt ttcctgaaag tgtcgtgttt ctcacctcta 540

gattgttatt ctcatcagtt acatgtgggt ttcacaaatt tatttctcag aatgcaagtc 600

tgtctcttat atcctcggga aacacacctt tatatcccag ttagtactga caaaaattaa 660

actagggact ggccaaaaac agtgcctttc ctcactttaa tctcactaaa gtagataaga 720

ctcaagttat tttgttcttg caatggcatt gacaaatgtt tgcaccaaaa accatgttga 780

agttcattaa ggaaactgtg atccaagatc caaggtcaaa aaaacaaatt catcaattca 840

gcacaccacc aactcacagg ctaagcatct tactgctaat tcattgatgc tgccatttgt 900

caagtgccaa attgaattat tgatttgtca ataatttcct tctgttggtt acttatatag 960

tatattgcaa ttcttgttgc tgaagtcagc tacacttttt ctatttgaaa aacaatttct 1020

tgcatttggg atttcaggta tagtgattgt tacaaatatg aaggacttga attaacagca 1080

agttttcaag taaaacttta cttatgtata actgaatgag ttcttaaaga catttactaa 1140

caattttcca caaactaaaa atttataaaa caataaataa aatagacttt aaaaaaaagc 1200

gtgtcacaca gctgcttgtt ttttgtttgt ttcttttgttt gtttttttagt agtgaa 1256

atg gtg aaa aat cag aca atg gtc aca gag ttc ctc cta ctg gga ttt 1304
Met Val Lys Asn Gln Thr Met Val Thr Glu Phe Leu Leu Leu Gly Phe
1 5 10 15

ctc ctg ggc cca agg att cag atg ctc ctc ttt ggg ctc ttc tcc ctg 1352
Leu Leu Gly Pro Arg Ile Gln Met Leu Leu Phe Gly Leu Phe Ser Leu
17 22 27 32

ttc tat gtc ttc acc ctg ctg ggg aat ggg acc atc ctg ggg ctc atc 1400
Phe Tyr Val Phe Thr Leu Leu Gly Asn Gly Thr Ile Leu Gly Leu Ile
33 38 43 48

tca ctg gac tcc aga ctc cac acc ccc atg tac ttc ttc ctc tca cac 1448
Ser Leu Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser His
49 54 59 64

ctg gcc gtc gtc aac atc gcc tat gcc tgc aac aca gtg ccc cag atg 1496
Leu Ala Val Val Asn Ile Ala Tyr Ala Cys Asn Thr Val Pro Gln Met
65 70 75 80

ctg gtg aac ctc ctg cat cca gcc aag ccc atc tcc ttt gct ggc tgc 1544
Leu Val Asn Leu Leu His Pro Ala Lys Pro Ile Ser Phe Ala Gly Cys
81 86 91 96

atg aca cag acc ttt ctc ttt ttg agt ttt gca cat act gaa tgc ctc 1592
Met Thr Gln Thr Phe Leu Phe Leu Ser Phe Ala His Thr Glu Cys Leu
97 102 107 112

ctg ttg gtg ctg atg tcc tac gat cgg tac gtg gcc atc tgc cac cct 1640

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Leu Leu Val Leu Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys His Pro
113                 118                 123                 128

ctc cga tat ttc atc atc atg acc tgg aaa gtc tgc atc act ctg gcc     1688
Leu Arg Tyr Phe Ile Ile Met Thr Trp Lys Val Cys Ile Thr Leu Ala
129                 134                 139                 144

atc act tcc tgg aca tgt ggc tcc ctc ctg gct atg gtc cat gtg agc     1736
Ile Thr Ser Trp Thr Cys Gly Ser Leu Leu Ala Met Val His Val Ser
145                 150                 155                 160

ctc atc cta aga ctg ccc ttt tgt ggg cct cgt gaa atc aac cac ttc     1784
Leu Ile Leu Arg Leu Pro Phe Cys Gly Pro Arg Glu Ile Asn His Phe
161                 166                 171                 176

ttc tgt gaa atc ctg tct gtc ctc agg ctg gcc tgt gct gat acc tgg     1832
Phe Cys Glu Ile Leu Ser Val Leu Arg Leu Ala Cys Ala Asp Thr Trp
177                 182                 187                 192

ctc aac cag gtg gtc atc ttt gca gcc tgc atg ttc atc ctg gtg gga     1880
Leu Asn Gln Val Val Ile Phe Ala Ala Cys Met Phe Ile Leu Val Gly
193                 198                 203                 208

cca ctc tgc ctg gtg ctg gtc tcc tac tca cac atc ctg gcg gcc atc     1928
Pro Leu Cys Leu Val Leu Val Ser Tyr Ser His Ile Leu Ala Ala Ile
209                 214                 219                 224

ctg agg atc cag tct ggg gag ggc cgc aga aag gcc ttc tcc acc tgc     1976
Leu Arg Ile Gln Ser Gly Glu Gly Arg Arg Lys Ala Phe Ser Thr Cys
225                 230                 235                 240

tcc tcc cac ctc tgc gta gtg gga ctc ttc ttt ggc agc gcc atc gtc     2024
Ser Ser His Leu Cys Val Val Gly Leu Phe Phe Gly Ser Ala Ile Val
241                 246                 251                 256

atg tac atg gcc cct aag tcc cgc cat cct gag gag cag cag aag gtc     2072
Met Tyr Met Ala Pro Lys Ser Arg His Pro Glu Glu Gln Gln Lys Val
257                 262                 267                 272

ctt ttt cta ttt tac agt tct ttc aac ccg atg cta aac ccc ctg att     2120
Leu Phe Leu Phe Tyr Ser Ser Phe Asn Pro Met Leu Asn Pro Leu Ile
273                 278                 283                 288

tac aac ctg agg aat gta gag gtc aag ggt gcc ctg agg aga gca ctg     2168
Tyr Asn Leu Arg Asn Val Glu Val Lys Gly Ala Leu Arg Arg Ala Leu
289                 294                 299                 304

tgc aag gaa agt cat tcc taa ga ggtgtgacat ttgaactgcc agcctcagtt     2221
Cys Lys Glu Ser His Ser  *
305                 310

gtcacgtgga ctctttgatg cccaattatt tgcctcaatc cagaaaagtt tacttcttct   2281

t                                                                   2282
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ggcagccgga agcgcgcgca tgctctggac tcctgcagcc gccgaaacgg tcaggttttc 180

cttgttcccg catgttcagc caatcgtgtt taaggagaaa ctaacaatga aaacggactc 240

gttgatggag gaaaagttgg aatgcagcct ctggtgctgt ttgagcgatc cctctacccc 300

gggtcgctgc tgtgttctgg aaaggcgcat tgtaccctgg atgcagcagg aatcctattc 360

atcttcttca ccgatatggt ctgtggactc tgatgagcca aatctgacat cagttctgga 420

acgtctagaa gatactaagg acaacagttc gcttccttct ttggttagaa ccacccggag 480

gtgactgtgg cc atg gct ctg act gac ata gac ctg cag ctg cag ttc 528
Met Ala Leu Thr Asp Ile Asp Leu Gln Leu Gln Phe
1 5 10

tcc atg tcc caa ccc gaa gcc ctc ctt ctc ctg gca gca ggc cca gct 576
Ser Met Ser Gln Pro Glu Ala Leu Leu Leu Leu Ala Ala Gly Pro Ala
13 18 23 28

gac cac ctc ctg ctg cag ctc tac tct gga cac ctg cag gtc aga ctt 624
Asp His Leu Leu Leu Gln Leu Tyr Ser Gly His Leu Gln Val Arg Leu
29 34 39 44

gtt ctg ggc cag gag gag ctg agg ctg cag act cca gca gag acg ctg 672
Val Leu Gly Gln Glu Glu Leu Arg Leu Gln Thr Pro Ala Glu Thr Leu
45 50 55 60

ctg agt gac tcc atc ccc cac act gtg gtg ctg act gtc gta gag ggc 720
Leu Ser Asp Ser Ile Pro His Thr Val Val Leu Thr Val Val Glu Gly
61 66 71 76

tgg gcc acg ttg tca gtc gat ggg ttt ctg aac gcc tcc tca gca gtc 768
Trp Ala Thr Leu Ser Val Asp Gly Phe Leu Asn Ala Ser Ser Ala Val
77 82 87 92

cca gga gcc ccc cta gag gtc ccc tat ggg ctc ttt gtt ggg ggc act 816
Pro Gly Ala Pro Leu Glu Val Pro Tyr Gly Leu Phe Val Gly Gly Thr
93 98 103 108

ggg acc ctt ggc ctg ccc tac ctg agg gga acc agc cga ccc ctg agg 864
Gly Thr Leu Gly Leu Pro Tyr Leu Arg Gly Thr Ser Arg Pro Leu Arg

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109                 114                 119                 124

ggt tgc ctc cat gca gcc acc ctc aat ggc cgc agc ctc ctc cgg cct      912
Gly Cys Leu His Ala Ala Thr Leu Asn Gly Arg Ser Leu Leu Arg Pro
125                 130                 135                 140

ctg acc ccc gat gtg cat gag ggc tgt gct gaa gag ttt tct gcc agt      960
Leu Thr Pro Asp Val His Glu Gly Cys Ala Glu Glu Phe Ser Ala Ser
141                 146                 151                 156

gat gat gtg gcc ctg ggc ttc tct ggg ccc cac tct ctg gct gcc ttc     1008
Asp Asp Val Ala Leu Gly Phe Ser Gly Pro His Ser Leu Ala Ala Phe
157                 162                 167                 172

cct gcc tgg ggc act cag gac gaa gga acc cta gag ttt aca ctc acc     1056
Pro Ala Trp Gly Thr Gln Asp Glu Gly Thr Leu Glu Phe Thr Leu Thr
173                 178                 183                 188

aca cag agc cgg cag gca ccc ttg gcc ttc cag gca ggg ggc cgg cgt     1104
Thr Gln Ser Arg Gln Ala Pro Leu Ala Phe Gln Ala Gly Gly Arg Arg
189                 194                 199                 204

ggg gac ttc atc tat gtg gac ata ttt gag ggc cac ctg cgg gcc gtg     1152
Gly Asp Phe Ile Tyr Val Asp Ile Phe Glu Gly His Leu Arg Ala Val
205                 210                 215                 220

gtg gag aag ggc cag ggt acc gta ttg ctc cac aac agt gtg cct gtg     1200
Val Glu Lys Gly Gln Gly Thr Val Leu Leu His Asn Ser Val Pro Val
221                 226                 231                 236

gcc gat ggg cag ccc cat gag gtc agt gtc cac atc aat gct cac cgg     1248
Ala Asp Gly Gln Pro His Glu Val Ser Val His Ile Asn Ala His Arg
237                 242                 247                 252

ctg gaa atc tcc gtg gac cag tac cct acg cat act tcg aac cga gga     1296
Leu Glu Ile Ser Val Asp Gln Tyr Pro Thr His Thr Ser Asn Arg Gly
253                 258                 263                 268

gtc ctc agc tac ctg gag cca cgg ggc agt ctc ctt ctc ggg ggg ctg     1344
Val Leu Ser Tyr Leu Glu Pro Arg Gly Ser Leu Leu Leu Gly Gly Leu
269                 274                 279                 284

gat gca gag gcc tct cgt cac ctc cag gaa cac cgc ctg ggc ctg aca     1392
Asp Ala Glu Ala Ser Arg His Leu Gln Glu His Arg Leu Gly Leu Thr
285                 290                 295                 300

cca gag gcc acc aat gcc tcc ctg ctg ggc tgc atg gaa gac ctc agt     1440
Pro Glu Ala Thr Asn Ala Ser Leu Leu Gly Cys Met Glu Asp Leu Ser
301                 306                 311                 316

gtc aat ggc cag agg cgg ggg ctg cgg gaa gct ttg ctg acg cgc aac     1488
Val Asn Gly Gln Arg Arg Gly Leu Arg Glu Ala Leu Leu Thr Arg Asn
317                 322                 327                 332

atg gca gcc ggc tgc agg ctg gag gag gag gag tat gag gac gat gcc     1536
Met Ala Ala Gly Cys Arg Leu Glu Glu Glu Glu Tyr Glu Asp Asp Ala
333                 338                 343                 348
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tat ggc cat tat gaa gct ttc tcc acc ctg gct ccc gag gct tgg cca      1584
Tyr Gly His Tyr Glu Ala Phe Ser Thr Leu Ala Pro Glu Ala Trp Pro
349                 354                 359                 364

gcc atg gag ctg cct gag cca tgc gtg cct gag cca ggg ctg cct cct      1632
Ala Met Glu Leu Pro Glu Pro Cys Val Pro Glu Pro Gly Leu Pro Pro
365                 370                 375                 380

gtc ttt gcc aat ttc acc cag ctg ctg act atc agc cca ctg gtg gtg      1680
Val Phe Ala Asn Phe Thr Gln Leu Leu Thr Ile Ser Pro Leu Val Val
381                 386                 391                 396

gcc gag ggt ggc aca gcc tgg ctt gag tgg agg cat gtg cag ccc acg      1728
Ala Glu Gly Gly Thr Ala Trp Leu Glu Trp Arg His Val Gln Pro Thr
397                 402                 407                 412

ctg gac ctg atg gag gct gag ctg cgc aaa tcc cag gtg ctg ttc agc      1776
Leu Asp Leu Met Glu Ala Glu Leu Arg Lys Ser Gln Val Leu Phe Ser
413                 418                 423                 428

gtg acc cga ggg gca cac tat ggc gag ctc gag ctg gac atc ctg ggt      1824
Val Thr Arg Gly Ala His Tyr Gly Glu Leu Glu Leu Asp Ile Leu Gly
429                 434                 439                 444

gcc cag gca cga aaa atg ttc acc ctc ctg gac gtg gtg aac cgc aag      1872
Ala Gln Ala Arg Lys Met Phe Thr Leu Leu Asp Val Val Asn Arg Lys
445                 450                 455                 460

gcc cgc ttc atc cac gat ggc cct gag gac acc tct gac cag ctg gtg      1920
Ala Arg Phe Ile His Asp Gly Pro Glu Asp Thr Ser Asp Gln Leu Val
461                 466                 471                 476

ctg gag gtg tca gtg atg gct tgg ttg ccc atg ccc tca tgc ctg cgg      1968
Leu Glu Val Ser Val Met Ala Trp Leu Pro Met Pro Ser Cys Leu Arg
477                 482                 487                 492

agg ggc caa aca gac ctc ctg ccc atc cag gtc aac cct gtc aat gac      2016
Arg Gly Gln Thr Asp Leu Leu Pro Ile Gln Val Asn Pro Val Asn Asp
493                 498                 503                 508

cca ccc cac atc atc ttc cca cat ggc agc ctt atg gtg atc ctg gaa      2064
Pro Pro His Ile Ile Phe Pro His Gly Ser Leu Met Val Ile Leu Glu
509                 514                 519                 524

cac aca cag aag ccg ctg ggg cct gag gtt ctc cag gcc tat gac ctg      2112
His Thr Gln Lys Pro Leu Gly Pro Glu Val Leu Gln Ala Tyr Asp Leu
525                 530                 535                 540

gac tct gcc tgt gag ggc ctc acc ttc cag ctc ctt ggc acc ccc tct      2160
Asp Ser Ala Cys Glu Gly Leu Thr Phe Gln Leu Leu Gly Thr Pro Ser
541                 546                 551                 556

ggc ctc ccc gtg gag cac cga gac cag cct ggg gag ccg gcg acc gag      2208
Gly Leu Pro Val Glu His Arg Asp Gln Pro Gly Glu Pro Ala Thr Glu
557                 562                 567                 572
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ttc tcc tgc cgg gag ttg gag gcc ggc agc cta gtc tat gtc cac tgc      2256
Phe Ser Cys Arg Glu Leu Glu Ala Gly Ser Leu Val Tyr Val His Cys
573                 578                 583                 588

ggt ggt cct gca cag gac ttg acg ttc cgg gtc agc gat gga ctg cag      2304
Gly Gly Pro Ala Gln Asp Leu Thr Phe Arg Val Ser Asp Gly Leu Gln
589                 594                 599                 604

gcc agc ccc ccg gcc acg ctg aag gtg gtg gcc atc cgg ccg gcc ata      2352
Ala Ser Pro Pro Ala Thr Leu Lys Val Val Ala Ile Arg Pro Ala Ile
605                 610                 615                 620

cag atc cac cgc agc aca ggg ttg cga ctg gcc caa ggc tct gcc atg      2400
Gln Ile His Arg Ser Thr Gly Leu Arg Leu Ala Gln Gly Ser Ala Met
621                 626                 631                 636

ccc atc ttg ccc gcc aac ctg tcg gtg gag acc aat gcc gtg ggg cag      2448
Pro Ile Leu Pro Ala Asn Leu Ser Val Glu Thr Asn Ala Val Gly Gln
637                 642                 647                 652

gat gtg agc gtg ctg ttc cgc gtc act ggg gcc ctg cag ttt ggg gag      2496
Asp Val Ser Val Leu Phe Arg Val Thr Gly Ala Leu Gln Phe Gly Glu
653                 658                 663                 668

ctg cag aag cat agt aca ggt ggg gtg gag ggt gct gag tgg tgg gcc      2544
Leu Gln Lys His Ser Thr Gly Gly Val Glu Gly Ala Glu Trp Trp Ala
669                 674                 679                 684

aca cag gcg ttc cac cag cgg gat gtg gag cag ggc cgc gtg agg tac      2592
Thr Gln Ala Phe His Gln Arg Asp Val Glu Gln Gly Arg Val Arg Tyr
685                 690                 695                 700

ctg agc act gac cca cag cac cac gct tac gac acc gtg gag aac ctg      2640
Leu Ser Thr Asp Pro Gln His His Ala Tyr Asp Thr Val Glu Asn Leu
701                 706                 711                 716

gcc ctg gag gtg cag gtg ggc cag gag atc ctg agc aat ctg tcc ttc      2688
Ala Leu Glu Val Gln Val Gly Gln Glu Ile Leu Ser Asn Leu Ser Phe
717                 722                 727                 732

cca gtg acc atc cag aga gcc act gtg tgg atg ctg cgg ctg gag cca      2736
Pro Val Thr Ile Gln Arg Ala Thr Val Trp Met Leu Arg Leu Glu Pro
733                 738                 743                 748

ctg cac act cag aac acc cag cag gag acc ctc acc aca gcc cac ctg      2784
Leu His Thr Gln Asn Thr Gln Gln Glu Thr Leu Thr Thr Ala His Leu
749                 754                 759                 764

gag gcc acc ctg gag gag gca ggc cca agc ccc cca acc ttc cat tat      2832
Glu Ala Thr Leu Glu Glu Ala Gly Pro Ser Pro Pro Thr Phe His Tyr
765                 770                 775                 780

gag gtg gtt cag gct ccc agg aaa ggc aac ctt caa cta cag ggc aca      2880
Glu Val Val Gln Ala Pro Arg Lys Gly Asn Leu Gln Leu Gln Gly Thr
781                 786                 791                 796

agg ctg tca gat ggc cag ggc ttc acc cag gat gac ata cag gct ggc      2928
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Arg Leu Ser Asp Gly Gln Gly Phe Thr Gln Asp Asp Ile Gln Ala Gly
797                 802                 807                 812

cgg gtg acc tat ggg gcc aca gct cgt gcc tca gag gca gtc gag gac     2976
Arg Val Thr Tyr Gly Ala Thr Ala Arg Ala Ser Glu Ala Val Glu Asp
813                 818                 823                 828

acc ttc cgt ttc cgt gtc aca gct cca cca tat ttc tcc cca ctc tat     3024
Thr Phe Arg Phe Arg Val Thr Ala Pro Pro Tyr Phe Ser Pro Leu Tyr
829                 834                 839                 844

acc ttc ccc atc cac att ggt ggt gac cca gat gcg cct gtc ctc acc     3072
Thr Phe Pro Ile His Ile Gly Gly Asp Pro Asp Ala Pro Val Leu Thr
845                 850                 855                 860

aat gtc ctc ctc gtg gtg cct gag ggt ggt gag ggt gtc ctc tct gct     3120
Asn Val Leu Leu Val Val Pro Glu Gly Gly Glu Gly Val Leu Ser Ala
861                 866                 871                 876

gac cac ctc ttt gtc aag agt ctc aac agt gcc agc tac ctc tat gag     3168
Asp His Leu Phe Val Lys Ser Leu Asn Ser Ala Ser Tyr Leu Tyr Glu
877                 882                 887                 892

gtc atg gag cgg ccc cgc ctt ggg agg ttg gct tgg cgt ggg aca cag     3216
Val Met Glu Arg Pro Arg Leu Gly Arg Leu Ala Trp Arg Gly Thr Gln
893                 898                 903                 908

gac aag acc act atg gtg aca tcc ttc acc aat gaa gac ctg ttg cgt     3264
Asp Lys Thr Thr Met Val Thr Ser Phe Thr Asn Glu Asp Leu Leu Arg
909                 914                 919                 924

ggc cgg ctg gtc tac cag cat gat gac tcc gag acc aca gaa gat gat     3312
Gly Arg Leu Val Tyr Gln His Asp Asp Ser Glu Thr Thr Glu Asp Asp
925                 930                 935                 940

atc cca ttt gtt gct acc cgc cag ggc gag agc agt ggt gac atg gcc     3360
Ile Pro Phe Val Ala Thr Arg Gln Gly Glu Ser Ser Gly Asp Met Ala
941                 946                 951                 956

tgg gag gag gta cgg ggt gtc ttc cga gtg gcc atc cag ccc gtg aat     3408
Trp Glu Glu Val Arg Gly Val Phe Arg Val Ala Ile Gln Pro Val Asn
957                 962                 967                 972

gac cac gcc cct gtg cag acc atc agc cgg atc ttc cat gtg gcc cgg     3456
Asp His Ala Pro Val Gln Thr Ile Ser Arg Ile Phe His Val Ala Arg
973                 978                 983                 988

ggt ggg cgg cgg ctg ctg act aca gac gac gtg gcc ttc agc gat gct     3504
Gly Gly Arg Arg Leu Leu Thr Thr Asp Asp Val Ala Phe Ser Asp Ala
989                 994                 999                1004

gac tcg ggc ttt gct gac gcc cag ctg gtg ctt acc cgc aag gac ctc     3552
Asp Ser Gly Phe Ala Asp Ala Gln Leu Val Leu Thr Arg Lys Asp Leu
1005                1010                1015                1020

ctc ttt ggc agt atc gtg gcc gta gat gag ccc acg cgg ccc atc tac     3600
Leu Phe Gly Ser Ile Val Ala Val Asp Glu Pro Thr Arg Pro Ile Tyr
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1021                1026                1031                1036

 cgc ttc acc cag gag gac ctc agg aag agg cga gta ctg ttc gtg cac     3648
 Arg Phe Thr Gln Glu Asp Leu Arg Lys Arg Arg Val Leu Phe Val His
1037                1042                1047                1052

 tca ggg gct gac cgt ggc tgg atc cag ctg cag gtg tcc gac ggg caa     3696
 Ser Gly Ala Asp Arg Gly Trp Ile Gln Leu Gln Val Ser Asp Gly Gln
1053                1058                1063                1068

 cac cag gcc act gcg ctg ctg gag gtg cag gcc tcg gaa ccc tac ctc     3744
 His Gln Ala Thr Ala Leu Leu Glu Val Gln Ala Ser Glu Pro Tyr Leu
1069                1074                1079                1084

 cgt gtg gcc aac ggc tcc agc ctt gtg gtc cct caa gga ggc cag ggc     3792
 Arg Val Ala Asn Gly Ser Ser Leu Val Val Pro Gln Gly Gly Gln Gly
1085                1090                1095                1100

 acc atc gac acg gcc gtg ctc cac ctg gac acc aac ctc gac atc cgc     3840
 Thr Ile Asp Thr Ala Val Leu His Leu Asp Thr Asn Leu Asp Ile Arg
1101                1106                1111                1116

 agt ggg gat gag gtc cac tac cac gtc aca gct ggc cct cgc tgg gga     3888
 Ser Gly Asp Glu Val His Tyr His Val Thr Ala Gly Pro Arg Trp Gly
1117                1122                1127                1132

 caa cta gtc cgg gct ggt cag cca gcc aca gcc ttc tcc cag cag gac     3936
 Gln Leu Val Arg Ala Gly Gln Pro Ala Thr Ala Phe Ser Gln Gln Asp
1133                1138                1143                1148

 ctg ctg gat ggg gcc gtt ctc tat agc cac aat ggc agc ctc agc ccc     3984
 Leu Leu Asp Gly Ala Val Leu Tyr Ser His Asn Gly Ser Leu Ser Pro
1149                1154                1159                1164

 cga gac acc atg gcc ttc tcc gtg gaa gca ggg cca gtg cac acg gat     4032
 Arg Asp Thr Met Ala Phe Ser Val Glu Ala Gly Pro Val His Thr Asp
1165                1170                1175                1180

 gcc acc cta caa gtg acc att gcc cta gag ggc cca ctg gcc cca ctg     4080
 Ala Thr Leu Gln Val Thr Ile Ala Leu Glu Gly Pro Leu Ala Pro Leu
1181                1186                1191                1196

 aag ctg gtc cgg cac aag aag atc tac gtc ttc cag gga gag gca gct     4128
 Lys Leu Val Arg His Lys Lys Ile Tyr Val Phe Gln Gly Glu Ala Ala
1197                1202                1207                1212

 gag atc aga agg gac cag ctg gag gca gcc cag gag gca gtg cca cct     4176
 Glu Ile Arg Arg Asp Gln Leu Glu Ala Ala Gln Glu Ala Val Pro Pro
1213                1218                1223                1228

 gca gac atc gta ttc tca gtg aag agc cca ccg agt gcc ggc tac ctg     4224
 Ala Asp Ile Val Phe Ser Val Lys Ser Pro Pro Ser Ala Gly Tyr Leu
1229                1234                1239                1244

 gtg atg gtg tcg cgt ggc gcc ttg gca gat gag cca ccc agc ctg gac     4272
 Val Met Val Ser Arg Gly Ala Leu Ala Asp Glu Pro Pro Ser Leu Asp
1245                1250                1255                1260
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ccc gtg cag agc ttc tcc cag gag gca gtg gac aca ggc agg gtc ctg      4320
 Pro Val Gln Ser Phe Ser Gln Glu Ala Val Asp Thr Gly Arg Val Leu
1261                1266                1271                1276

tac ctg cac tcc cgc cct gag gcc tgg agc gat gcc ttc tcg ctg gat      4368
 Tyr Leu His Ser Arg Pro Glu Ala Trp Ser Asp Ala Phe Ser Leu Asp
1277                1282                1287                1292

gtg gcc tca ggc ctg ggt gct ccc ctc gag ggc gtc ctt gtg gag ctg      4416
 Val Ala Ser Gly Leu Gly Ala Pro Leu Glu Gly Val Leu Val Glu Leu
1293                1298                1303                1308

gag gtg ctg ccc gct gcc atc cca cta gag gcg caa aac ttc agc gtc      4464
 Glu Val Leu Pro Ala Ala Ile Pro Leu Glu Ala Gln Asn Phe Ser Val
1309                1314                1319                1324

cct gag ggt ggc agc ctc acc ctg gcc cct cca ctg ctc cgt gtc tcc      4512
 Pro Glu Gly Gly Ser Leu Thr Leu Ala Pro Pro Leu Leu Arg Val Ser
1325                1330                1335                1340

ggg ccc tac ttc ccc act ctc ctg ggc ctc agc ctg cag gtg ctg gag      4560
 Gly Pro Tyr Phe Pro Thr Leu Leu Gly Leu Ser Leu Gln Val Leu Glu
1341                1346                1351                1356

cca ccc cag cat gga ccc ctg cag aag gag gac gga cct caa gcc agg      4608
 Pro Pro Gln His Gly Pro Leu Gln Lys Glu Asp Gly Pro Gln Ala Arg
1357                1362                1367                1372

acc ctc agc gcc ttc tcc tgg aga atg gtg gaa gag cag ctg atc cgc      4656
 Thr Leu Ser Ala Phe Ser Trp Arg Met Val Glu Glu Gln Leu Ile Arg
1373                1378                1383                1388

tac gtg cat gac ggg agc gag aca ctg aca gac agt ttt gtc ctg atg      4704
 Tyr Val His Asp Gly Ser Glu Thr Leu Thr Asp Ser Phe Val Leu Met
1389                1394                1399                1404

gct aat gcc tcc gag atg gat cgc cag agc cat cct gtg gcc ttc act      4752
 Ala Asn Ala Ser Glu Met Asp Arg Gln Ser His Pro Val Ala Phe Thr
1405                1410                1415                1420

gtc act gtc ctg cct gtc aat gac caa ccc ccc atc ctc act aca aac      4800
 Val Thr Val Leu Pro Val Asn Asp Gln Pro Pro Ile Leu Thr Thr Asn
1421                1426                1431                1436

aca ggc ctg cag atg tgg gag ggg gcc act gcg ccc atc cct gcg gag      4848
 Thr Gly Leu Gln Met Trp Glu Gly Ala Thr Ala Pro Ile Pro Ala Glu
1437                1442                1447                1452

gct ctg agg agc acg gac ggc gac tct ggg tct gag gat ctg gtc tac      4896
 Ala Leu Arg Ser Thr Asp Gly Asp Ser Gly Ser Glu Asp Leu Val Tyr
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acc atc gag cag ccc agc aac ggg cgg gta gtg ctg cgg ggg gcg ccg      4944
 Thr Ile Glu Gln Pro Ser Asn Gly Arg Val Val Leu Arg Gly Ala Pro
1469                1474                1479                1484
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Gly Thr Glu Val Arg Ser Phe Thr Gln Ala Gln Leu Asp Gly Gly Leu
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gtg ctg ttc tca cac aga gga acc ctg gat gga ggc ttc ccg ttc cgc     5040
Val Leu Phe Ser His Arg Gly Thr Leu Asp Gly Gly Phe Pro Phe Arg
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ctc tct gac ggc gag cac act tcc ccc gga cac ttc ttc cga gtg acg     5088
Leu Ser Asp Gly Glu His Thr Ser Pro Gly His Phe Phe Arg Val Thr
1517                1522                1527                1532

gcc cag aag caa gtg ctc ctc tcg ctg aag ggc agc cag aca ctg act     5136
Ala Gln Lys Gln Val Leu Leu Ser Leu Lys Gly Ser Gln Thr Leu Thr
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gtc tgc cca ggg tcc gtc cag cca ctc agc agt cag acc ctc agg gcc     5184
Val Cys Pro Gly Ser Val Gln Pro Leu Ser Ser Gln Thr Leu Arg Ala
1549                1554                1559                1564

agc tcc agc gca ggc act gac ccc cag ctc ctg ctc tac cgt gtg gtg     5232
Ser Ser Ser Ala Gly Thr Asp Pro Gln Leu Leu Leu Tyr Arg Val Val
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cgg ggc ccc cag cta ggc cgg ctg ttc cac gcc cag cag gac agc aca     5280
Arg Gly Pro Gln Leu Gly Arg Leu Phe His Ala Gln Gln Asp Ser Thr
1581                1586                1591                1596

ggg gag gcc ctg gtg aac ttc act cag gca gag gtc tac gct ggg aat     5328
Gly Glu Ala Leu Val Asn Phe Thr Gln Ala Glu Val Tyr Ala Gly Asn
1597                1602                1607                1612

att ctg tat gag cat gag atg ccc ccc gag ccc ttt tgg gag gcc cat     5376
Ile Leu Tyr Glu His Glu Met Pro Pro Glu Pro Phe Trp Glu Ala His
1613                1618                1623                1628

gat acc cta gag ctc cag ctg tcc tcg ccg cct gcc cgg gac gtg gcc     5424
Asp Thr Leu Glu Leu Gln Leu Ser Ser Pro Pro Ala Arg Asp Val Ala
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gcc acc ctt gct gtg gct gtg tct ttt gag gct gcc tgt ccc cag cgc     5472
Ala Thr Leu Ala Val Ala Val Ser Phe Glu Ala Ala Cys Pro Gln Arg
1645                1650                1655                1660

ccc agc cac ctc tgg aag aac aaa ggt ctc tgg gtc ccc gag ggc cag     5520
Pro Ser His Leu Trp Lys Asn Lys Gly Leu Trp Val Pro Glu Gly Gln
1661                1666                1671                1676

cgg gcc agg atc acc gtg gct gct ctg gat gcc tcc aat ctc ttg gcc     5568
Arg Ala Arg Ile Thr Val Ala Ala Leu Asp Ala Ser Asn Leu Leu Ala
1677                1682                1687                1692

agc gtt cca tca ccc cag cgc tca gag cat gat gtg ctc ttc cag gtc     5616
Ser Val Pro Ser Pro Gln Arg Ser Glu His Asp Val Leu Phe Gln Val
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aca cag ttc ccc agc cgg ggc cag ctg ttg gtg tcc gag gag ccc ctc     5664
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 Thr Gln Phe Pro Ser Arg Gly Gln Leu Leu Val Ser Glu Glu Pro Leu
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 His Ala Gly Gln Pro His Phe Leu Gln Ser Gln Leu Ala Ala Gly Gln
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 cta gtg tat gcc cac ggc ggt ggg ggc acc cag cag gat ggc ttc cac     5760
 Leu Val Tyr Ala His Gly Gly Gly Gly Thr Gln Gln Asp Gly Phe His
1741                1746                1751                1756

 ttt cgt gcc cac ctc cag ggg cca gca ggg gcc tcc gtg gct gga ccc     5808
 Phe Arg Ala His Leu Gln Gly Pro Ala Gly Ala Ser Val Ala Gly Pro
1757                1762                1767                1772

 caa acc tca gag gcc ttt gcc atc acg gtg agg gat gta aat gag cgg     5856
 Gln Thr Ser Glu Ala Phe Ala Ile Thr Val Arg Asp Val Asn Glu Arg
1773                1778                1783                1788

 ccc cct cag cca cag gcc tct gtc cca ctc cgg ctc acc cga ggc tct     5904
 Pro Pro Gln Pro Gln Ala Ser Val Pro Leu Arg Leu Thr Arg Gly Ser
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 cgt gcc ccc atc tcc cgg gcc cag ctg agt gtg gtg gac cca gac tca     5952
 Arg Ala Pro Ile Ser Arg Ala Gln Leu Ser Val Val Asp Pro Asp Ser
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 Ala Pro Gly Glu Ile Glu Tyr Glu Val Gln Arg Ala Pro His Asn Gly
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 Phe Leu Ser Leu Val Gly Gly Gly Leu Gly Pro Val Thr Arg Phe Thr
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 Gln Ala Asp Val Asp Ser Gly Arg Leu Ala Phe Val Ala Asn Gly Ser
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 Ser Val Ala Gly Ile Phe Gln Leu Ser Met Ser Asp Gly Ala Ser Pro
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 Pro Leu Pro Met Ser Leu Ala Val Asp Ile Leu Pro Ser Ala Ile Glu
1885                1890                1895                1900

 gtg cag ctg cgg gca ccc ctg gag gtg ccc caa gct ttg ggg cgc tcc     6240
 Val Gln Leu Arg Ala Pro Leu Glu Val Pro Gln Ala Leu Gly Arg Ser
1901                1906                1911                1916

 tca ctg agc cag cag cag ctc cgg gtg gtt tca gat cgg gag gag cca     6288
 Ser Leu Ser Gln Gln Gln Leu Arg Val Val Ser Asp Arg Glu Glu Pro
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 Glu Ala Ala Tyr Arg Leu Ile Gln Gly Pro Gln Tyr Gly His Leu Leu
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 Val Gly Gly Arg Pro Thr Ser Ala Phe Ser Gln Phe Gln Ile Asp Gln
1949                1954                1959                1964

 ggc gag gtg gtc ttt gcc ttc acc aac ttc tcc tcc tct cat gac cac     6432
 Gly Glu Val Val Phe Ala Phe Thr Asn Phe Ser Ser Ser His Asp His
1965                1970                1975                1980

 ttc aga gtc ctg gca ctg gct agg ggt gtc aat gca tca gcc gta gtg     6480
 Phe Arg Val Leu Ala Leu Ala Arg Gly Val Asn Ala Ser Ala Val Val
1981                1986                1991                1996

 aac gtc act gtg agg gct ctg ctg cat gtg tgg gca ggt ggg cca tgg     6528
 Asn Val Thr Val Arg Ala Leu Leu His Val Trp Ala Gly Gly Pro Trp
1997                2002                2007                2012

 cca gag ggt gcc acc ctg cgc ctg gac ccc acc gtc cta gat gct ggc     6576
 Pro Glu Gly Ala Thr Leu Arg Leu Asp Pro Thr Val Leu Asp Ala Gly
2013                2018                2023                2028

 gag ctg gcc aac cgc aca ggc agt gtg ccg cgc ttc cgc ctc ctg gag     6624
 Glu Leu Ala Asn Arg Thr Gly Ser Val Pro Arg Phe Arg Leu Leu Glu
2029                2034                2039                2044

 gga ccc cgg cat ggc cgc gtg gtc cgc gtg ccc cga gcc agg acg gag     6672
 Gly Pro Arg His Gly Arg Val Val Arg Val Pro Arg Ala Arg Thr Glu
2045                2050                2055                2060

 ccc ggg ggc agc cag ctg gtg gag cag ttc act cag cag gac ctt gag     6720
 Pro Gly Gly Ser Gln Leu Val Glu Gln Phe Thr Gln Gln Asp Leu Glu
2061                2066                2071                2076

 gac ggg agg ctg ggg ctg gag gtg ggc agg cca gag ggg agg gcc ccc     6768
 Asp Gly Arg Leu Gly Leu Glu Val Gly Arg Pro Glu Gly Arg Ala Pro
2077                2082                2087                2092

 ggc ccc gca ggt gac agt ctc act ctg gag ctg tgg gca cag ggc gtc     6816
 Gly Pro Ala Gly Asp Ser Leu Thr Leu Glu Leu Trp Ala Gln Gly Val
2093                2098                2103                2108

 ccg cct gct gtg gcc tcc ctg gac ttt gcc act gag cct tac aat gct     6864
 Pro Pro Ala Val Ala Ser Leu Asp Phe Ala Thr Glu Pro Tyr Asn Ala
2109                2114                2119                2124

 gcc cgg ccc tac agc gtg gcc ctg ctc agt gtc ccc gag gcc gcc cgg     6912
 Ala Arg Pro Tyr Ser Val Ala Leu Leu Ser Val Pro Glu Ala Ala Arg
2125                2130                2135                2140

 acg gaa gca ggg aag cca gag agc agc acc ccc aca ggc gag cca ggc     6960
 Thr Glu Ala Gly Lys Pro Glu Ser Ser Thr Pro Thr Gly Glu Pro Gly
2141                2146                2151                2156

 ccc atg gca tcc agc cct gag ccc gct gtg gcc aag gga ggc ttc ctg     7008
 Pro Met Ala Ser Ser Pro Glu Pro Ala Val Ala Lys Gly Gly Phe Leu
2157                2162                2167                2172
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 Ser Phe Leu Glu Ala Asn Met Phe Ser Val Ile Ile Pro Met Cys Leu
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 gta ctt ctg ctc ctg gcg ctc atc ctg ccc ctg ctc ttc tac ctc cga      7104
 Val Leu Leu Leu Leu Ala Leu Ile Leu Pro Leu Leu Phe Tyr Leu Arg
2189                 2194                 2199                 2204

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 Lys Arg Asn Lys Thr Gly Lys His Asp Val Gln Val Leu Thr Ala Lys
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 Pro Arg Asn Gly Leu Ala Gly Asp Thr Glu Thr Phe Arg Lys Val Glu
2221                 2226                 2231                 2236

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 Pro Gly Gln Ala Ile Pro Leu Thr Ala Val Pro Gly Gln Gly Pro Pro
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 Pro Gly Gly Gln Pro Asp Pro Glu Leu Leu Gln Phe Cys Arg Thr Pro
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 Asn Pro Ala Leu Lys Asn Gly Gln Tyr Trp Val  *
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Met Asp Ala Leu Lys Pro Pro
1 5

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Cys Leu Trp Arg Asn His Glu Arg Gly Lys Lys Asp Arg Asp Ser Cys
8 13 18 23

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Gly Arg Lys Asn Ser Glu Pro Gly Ser Pro His Ser Leu Glu Ala Leu
24 29 34 39

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72 77 82 87

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88 93 98 103

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Ser Val Gly Ile Glu Gly Gly Ala Arg Lys Gly Val Ser Gln Lys Asn
104                 109                 114                 119

aat gac cta aca agt tgc tgc ttc tca gat gcc aag act atg tat gag      495
Asn Asp Leu Thr Ser Cys Cys Phe Ser Asp Ala Lys Thr Met Tyr Glu
120                 125                 130                 135

gtt ttc caa aga gga ctc gct gtg tct gac aat ggg ccc tgc ttg gga      543
Val Phe Gln Arg Gly Leu Ala Val Ser Asp Asn Gly Pro Cys Leu Gly
136                 141                 146                 151

tat aga aaa cca aac cag ccc tac aga tgg cta tct tac aaa cag gtg      591
Tyr Arg Lys Pro Asn Gln Pro Tyr Arg Trp Leu Ser Tyr Lys Gln Val
152                 157                 162                 167

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Ser Asp Arg Ala Glu Tyr Leu Gly Ser Cys Leu Leu His Lys Gly Tyr
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Lys Ser Ser Pro Asp Gln Phe Val Gly Ile Phe Ala Gln Asn Arg Pro
184                 189                 194                 199

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200                 205                 210                 215

gta cct ctg tat gac acc ttg gga cca gaa gcc atc gta cat att gtc      783
Val Pro Leu Tyr Asp Thr Leu Gly Pro Glu Ala Ile Val His Ile Val
216                 221                 226                 231

aac aag gct gat atc gcc atg gtg atc tgt gac aca ccc caa aag gca      831
Asn Lys Ala Asp Ile Ala Met Val Ile Cys Asp Thr Pro Gln Lys Ala
232                 237                 242                 247

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Leu Val Leu Ile Gly Asn Val Glu Lys Gly Phe Thr Pro Ser Leu Lys
248                 253                 258                 263

gtg atc atc ctt atg gac ccc ttt gat gat gac ctg aag caa aga ggg      927
Val Ile Ile Leu Met Asp Pro Phe Asp Asp Asp Leu Lys Gln Arg Gly
264                 269                 274                 279

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Glu Lys Ser Gly Ile Glu Ile Leu Ser Leu Tyr Asp Ala Glu Asn Leu
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ggc aaa gag cac ttc aga aaa cct gtg cct cct agc cca gaa gac ctg     1023
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296                 301                 306                 311

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360                 365                 370                 375

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376                 381                 386                 391

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Leu Ala Asp Asp Met Lys Thr Leu Lys Pro Thr Leu Phe Pro Ala Val
392                 397                 402                 407

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Pro Arg Leu Leu Asn Arg Ile Tyr Asp Lys Val Gln Asn Glu Ala Lys
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424                 429                 434                 439

aaa gag ctt caa aag ggt atc atc agg cat gat agt ttc tgg gac aag     1455
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cgg gca gca atg gga tgt cag gtg tat gaa gct tat ggt caa aca gaa     1599
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tgc aca ggt ggc tgt aca ttt aca tta cct ggg gac tgg aca tca ggt     1647
Cys Thr Gly Gly Cys Thr Phe Thr Leu Pro Gly Asp Trp Thr Ser Gly
504                 509                 514                 519

cac gtt ggg gtg ccc ctg gct tgc aat tac gtg aag ctg gaa gat gtg     1695
His Val Gly Val Pro Leu Ala Cys Asn Tyr Val Lys Leu Glu Asp Val
520                 525                 530                 535

gct gac atg aac tac ttt aca gtg aat aat gaa gga gag gtc tgc atc     1743
Ala Asp Met Asn Tyr Phe Thr Val Asn Asn Glu Gly Glu Val Cys Ile
536                 541                 546                 551

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568                 573                 578                 583

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Arg Trp Leu Pro Asn Gly Thr Leu Lys Ile Ile Asp Arg Lys Lys Asn
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Ile Phe Lys Leu Ala Gln Gly Glu Tyr Ile Ala Pro Glu Lys Ile Glu
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Glu Leu Cys Gln Asn Gln Val Val Arg Glu Ala Ile Leu Glu Asp Leu
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cag aaa att ggg aaa gaa agt ggc ctt aaa act ttt gaa cag gtc aaa     2175
Gln Lys Ile Gly Lys Glu Ser Gly Leu Lys Thr Phe Glu Gln Val Lys
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<222> (1)...(1751)
<223> n = a,t,c or g

<400> 95
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cgagccggga gccggtcgcg ggggctccgg gctgtgggac cgctgggccc ccagcg 116

atg gcg acc ctg tgg gga ggc ctt ctt cgg ctt ggc tcc ttg ctc agc 164
Met Ala Thr Leu Trp Gly Gly Leu Leu Arg Leu Gly Ser Leu Leu Ser
1 5 10 15

ctg tcg tgc ctg gcg ctt tcc gtg ctg ctg ctg gcg cag ctg tca gac 212
Leu Ser Cys Leu Ala Leu Ser Val Leu Leu Leu Ala Gln Leu Ser Asp
17 22 27 32

gcc gcc aag aat ttc gag gat gtc aga tgt aaa tgt atc tgc cct ccc 260
Ala Ala Lys Asn Phe Glu Asp Val Arg Cys Lys Cys Ile Cys Pro Pro
33 38 43 48

tat aaa gaa aat tct ggg cat att tat aat aag aac ata tct cag aaa 308
Tyr Lys Glu Asn Ser Gly His Ile Tyr Asn Lys Asn Ile Ser Gln Lys
49 54 59 64

gat tgt gat tgc ctt cat gtt gtg gag ccc atg cct gtg cgg ggg cct 356
Asp Cys Asp Cys Leu His Val Val Glu Pro Met Pro Val Arg Gly Pro
65 70 75 80

gat gta gaa gca tac tgt cta cgc tgt gaa tgc aaa tat gaa gaa aga 404
Asp Val Glu Ala Tyr Cys Leu Arg Cys Glu Cys Lys Tyr Glu Glu Arg
81 86 91 96

agc tct gtc aca atc aag gtt acc att ata att tat ctc tcc att ttg 452
Ser Ser Val Thr Ile Lys Val Thr Ile Ile Ile Tyr Leu Ser Ile Leu
97 102 107 112

ggc ctt cta ctt ctg tac atg gta tat ctt act ctg gtt gag ccc ata 500
Gly Leu Leu Leu Leu Tyr Met Val Tyr Leu Thr Leu Val Glu Pro Ile
113 118 123 128

ctg aag agg cgc ctc ttt gga cat gca cag ttg ata cag agt gat gat 548
Leu Lys Arg Arg Leu Phe Gly His Ala Gln Leu Ile Gln Ser Asp Asp
129 134 139 144

gat att ggg gat cac cag cct ttt gca aat gca cac gat gtg cta gcc 596
Asp Ile Gly Asp His Gln Pro Phe Ala Asn Ala His Asp Val Leu Ala
145 150 155 160

cgc tcc cgc agt cga gcc aac gtg ctg aac aag gta gaa tat gca cag 644
Arg Ser Arg Ser Arg Ala Asn Val Leu Asn Lys Val Glu Tyr Ala Gln

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161                 166                 171                 176

cag cgc tgg aag ctt caa gtc caa gag cag cga aag tct gtc ttt gac      692
Gln Arg Trp Lys Leu Gln Val Gln Glu Gln Arg Lys Ser Val Phe Asp
177                 182                 187                 192

cgg cat gtt gtc ctc agc taa tt gggaattgaa ttcaaggtga ctagaaagaa      745
Arg His Val Val Leu Ser  *
193                 198

acaggcagac aactggaaag aactgactgg gttttgctgg gtttcatttt aataccttgt    805

tgatttcacc aactgttgct ggaagattca aaactggaag caaaaacttg cttgattttt    865

ttttcttgtt aacgtaataa tagagacatt tttaaaagca cacagctcaa agtcagccaa    925

taagtctttt cctatttgtg acttttacta ataaaaataa atctgcctgt aaattatctt    985

gaagtccttt acctggaaca agcactctct ttttcaccac atagttttaa cttgactttc   1045

aagataattt tcagggtttt tgttgttgtt gtttttgtt tgtttgtttt ggtgggagag   1105

gggagggatg cctgggaagt ggttaacaac ttttttcaag tcactttact aaacaaactt   1165

ttgtaaatag accttacctt ctattttcga gtttcattta tattttgcag tgtagccagc   1225

ctcatcaaag agctgactta ctcatttgac ttttgcactg actgtattat ctgggtatct   1285

gctgtgtctg cacttcatgg taaacgggat ctaaaatgcc tggtggcttt tcacaaaaag   1345

cagattttct tcatgtactg tgatgtctga tgcaatgcat cctagaacaa actggccatt   1405

tgctagttta ctctaaagac taaacatagt cttggtgtgt gtggtcttac tcatcttcta   1465

gtacctttaa ggacaaatcc taaggacttg gacacttgca ataaagaaat tttattttaa   1525

acccaagcct ccctggattg ataatatata cacatttgtc agcatttccg gtcgtggtga   1585

gaggcagctg tttgagctcc aatgtgtgca gctttgaact agggctgggg ttgtgggtgc   1645

ctcttctgaa aggtctaacc attattggat aactggcttt tttcttccta tgtcctcttt   1705

ggaatgtaac aataaaaata atttttgaaa catcaaaaaa aaaaaa                  1751
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<210> 96
<211> 2396
<212> DNA
<213> Homo sapiens

<220>
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<222> (888)..(2396)

<400> 96

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agccctcctc gtgagccgca gcagcctcgg tgccagcccc cgccgcagct gggcccagcg     120

gtccgcctgt ccctcgttgc ggcttgtcga cctctgcgcg ggcggctcgg cccttcacgc     180

ccttttcgtt cacgaatccg agcccgctcg cctctctcca gcgaaccgac catgtctggc     240

ggcgccgcag agaagcagag cagcactccc ggttccctgt tcctctcgcc gccggctcct     300

gcccccaaga atggctccag ctccgattcc tccgtggggg agaaactggg agccgcggcc     360

gccgacgctg tgaccggcag gaccgaggag tacaggcgcc gccgccacac tatggacaag     420

gacagccgtg gggcggccgc gaccactacc accactgagc accgcttctt ccgccggagc     480

gtcatctgcg actccaatgc cactgcactg gagcttcccg gccttcctct ttccctgccc     540

cagcccagca tccccgcggc tgtcccgcag agtgctccac cggagcccca ccgggaagag     600

accgtgaccg ccaccgccac ttcccaggta gcccagcagc ctccagccgc tgccgccccc     660

ggggaacagg ccgtcgcggg ccctgccccc tcgactgtcc ccagcagtac cagcaaagac     720

cgcccagtgt cccagcctag ccttgtgggg agcaaagagg agccgccgcc ggcgagaaag     780

tggcagcggc ggcgaagcgc aaaagggaag cccacaagga aggaacggag ccagcagcag     840

gatgatatcg aagagcttgg agaccaaggc cgtgggaatg tctaacg  atg gcc gct      896
                                                     Met Ala Ala
                                                       1

ttc tca agt ttt gac atc gaa atc ggc aga ggc tcc ttt aag acg gtc      944
Phe Ser Ser Phe Asp Ile Glu Ile Gly Arg Gly Ser Phe Lys Thr Val
  4                   9                  14                  19

tac aaa ggt ctg gac act gaa acc acc gtg gaa gtc gcc tgg tgt gaa      992
Tyr Lys Gly Leu Asp Thr Glu Thr Thr Val Glu Val Ala Trp Cys Glu
 20                  25                  30                  35

ctg cag gat cga aaa tta aca aag tct gag agg cag aga ttt aaa gaa     1040
Leu Gln Asp Arg Lys Leu Thr Lys Ser Glu Arg Gln Arg Phe Lys Glu
 36                  41                  46                  51

gaa gct gaa atg tta aaa ggt ctt cag cat ccc aat att gtt aga ttt     1088
Glu Ala Glu Met Leu Lys Gly Leu Gln His Pro Asn Ile Val Arg Phe
 52                  57                  62                  67

tat gat tcc tgg gaa tcc aca gta aaa gga aag aag tgc att gtt ttg     1136
Tyr Asp Ser Trp Glu Ser Thr Val Lys Gly Lys Lys Cys Ile Val Leu
 68                  73                  78                  83

gtg act gaa ctt atg acg tct gga aca ctt aaa acg tat ctg aaa agg     1184
Val Thr Glu Leu Met Thr Ser Gly Thr Leu Lys Thr Tyr Leu Lys Arg
 84                  89                  94                  99

ttt aaa gtg atg aag atc aaa gtt cta aga agc tgg tgc cgt cag atc     1232
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Phe Lys Val Met Lys Ile Lys Val Leu Arg Ser Trp Cys Arg Gln Ile
100                 105                 110                 115

ctt aaa ggt ctt cag ttt ctt cat act cga act cca cct atc att cac     1280
Leu Lys Gly Leu Gln Phe Leu His Thr Arg Thr Pro Pro Ile Ile His
116                 121                 126                 131

cgc gat ctt aaa tgt gac aac atc ttt atc acc ggc cct act ggc tca     1328
Arg Asp Leu Lys Cys Asp Asn Ile Phe Ile Thr Gly Pro Thr Gly Ser
132                 137                 142                 147

gtc aag att gga gac ctc ggt ctg gca acc ctg aag cgg gct tct ttt     1376
Val Lys Ile Gly Asp Leu Gly Leu Ala Thr Leu Lys Arg Ala Ser Phe
148                 153                 158                 163

gcc aag agt gtg ata ggt acc cca gag ttc atg gcc cct gag atg tat     1424
Ala Lys Ser Val Ile Gly Thr Pro Glu Phe Met Ala Pro Glu Met Tyr
164                 169                 174                 179

gag gag aaa tat gat gaa tcc gtt gac gtt tat gct ttt ggg atg tgc     1472
Glu Glu Lys Tyr Asp Glu Ser Val Asp Val Tyr Ala Phe Gly Met Cys
180                 185                 190                 195

atg ctt gag atg gct aca tct gaa tat cct tac tcg gag tgc caa aat     1520
Met Leu Glu Met Ala Thr Ser Glu Tyr Pro Tyr Ser Glu Cys Gln Asn
196                 201                 206                 211

gct gca cag atc tac cgt cgc gtg acc agt ggg gtg aag cca gcc agt     1568
Ala Ala Gln Ile Tyr Arg Arg Val Thr Ser Gly Val Lys Pro Ala Ser
212                 217                 222                 227

ttt gac aaa gta gca att cct gaa gtg aag gaa att att gaa gga tgc     1616
Phe Asp Lys Val Ala Ile Pro Glu Val Lys Glu Ile Ile Glu Gly Cys
228                 233                 238                 243

ata cga caa aac aaa gat gaa aga tat tcc atc aaa gac ctt ttg aac     1664
Ile Arg Gln Asn Lys Asp Glu Arg Tyr Ser Ile Lys Asp Leu Leu Asn
244                 249                 254                 259

cat gcc ttc ttc caa gag gaa aca gga gta cgg gta gaa tta gca gaa     1712
His Ala Phe Phe Gln Glu Glu Thr Gly Val Arg Val Glu Leu Ala Glu
260                 265                 270                 275

gaa gat gat gga gaa aaa ata gcc ata aaa tta tgg cta cgt att gaa     1760
Glu Asp Asp Gly Glu Lys Ile Ala Ile Lys Leu Trp Leu Arg Ile Glu
276                 281                 286                 291

gat att aag aaa tta aag gga aaa tac aaa gat aat gaa gct att gag     1808
Asp Ile Lys Lys Leu Lys Gly Lys Tyr Lys Asp Asn Glu Ala Ile Glu
292                 297                 302                 307

ttt tct ttt gat tta gag aga gat gtc cca gaa gat gtt gca caa gaa     1856
Phe Ser Phe Asp Leu Glu Arg Asp Val Pro Glu Asp Val Ala Gln Glu
308                 313                 318                 323

atg gta gag tct ggg tat gtc tgt gaa ggt gat cac aag acc atg gct     1904
Met Val Glu Ser Gly Tyr Val Cys Glu Gly Asp His Lys Thr Met Ala
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09050-7P2US

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324                 329                 334                 339

aaa gct atc aaa gac aga gta tca tta att aag agg aaa cga gag cag     1952
Lys Ala Ile Lys Asp Arg Val Ser Leu Ile Lys Arg Lys Arg Glu Gln
340                 345                 350                 355

cgg cag ttg gta cgg gag gag caa gaa aaa aaa aag cag gaa gag agc     2000
Arg Gln Leu Val Arg Glu Glu Gln Glu Lys Lys Lys Gln Glu Glu Ser
356                 361                 366                 371

agt ctc aaa cag cag gta gaa caa tcc agt gct tcc cag aca gga atc     2048
Ser Leu Lys Gln Gln Val Glu Gln Ser Ser Ala Ser Gln Thr Gly Ile
372                 377                 382                 387

aag cag ctc cct tct gct agc acc ggc ata cct act gct tct acc act     2096
Lys Gln Leu Pro Ser Ala Ser Thr Gly Ile Pro Thr Ala Ser Thr Thr
388                 393                 398                 403

tca gct tca gtt tct aca caa gta gaa cct gaa gaa cct gag gca gat     2144
Ser Ala Ser Val Ser Thr Gln Val Glu Pro Glu Glu Pro Glu Ala Asp
404                 409                 414                 419

caa cat caa caa cta cag tac cag caa ccc agt ata tct gtg tta tct     2192
Gln His Gln Gln Leu Gln Tyr Gln Gln Pro Ser Ile Ser Val Leu Ser
420                 425                 430                 435

gat ggg acg gtt gac agt ggt cag gga tcc tct gtc ttc aca gaa tct     2240
Asp Gly Thr Val Asp Ser Gly Gln Gly Ser Ser Val Phe Thr Glu Ser
436                 441                 446                 451

cga gtg agc agc caa cag aca gtt tca tat ggt tcc caa cat gaa cag     2288
Arg Val Ser Ser Gln Gln Thr Val Ser Tyr Gly Ser Gln His Glu Gln
452                 457                 462                 467

gca cat tct aca ggc aca gtc cca ggg cat ata cct tct act gtc caa     2336
Ala His Ser Thr Gly Thr Val Pro Gly His Ile Pro Ser Thr Val Gln
468                 473                 478                 483

gca cag tct cag ccc cat ggg gta tat cca ccc tca agt gtg gaa tgt     2384
Ala Gln Ser Gln Pro His Gly Val Tyr Pro Pro Ser Ser Val Glu Cys
484                 489                 494                 499

ggc tta caa taa                                                    2396
Gly Leu Gln  *
500
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<210> 97
<211> 2663
<212> DNA
<213> Homo sapiens

<220>
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<222> (888)..(2663)

<400> 97

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ccttttcgtt cacgaatccg agcccgctcg cctctctcca gcgaaccgac catgtctggc     240

ggcgccgcag agaagcagag cagcactccc ggttccctgt tcctctcgcc gccggctcct     300

gcccccaaga atggctccag ctccgattcc tccgtggggg agaaactggg agccgcggcc     360

gccgacgctg tgaccggcag gaccgaggag tacaggcgcc gccgccacac tatggacaag     420

gacagccgtg gggcggccgc gaccactacc accactgagc accgcttctt ccgccggagc     480

gtcatctgcg actccaatgc cactgcactg gagcttcccg gccttcctct ttccctgccc     540

cagcccagca tccccgcggc tgtcccgcag agtgctccac cggagcccca ccgggaagag     600

accgtgaccg ccaccgccac ttcccaggta gcccagcagc ctccagccgc tgccgccccc     660

ggggaacagg ccgtcgcggg ccctgccccc tcgactgtcc ccagcagtac cagcaaagac     720

cgcccagtgt cccagcctag ccttgtgggg agcaaagagg agccgccgcc ggcgagaaag     780

tggcagcggc ggcgaagcgc aaaagggaag cccacaagga aggaacggag ccagcagcag     840

gatgatatcg aagagcttgg agaccaaggc cgtgggaatg tctaacg  atg gcc gct      896
                                                     Met Ala Ala
                                                       1

ttc tca agt ttt gac atc gaa atc ggc aga ggc tcc ttt aag acg gtc      944
Phe Ser Ser Phe Asp Ile Glu Ile Gly Arg Gly Ser Phe Lys Thr Val
  4                   9                  14                  19

tac aaa ggt ctg gac act gaa acc acc gtg gaa gtc gcc tgg tgt gaa      992
Tyr Lys Gly Leu Asp Thr Glu Thr Thr Val Glu Val Ala Trp Cys Glu
 20                  25                  30                  35

ctg cag gat cga aaa tta aca aag tct gag agg cag aga ttt aaa gaa     1040
Leu Gln Asp Arg Lys Leu Thr Lys Ser Glu Arg Gln Arg Phe Lys Glu
 36                  41                  46                  51

gaa gct gaa atg tta aaa ggt ctt cag cat ccc aat att gtt aga ttt     1088
Glu Ala Glu Met Leu Lys Gly Leu Gln His Pro Asn Ile Val Arg Phe
 52                  57                  62                  67

tat gat tcc tgg gaa tcc aca gta aaa gga aag aag tgc att gtt ttg     1136
Tyr Asp Ser Trp Glu Ser Thr Val Lys Gly Lys Lys Cys Ile Val Leu
 68                  73                  78                  83

gtg act gaa ctt atg acg tct gga aca ctt aaa acg agc cag agc tca     1184
Val Thr Glu Leu Met Thr Ser Gly Thr Leu Lys Thr Ser Gln Ser Ser
```

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84                  89                  94                  99

ggt ggt aat gcg agc agt gag gga gcg gct gta aat aca gat gaa gct     1232
Gly Gly Asn Ala Ser Ser Glu Gly Ala Ala Val Asn Thr Asp Glu Ala
100                 105                 110                 115

ttg ctt gct cgc ctg cca ctc acc tcc tgc tgt gtg gcc agg ttc cta     1280
Leu Leu Ala Arg Leu Pro Leu Thr Ser Cys Cys Val Ala Arg Phe Leu
116                 121                 126                 131

aaa ggc cat gga ctg ata ttg atc tgt ggc tca gtg gtt ggg gac ccc     1328
Lys Gly His Gly Leu Ile Leu Ile Cys Gly Ser Val Val Gly Asp Pro
132                 137                 142                 147

tgg tat ctt aga gga tct gtt ttt act cag aga aga acc tgt aat ctg     1376
Trp Tyr Leu Arg Gly Ser Val Phe Thr Gln Arg Arg Thr Cys Asn Leu
148                 153                 158                 163

tgc tgt cca gta gaa ctt tct gcc att atg gaa atg ttg tat aac gta     1424
Cys Cys Pro Val Glu Leu Ser Ala Ile Met Glu Met Leu Tyr Asn Val
164                 169                 174                 179

cac cat cca gaa tgg tat ctg aaa agg ttt aaa gtg atg aag atc aaa     1472
His His Pro Glu Trp Tyr Leu Lys Arg Phe Lys Val Met Lys Ile Lys
180                 185                 190                 195

gtt cta aga agc tgg tgc cgt cag atc ctt aaa ggt ctt cag ttt ctt     1520
Val Leu Arg Ser Trp Cys Arg Gln Ile Leu Lys Gly Leu Gln Phe Leu
196                 201                 206                 211

cat act cga act cca cct atc att cac cgc gat ctt aaa tgt gac aac     1568
His Thr Arg Thr Pro Pro Ile Ile His Arg Asp Leu Lys Cys Asp Asn
212                 217                 222                 227

atc ttt atc acc ggc cct act ggc tca gtc aag att gga gac ctc ggt     1616
Ile Phe Ile Thr Gly Pro Thr Gly Ser Val Lys Ile Gly Asp Leu Gly
228                 233                 238                 243

ctg gca acc ctg aag cgg gct tct ttt gcc aag agt gtg ata ggt acc     1664
Leu Ala Thr Leu Lys Arg Ala Ser Phe Ala Lys Ser Val Ile Gly Thr
244                 249                 254                 259

cca gag ttc atg gcc cct gag atg tat gag gag aaa tat gat gaa tcc     1712
Pro Glu Phe Met Ala Pro Glu Met Tyr Glu Glu Lys Tyr Asp Glu Ser
260                 265                 270                 275

gtt gac gtt tat gct ttt ggg atg tgc atg ctt gag atg gct aca tct     1760
Val Asp Val Tyr Ala Phe Gly Met Cys Met Leu Glu Met Ala Thr Ser
276                 281                 286                 291

gaa tat cct tac tcg gag tgc caa aat gct gca cag atc tac cgt cgc     1808
Glu Tyr Pro Tyr Ser Glu Cys Gln Asn Ala Ala Gln Ile Tyr Arg Arg
292                 297                 302                 307

gtg acc agt ggg gtg aag cca gcc agt ttt gac aaa gta gca att cct     1856
Val Thr Ser Gly Val Lys Pro Ala Ser Phe Asp Lys Val Ala Ile Pro
308                 313                 318                 323
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gaa gtg aag gaa att att gaa gga tgc ata cga caa aac aaa gat gaa     1904
Glu Val Lys Glu Ile Ile Glu Gly Cys Ile Arg Gln Asn Lys Asp Glu
324                 329                 334                 339

aga tat tcc atc aaa gac ctt ttg aac cat gcc ttc ttc caa gag gaa     1952
Arg Tyr Ser Ile Lys Asp Leu Leu Asn His Ala Phe Phe Gln Glu Glu
340                 345                 350                 355

aca gga gta cgg gta gaa tta gca gaa gaa gat gat gga gaa aaa ata     2000
Thr Gly Val Arg Val Glu Leu Ala Glu Glu Asp Asp Gly Glu Lys Ile
356                 361                 366                 371

gcc ata aaa tta tgg cta cgt att gaa gat att aag aaa tta aag gga     2048
Ala Ile Lys Leu Trp Leu Arg Ile Glu Asp Ile Lys Lys Leu Lys Gly
372                 377                 382                 387

aaa tac aaa gat aat gaa gct att gag ttt tct ttt gat tta gag aga     2096
Lys Tyr Lys Asp Asn Glu Ala Ile Glu Phe Ser Phe Asp Leu Glu Arg
388                 393                 398                 403

gat gtc cca gaa gat gtt gca caa gaa atg gta gag tct ggg tat gtc     2144
Asp Val Pro Glu Asp Val Ala Gln Glu Met Val Glu Ser Gly Tyr Val
404                 409                 414                 419

tgt gaa ggt gat cac aag acc atg gct aaa gct atc aaa gac aga gta     2192
Cys Glu Gly Asp His Lys Thr Met Ala Lys Ala Ile Lys Asp Arg Val
420                 425                 430                 435

tca tta att aag agg aaa cga gag cag cgg cag ttg gta cgg gag gag     2240
Ser Leu Ile Lys Arg Lys Arg Glu Gln Arg Gln Leu Val Arg Glu Glu
436                 441                 446                 451

caa gaa aaa aaa aag cag gaa gag agc agt ctc aaa cag cag gta gaa     2288
Gln Glu Lys Lys Lys Gln Glu Glu Ser Ser Leu Lys Gln Gln Val Glu
452                 457                 462                 467

caa tcc agt gct tcc cag aca gga atc aag cag ctc cct tct gct agc     2336
Gln Ser Ser Ala Ser Gln Thr Gly Ile Lys Gln Leu Pro Ser Ala Ser
468                 473                 478                 483

acc ggc ata cct act gct tct acc act tca gct tca gtt tct aca caa     2384
Thr Gly Ile Pro Thr Ala Ser Thr Thr Ser Ala Ser Val Ser Thr Gln
484                 489                 494                 499

gta gaa cct gaa gaa cct gag gca gat caa cat caa caa cta cag tac     2432
Val Glu Pro Glu Glu Pro Glu Ala Asp Gln His Gln Gln Leu Gln Tyr
500                 505                 510                 515

cag caa ccc agt ata tct gtg tta tct gat ggg acg gtt gac agt ggt     2480
Gln Gln Pro Ser Ile Ser Val Leu Ser Asp Gly Thr Val Asp Ser Gly
516                 521                 526                 531

cag gga tcc tct gtc ttc aca gaa tct cga gtg agc agc caa cag aca     2528
Gln Gly Ser Ser Val Phe Thr Glu Ser Arg Val Ser Ser Gln Gln Thr
532                 537                 542                 547
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gtt tca tat ggt tcc caa cat gaa cag gca cat tct aca ggc aca gtc     2576
Val Ser Tyr Gly Ser Gln His Glu Gln Ala His Ser Thr Gly Thr Val
548                 553                 558                 563

cca ggg cat ata cct tct act gtc caa gca cag tct cag ccc cat ggg     2624
Pro Gly His Ile Pro Ser Thr Val Gln Ala Gln Ser Gln Pro His Gly
564                 569                 574                 579

gta tat cca ccc tca agt gtg gaa tgt ggc tta caa taa                 2663
Val Tyr Pro Pro Ser Ser Val Glu Cys Gly Leu Gln  *
580                 585                 590
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<210> 98
<211> 1372
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (118)..(1095)

<400> 98

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cgcggacgcg tgggtcgccc acgcgtccgc gaggcgggag gatgaagttg attgact   117

atg gtc tct ccg gct acc agg aag agt ctg ccg aag gtg aag gcc atg      165
Met Val Ser Pro Ala Thr Arg Lys Ser Leu Pro Lys Val Lys Ala Met
  1               5                  10                  15

gac ttc atc acc tcc aca gcc atc ctg ccc ctg ctg ttc ggc tgc ctg      213
Asp Phe Ile Thr Ser Thr Ala Ile Leu Pro Leu Leu Phe Gly Cys Leu
 17                  22                  27                  32

ggc gtc ttc ggc ctc ttc cgg ctg ctg cag tgg gtg cgc ggg aag gcc      261
Gly Val Phe Gly Leu Phe Arg Leu Leu Gln Trp Val Arg Gly Lys Ala
 33                  38                  43                  48

tac ctg cgg aat gct gtg gtg gtg atc aca ggc gcc acc tca ggg ctg      309
Tyr Leu Arg Asn Ala Val Val Val Ile Thr Gly Ala Thr Ser Gly Leu
 49                  54                  59                  64

ggc aaa gaa tgt gca aaa gtc ttc tat gct gcg ggt gct aaa ctg gtg      357
Gly Lys Glu Cys Ala Lys Val Phe Tyr Ala Ala Gly Ala Lys Leu Val
 65                  70                  75                  80

ctc tgt ggc cgg aat ggt ggg gcc cta gaa gag ctc atc aga gaa ctc      405
Leu Cys Gly Arg Asn Gly Gly Ala Leu Glu Glu Leu Ile Arg Glu Leu
 81                  86                  91                  96

acc gct tct cat gcc acc aag gtg cag aca cac aag cct tac ttg gtg      453
Thr Ala Ser His Ala Thr Lys Val Gln Thr His Lys Pro Tyr Leu Val
 97                 102                 107                 112
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```
acc ttc gac ctc aca gac tct ggg gcc ata gtt gca gca gca gct gag      501
Thr Phe Asp Leu Thr Asp Ser Gly Ala Ile Val Ala Ala Ala Ala Glu
113                 118                 123                 128

atc ctg cag tgc ttt ggc tat gtc gac ata ctt gtc aac aat gct ggg      549
Ile Leu Gln Cys Phe Gly Tyr Val Asp Ile Leu Val Asn Asn Ala Gly
129                 134                 139                 144

atc agc tac cgt ggt acc atc atg gac acc aca gtg gat gtg gac aag      597
Ile Ser Tyr Arg Gly Thr Ile Met Asp Thr Thr Val Asp Val Asp Lys
145                 150                 155                 160

agg gtc atg gag aca aac tac ttt ggc cca gtt gct cta acg aaa gca      645
Arg Val Met Glu Thr Asn Tyr Phe Gly Pro Val Ala Leu Thr Lys Ala
161                 166                 171                 176

ctc ctg ccc tcc atg atc aag agg agg caa ggc cac att gtc gcc atc      693
Leu Leu Pro Ser Met Ile Lys Arg Arg Gln Gly His Ile Val Ala Ile
177                 182                 187                 192

agc agc atc cag ggc aag atg agc att cct ttt cga tca gca tat gca      741
Ser Ser Ile Gln Gly Lys Met Ser Ile Pro Phe Arg Ser Ala Tyr Ala
193                 198                 203                 208

gcc tcc aag cac gca acc cag gct ttc ttt gac tgt ctg cgt gcc gag      789
Ala Ser Lys His Ala Thr Gln Ala Phe Phe Asp Cys Leu Arg Ala Glu
209                 214                 219                 224

atg gaa cag tat gaa att gag gtg acc gtc atc agc ccc ggc tac atc      837
Met Glu Gln Tyr Glu Ile Glu Val Thr Val Ile Ser Pro Gly Tyr Ile
225                 230                 235                 240

cac acc aac ctc tct gta aat gcc atc acc gcg gat gga tct agg tat      885
His Thr Asn Leu Ser Val Asn Ala Ile Thr Ala Asp Gly Ser Arg Tyr
241                 246                 251                 256

gga gtt atg gac acc acc aca gcc cag ggc cga agc cct gtg gag gtg      933
Gly Val Met Asp Thr Thr Thr Ala Gln Gly Arg Ser Pro Val Glu Val
257                 262                 267                 272

gcc cag gat gtt ctt gct gct gtg ggg aag aag aag aaa gat gtg atc      981
Ala Gln Asp Val Leu Ala Ala Val Gly Lys Lys Lys Lys Asp Val Ile
273                 278                 283                 288

ctg gct gac tta ctg cct tcc ttg gct gtt tat ctt cga act ctg gct     1029
Leu Ala Asp Leu Leu Pro Ser Leu Ala Val Tyr Leu Arg Thr Leu Ala
289                 294                 299                 304

cct ggg ctc ttc ttc agc ctc atg gcc tcc agg gcc aga aaa gag cgg     1077
Pro Gly Leu Phe Phe Ser Leu Met Ala Ser Arg Ala Arg Lys Glu Arg
305                 310                 315                 320

aaa tcc aag aac tcc tag tactct gaccagccag ggccagggca gagaagcagc     1131
Lys Ser Lys Asn Ser  *
321                 326
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actcttaggc ttgcttactc tacaagggac agttgcattt gttgagactt taatggagat 1191

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Met Asp Pro Gln Arg Ser Pro Leu Leu Glu Val Lys Gly Asn
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Ile Glu Leu Lys Arg Pro Leu Ile Lys Ala Pro Ser Gln Leu Pro Leu
15 20 25 30

tca gga agc aga ctc aag agg agg cct gac cag atg gaa gat ggc ctg 323
Ser Gly Ser Arg Leu Lys Arg Arg Pro Asp Gln Met Glu Asp Gly Leu
31 36 41 46

gag cct gag aag aaa cgg aca aga ggc ctg ggt gca acg acc aaa att 371
Glu Pro Glu Lys Lys Arg Thr Arg Gly Leu Gly Ala Thr Thr Lys Ile
47 52 57 62

acc aca tcc cac cca aga gtt cca tcc ctc act aca gtg cca cag aca 419
Thr Thr Ser His Pro Arg Val Pro Ser Leu Thr Thr Val Pro Gln Thr
63 68 73 78

caa ggc cag acc aca gct caa aaa gtt tcc aag aag aca gga ccc cgg 467
Gln Gly Gln Thr Thr Ala Gln Lys Val Ser Lys Lys Thr Gly Pro Arg
79 84 89 94

tgt tcc aca gct att gcc aca ggg ttg aag aac cag aag cca gtt cct 515
Cys Ser Thr Ala Ile Ala Thr Gly Leu Lys Asn Gln Lys Pro Val Pro
95 100 105 110

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gct gtt cct gtc cag aag tct ggc aca tca ggt gtt cct ccc atg gca      563
Ala Val Pro Val Gln Lys Ser Gly Thr Ser Gly Val Pro Pro Met Ala
111                 116                 121                 126

gga ggg aag aaa ccc agc aaa cgt cca gcc tgg gac tta aag ggt cag      611
Gly Gly Lys Lys Pro Ser Lys Arg Pro Ala Trp Asp Leu Lys Gly Gln
127                 132                 137                 142

tta tgt gac cta aat gca gaa cta aaa cgg tgc cgt gag agg act caa      659
Leu Cys Asp Leu Asn Ala Glu Leu Lys Arg Cys Arg Glu Arg Thr Gln
143                 148                 153                 158

acg ttg gac caa gag aac cag cag ctt cag gac cag ctc aga gat gcc      707
Thr Leu Asp Gln Glu Asn Gln Gln Leu Gln Asp Gln Leu Arg Asp Ala
159                 164                 169                 174

cag cag cag gtc aag gcc ctg ggg aca gag cgc aca aca ctg gag ggg      755
Gln Gln Gln Val Lys Ala Leu Gly Thr Glu Arg Thr Thr Leu Glu Gly
175                 180                 185                 190

cat tta gcc aag gta cag gcc cag gct gag cag ggc caa cag gag ctg      803
His Leu Ala Lys Val Gln Ala Gln Ala Glu Gln Gly Gln Gln Glu Leu
191                 196                 201                 206

aag aac ttg cgt gct tgt gtc ctg gag ctg gaa gag cgg ctg agc acg      851
Lys Asn Leu Arg Ala Cys Val Leu Glu Leu Glu Glu Arg Leu Ser Thr
207                 212                 217                 222

cag gag ggc ttg gtg caa gag ctt cag aaa aaa cag gtg gaa ttg cag      899
Gln Glu Gly Leu Val Gln Glu Leu Gln Lys Lys Gln Val Glu Leu Gln
223                 228                 233                 238

gaa gaa cgg agg gga ctg atg tcc caa cta gag gag aag gag agg agg      947
Glu Glu Arg Arg Gly Leu Met Ser Gln Leu Glu Glu Lys Glu Arg Arg
239                 244                 249                 254

ctg cag aca tca gaa gca gcc ctg tca agc agc caa gca gag gtg gca      995
Leu Gln Thr Ser Glu Ala Ala Leu Ser Ser Ser Gln Ala Glu Val Ala
255                 260                 265                 270

tct ctg cgg cag gag act gtg gcc cag gca gcc tta ctg act gag cgg     1043
Ser Leu Arg Gln Glu Thr Val Ala Gln Ala Ala Leu Leu Thr Glu Arg
271                 276                 281                 286

gaa gaa cgt ctt cat ggg cta gaa atg gag cgc cgg cga ctg cac aac     1091
Glu Glu Arg Leu His Gly Leu Glu Met Glu Arg Arg Arg Leu His Asn
287                 292                 297                 302

cag ctg cag gaa ctc aag ggc aac atc cgt gta ttc tgc cgg gtc cgc     1139
Gln Leu Gln Glu Leu Lys Gly Asn Ile Arg Val Phe Cys Arg Val Arg
303                 308                 313                 318

cct gtc ctg ccg ggg gag ccc act cca ccc cct ggc ctc ctc ctg ttt     1187
Pro Val Leu Pro Gly Glu Pro Thr Pro Pro Pro Gly Leu Leu Leu Phe
319                 324                 329                 334

ccc tct ggc cct ggt ggg ccc tct gat cct cca acc cgc ctt agc ctc     1235
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Pro Ser Gly Pro Gly Gly Pro Ser Asp Pro Pro Thr Arg Leu Ser Leu
335                 340                 345                 350

tcc cgg tct gac gag cgg cgt ggg acc ctg agt ggg gca cca gct ccc     1283
Ser Arg Ser Asp Glu Arg Arg Gly Thr Leu Ser Gly Ala Pro Ala Pro
351                 356                 361                 366

cca act cgc cat gat ttt tcc ttt gac cgg gta ttc cca cca gga agt     1331
Pro Thr Arg His Asp Phe Ser Phe Asp Arg Val Phe Pro Pro Gly Ser
367                 372                 377                 382

gga cag gat gaa gtg ttt gaa gag att gcc atg ctt gtc cag tca gcc     1379
Gly Gln Asp Glu Val Phe Glu Glu Ile Ala Met Leu Val Gln Ser Ala
383                 388                 393                 398

ctg gat ggc tat cca gta tgc atc ttt gcc tat ggc cag aca ggc agt     1427
Leu Asp Gly Tyr Pro Val Cys Ile Phe Ala Tyr Gly Gln Thr Gly Ser
399                 404                 409                 414

ggc aag acc ttc aca atg gag ggt ggg cct ggg gga gac ccc cag ttg     1475
Gly Lys Thr Phe Thr Met Glu Gly Gly Pro Gly Gly Asp Pro Gln Leu
415                 420                 425                 430

gag ggg ctg atc cct cgg gcc ctg cgg cac ctc ttc tct gtg gct cag     1523
Glu Gly Leu Ile Pro Arg Ala Leu Arg His Leu Phe Ser Val Ala Gln
431                 436                 441                 446

gag ctg agt ggt cag ggc tgg acc tac agc ttt gta gca agc tac gta     1571
Glu Leu Ser Gly Gln Gly Trp Thr Tyr Ser Phe Val Ala Ser Tyr Val
447                 452                 457                 462

gag atc tac aat gag act gtc cgg gac ctg ctg gcc act gga acc cgg     1619
Glu Ile Tyr Asn Glu Thr Val Arg Asp Leu Leu Ala Thr Gly Thr Arg
463                 468                 473                 478

aag ggt caa ggg ggc gag tgt gag att cgc cgt gca ggg cca ggg agt     1667
Lys Gly Gln Gly Gly Glu Cys Glu Ile Arg Arg Ala Gly Pro Gly Ser
479                 484                 489                 494

gag gag ctc act gtc acc aat gct cga tat gtc cct gtc tcc tgt gag     1715
Glu Glu Leu Thr Val Thr Asn Ala Arg Tyr Val Pro Val Ser Cys Glu
495                 500                 505                 510

aaa gaa gtg gac gcc ctg ctt cat ctg gcc cgc cag aat cgg gct gtg     1763
Lys Glu Val Asp Ala Leu Leu His Leu Ala Arg Gln Asn Arg Ala Val
511                 516                 521                 526

gcc cgc aca gcc cag aat gaa cgg tca tca cgc agc cac agt gta ttc     1811
Ala Arg Thr Ala Gln Asn Glu Arg Ser Ser Arg Ser His Ser Val Phe
527                 532                 537                 542

cag cta cag att tct ggg gag cac tcc agc cga ggc ctg cag tgt ggg     1859
Gln Leu Gln Ile Ser Gly Glu His Ser Ser Arg Gly Leu Gln Cys Gly
543                 548                 553                 558

gcc ccc ctc agt ctt gtg gac ctg gcc ggg agt gag cga ctt gac ccc     1907
Ala Pro Leu Ser Leu Val Asp Leu Ala Gly Ser Glu Arg Leu Asp Pro
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559                 564                 569                 574

ggc tta gcc ctc ggc ccc ggg gag cgg gaa cgc ctt cgg gaa aca cag     1955
Gly Leu Ala Leu Gly Pro Gly Glu Arg Glu Arg Leu Arg Glu Thr Gln
575                 580                 585                 590

gcc att aac agc agc ctg tcc acg ctg ggg ctg gtt atc atg gcc ctg     2003
Ala Ile Asn Ser Ser Leu Ser Thr Leu Gly Leu Val Ile Met Ala Leu
591                 596                 601                 606

agc aac aag gag tcc cac gtg cct tac cgg aac agc aaa ctg acc tac     2051
Ser Asn Lys Glu Ser His Val Pro Tyr Arg Asn Ser Lys Leu Thr Tyr
607                 612                 617                 622

ctg ctg cag aac tct ctg ggt ggt agt gct aag atg ctc atg ttt gtg     2099
Leu Leu Gln Asn Ser Leu Gly Gly Ser Ala Lys Met Leu Met Phe Val
623                 628                 633                 638

aac att tct cca ctg gaa gag aac gtc tcc gag tcc ctc aac tct cta     2147
Asn Ile Ser Pro Leu Glu Glu Asn Val Ser Glu Ser Leu Asn Ser Leu
639                 644                 649                 654

cgc ttt gcc tcc aag gtg aac cag tgt gtt att ggt act gct cag gcc     2195
Arg Phe Ala Ser Lys Val Asn Gln Cys Val Ile Gly Thr Ala Gln Ala
655                 660                 665                 670

aac agg aag tga aga cggatccaga tctgtgtgtg tgtgtgtgtg tgtgtgtgtg     2250
Asn Arg Lys  *
671

tgtgtgtgtg tgtgtgtgtg tgtgtgtccc tatgtctatg tatcgggtga ggggtgggag   2310

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aatagtttgg ttttttttt aaataaaggt tttattagca tttgcccaag aaggcagata   2430

ctttcatatc tgtaaaagtg ggagctgtga tctgtaccct ctgccaaacg tttacgtggg   2490

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aggcacccct gccctcctga ggtcagctga gcggtta atg cgg aag gtt aag aaa 175
Met Arg Lys Val Lys Lys
1

ctg cgc ctg gac aag gag aac acc gga agt tgg aga agc ttc tcg ctg 223
Leu Arg Leu Asp Lys Glu Asn Thr Gly Ser Trp Arg Ser Phe Ser Leu
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aat tcc gag ggg gct gag agg atg gcc acc acc ggg acc cca acg gcc 271
Asn Ser Glu Gly Ala Glu Arg Met Ala Thr Thr Gly Thr Pro Thr Ala
23 28 33 38

gac cga ggc gac gca gcc gcc aca gat gac ccg gcc gcc cgc ttc cag 319
Asp Arg Gly Asp Ala Ala Ala Thr Asp Asp Pro Ala Ala Arg Phe Gln
39 44 49 54

gtg cag aag cac tcg tgg gac ggg ctc cgg agc atc atc cac ggc agc 367
Val Gln Lys His Ser Trp Asp Gly Leu Arg Ser Ile Ile His Gly Ser
55 60 65 70

cgc aag tac tcg ggc ctc att gtc aac aag gcg ccc cac gac ttc cag 415
Arg Lys Tyr Ser Gly Leu Ile Val Asn Lys Ala Pro His Asp Phe Gln
71 76 81 86

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Phe Val Gln Lys Thr Asp Glu Ser Gly Pro His Ser His Arg Leu Tyr
87 92 97 102

tac ctg ggt atg cca tat ggc agc cga gag aac tcc ctc ctc tac tct 511
Tyr Leu Gly Met Pro Tyr Gly Ser Arg Glu Asn Ser Leu Leu Tyr Ser
103 108 113 118

gag att ccc aag aag gtc cgg aaa gag gct ctg ctg ctc ctg tcc tgg 559
Glu Ile Pro Lys Lys Val Arg Lys Glu Ala Leu Leu Leu Leu Ser Trp
119 124 129 134

aag cag atg ctg gat cat ttc cag gcc acg ccc cac cat ggg gtc tac 607
Lys Gln Met Leu Asp His Phe Gln Ala Thr Pro His His Gly Val Tyr
135 140 145 150

tct cgg gag gag gag ctg ctg agg gag cgg aaa cgc ctg ggg gtc ttc 655
Ser Arg Glu Glu Glu Leu Leu Arg Glu Arg Lys Arg Leu Gly Val Phe
151 156 161 166

ggc atc acc tcc tac gac ttc cac agc gag agt ggc ctc ttc ctc ttc 703
Gly Ile Thr Ser Tyr Asp Phe His Ser Glu Ser Gly Leu Phe Leu Phe
167 172 177 182

cag gcc agc aac agc ctc ttc cac tgc cgc gac ggc ggc aag aac ggc 751
Gln Ala Ser Asn Ser Leu Phe His Cys Arg Asp Gly Gly Lys Asn Gly
183 188 193 198

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ttc atg gtg agc cct ggc cct ggc tgt gtg tcc cct atg aaa ccg ctg      799
Phe Met Val Ser Pro Gly Pro Gly Cys Val Ser Pro Met Lys Pro Leu
199                 204                 209                 214

gaa atc aag acc cag tgc tca ggg ccc cgg atg gac ccc aaa atc tgc      847
Glu Ile Lys Thr Gln Cys Ser Gly Pro Arg Met Asp Pro Lys Ile Cys
215                 220                 225                 230

cct gcc gac cct gcc ttc ttc tcc ttc atc aat aac agc gac ctg tgg      895
Pro Ala Asp Pro Ala Phe Phe Ser Phe Ile Asn Asn Ser Asp Leu Trp
231                 236                 241                 246

gtg gcc aac atc gag aca ggc gag gag cgg cgg ctg acc ttc tgc cac      943
Val Ala Asn Ile Glu Thr Gly Glu Glu Arg Arg Leu Thr Phe Cys His
247                 252                 257                 262

caa ggt tta tcc aat gtc ctg gat gac ccc aag tct gcg ggt gtg gcc      991
Gln Gly Leu Ser Asn Val Leu Asp Asp Pro Lys Ser Ala Gly Val Ala
263                 268                 273                 278

acc ttc gtc ata cag gaa gag ttc gac cgc ttc act ggg tac tgg tgg     1039
Thr Phe Val Ile Gln Glu Glu Phe Asp Arg Phe Thr Gly Tyr Trp Trp
279                 284                 289                 294

tgc ccc aca gcc tcc tgg gaa ggt tca gag ggc ctc aag acg ctg cga     1087
Cys Pro Thr Ala Ser Trp Glu Gly Ser Glu Gly Leu Lys Thr Leu Arg
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atc ctg tat gag gaa gtc gat gag tcc gag gtg gag gtc att cac gtc     1135
Ile Leu Tyr Glu Glu Val Asp Glu Ser Glu Val Glu Val Ile His Val
311                 316                 321                 326

ccc tct cct gcg cta gaa gaa agg aag acg gac tcg tat cgg tac ccc     1183
Pro Ser Pro Ala Leu Glu Glu Arg Lys Thr Asp Ser Tyr Arg Tyr Pro
327                 332                 337                 342

agg aca ggc agc aag aat ccc aag att gcc ttg aaa ctg gct gag ttc     1231
Arg Thr Gly Ser Lys Asn Pro Lys Ile Ala Leu Lys Leu Ala Glu Phe
343                 348                 353                 358

cag act gac agc cag ggc aag atc gtc tcg acc cag gag aag gag ctg     1279
Gln Thr Asp Ser Gln Gly Lys Ile Val Ser Thr Gln Glu Lys Glu Leu
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gtg cag ccc ttc agc tcg ctg ttc ccg aag gtg gag tac atc gcc agg     1327
Val Gln Pro Phe Ser Ser Leu Phe Pro Lys Val Glu Tyr Ile Ala Arg
375                 380                 385                 390

gcc ggg tgg acc cgg gat ggc aaa tac gcc tgg gcc atg ttc ctg gac     1375
Ala Gly Trp Thr Arg Asp Gly Lys Tyr Ala Trp Ala Met Phe Leu Asp
391                 396                 401                 406

cgg ccc cag cag tgg ctc cag ctc gtc ctc ctc ccc ccg gcc ctg ttc     1423
Arg Pro Gln Gln Trp Leu Gln Leu Val Leu Leu Pro Pro Ala Leu Phe
407                 412                 417                 422
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atc ccg agc aca gag aat gag gag cag gcg gct agc ctc tgc cag agc      1471
Ile Pro Ser Thr Glu Asn Glu Glu Gln Ala Ala Ser Leu Cys Gln Ser
423                 428                 433                 438

tgt ccc cag gaa tgt cca gcc gta tgt gtg tac gga gga ggt cac caa      1519
Cys Pro Gln Glu Cys Pro Ala Val Cys Val Tyr Gly Gly Gly His Gln
439                 444                 449                 454

cgt ctg gat caa tgt tca tga ca tcttctatcc cttcccccaa tcagagggag      1572
Arg Leu Asp Gln Cys Ser  *
455                 460

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aagtcaccgc cgttttaaaa tcccagggct acgattggag tgagcccttc agccccgggg    1692

aaggtgagca gagcctgacg aatgctatct gggtcaatga ggagaccaag ctggtgtact    1752

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ccggcgagat cgtacgcctc accacgcccg gcttctccca tagctgctcc atgagccaga    1872

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Application No. 10/765,950

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Glu Glu Tyr Ala Arg Leu Val Met Glu Ala Gln Pro Glu Trp Leu Arg
8 13 18 23

gcc gag gtg aag cgg ctg tcc cac gag ctg gcc gag acc acg cgt gag 210
Ala Glu Val Lys Arg Leu Ser His Glu Leu Ala Glu Thr Thr Arg Glu
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Lys Ile Gln Ala Ala Glu Tyr Gly Leu Ala Val Leu Glu Glu Lys His
40 45 50 55

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Gln Leu Lys Leu Gln Phe Glu Glu Leu Glu Val Asp Tyr Glu Ala Ile
56 61 66 71

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Arg Ser Glu Met Glu Gln Leu Lys Glu Ala Phe Gly Gln Ala His Thr
72 77 82 87

aac cac aag aag gtg gct gct gac gga gag agc cgg gag gag agc ctg 402
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88 93 98 103

atc cag gag tcg gcc tcc aag gag cag tac tac gtg cgg aag gtg cta 450
Ile Gln Glu Ser Ala Ser Lys Glu Gln Tyr Tyr Val Arg Lys Val Leu
104 109 114 119

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120 125 130 135

cag tcg gag aat gag cgc ctg gcc tct gtg gcc cag gag ctg aag gag 546
Gln Ser Glu Asn Glu Arg Leu Ala Ser Val Ala Gln Glu Leu Lys Glu
136 141 146 151

atc aac cag aat gtg gag atc cag cgt ggc cgc ctg cgg gat gac atc 594
Ile Asn Gln Asn Val Glu Ile Gln Arg Gly Arg Leu Arg Asp Asp Ile
152 157 162 167

aag gag tac aaa ttc cgg gaa gct cgt ctg ctg cag gac tac tcg gaa 642

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Lys Glu Tyr Lys Phe Arg Glu Ala Arg Leu Leu Gln Asp Tyr Ser Glu
168                 173                 178                 183

ctg gag gag gag aac atc agc ctg cag aag caa gtg tct gtg ctc aga      690
Leu Glu Glu Glu Asn Ile Ser Leu Gln Lys Gln Val Ser Val Leu Arg
184                 189                 194                 199

cag aac cag gtg gag ttt gag ggc ctc aag cat gag atc aag cgt ctg      738
Gln Asn Gln Val Glu Phe Glu Gly Leu Lys His Glu Ile Lys Arg Leu
200                 205                 210                 215

gag gag gag acc gag tac ctc aac agc cag ctg gag gat gcc atc cgc      786
Glu Glu Glu Thr Glu Tyr Leu Asn Ser Gln Leu Glu Asp Ala Ile Arg
216                 221                 226                 231

ctc aag gag atc tca gag cgg cag ctg gag gag gcg ctg gag acc ctg      834
Leu Lys Glu Ile Ser Glu Arg Gln Leu Glu Glu Ala Leu Glu Thr Leu
232                 237                 242                 247

aag acg gag cgc gaa cag aag aac agc ctg cgc aag gag ctg tca cac      882
Lys Thr Glu Arg Glu Gln Lys Asn Ser Leu Arg Lys Glu Leu Ser His
248                 253                 258                 263

tac atg agc atc aat gac tcc ttc tac acc agc cac ctg cat gtc tcg      930
Tyr Met Ser Ile Asn Asp Ser Phe Tyr Thr Ser His Leu His Val Ser
264                 269                 274                 279

ctg gat ggc ctc aag ttc agt gac gat gct gcc gag ccc aac aac gat      978
Leu Asp Gly Leu Lys Phe Ser Asp Asp Ala Ala Glu Pro Asn Asn Asp
280                 285                 290                 295

gcc gag gcc ctg gtc aat ggc ttt gag cac ggc ggc ctg gcc aag ctg     1026
Ala Glu Ala Leu Val Asn Gly Phe Glu His Gly Gly Leu Ala Lys Leu
296                 301                 306                 311

cca ctg gac aac aag acc tcc acg ccc aag aag gag ggc ctc gca ccg     1074
Pro Leu Asp Asn Lys Thr Ser Thr Pro Lys Lys Glu Gly Leu Ala Pro
312                 317                 322                 327

ccc tcc ccc agc ctc gtc tcc gac cta ctc agt gag ctc aac atc tct     1122
Pro Ser Pro Ser Leu Val Ser Asp Leu Leu Ser Glu Leu Asn Ile Ser
328                 333                 338                 343

gag atc cag aag ctg aag cag cag ctg atg cag atg gag cgg gaa aag     1170
Glu Ile Gln Lys Leu Lys Gln Gln Leu Met Gln Met Glu Arg Glu Lys
344                 349                 354                 359

gcg ggc ctg ctg gca acg ctg cag gac aca cag aag cag ctg gag cac     1218
Ala Gly Leu Leu Ala Thr Leu Gln Asp Thr Gln Lys Gln Leu Glu His
360                 365                 370                 375

acg cgg ggc tcc ctg tca gaa cag cag gag aag gtg acc cgc ctc aca     1266
Thr Arg Gly Ser Leu Ser Glu Gln Gln Glu Lys Val Thr Arg Leu Thr
376                 381                 386                 391

gag aat ctg agt gcc ctg cgg cgc ctg cag gcc agc aag gag cgg cag     1314
Glu Asn Leu Ser Ala Leu Arg Arg Leu Gln Ala Ser Lys Glu Arg Gln
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Case 2:15-cv-04062-GW-JEM Document 1-2 Filed 05/26/15 Page 391 of 450 Page ID #:391

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392                 397                 402                 407

aca gcc ctg gac aac gag aag gac cgt gac agc cat gag gat ggg gac     1362
Thr Ala Leu Asp Asn Glu Lys Asp Arg Asp Ser His Glu Asp Gly Asp
408                 413                 418                 423

tac tac gag gtg gac atc aac ggg cct gag atc ttg gcc tgc aag tac     1410
Tyr Tyr Glu Val Asp Ile Asn Gly Pro Glu Ile Leu Ala Cys Lys Tyr
424                 429                 434                 439

cat gtg gct gtg gct gag gct ggc gag ctc cgc gag cag ctc aag gca     1458
His Val Ala Val Ala Glu Ala Gly Glu Leu Arg Glu Gln Leu Lys Ala
440                 445                 450                 455

ctg cgc agc acg cac gag gct cgt gag gcc cag cac gcc gag gag aag     1506
Leu Arg Ser Thr His Glu Ala Arg Glu Ala Gln His Ala Glu Glu Lys
456                 461                 466                 471

ggc cgc tat gag gct gag ggc cag gca ctc acg gag aag gtc tcc ctg     1554
Gly Arg Tyr Glu Ala Glu Gly Gln Ala Leu Thr Glu Lys Val Ser Leu
472                 477                 482                 487

cta gag aag gcc agc cgc cag gac cgc gag ctg ctg gcc cgg ctg gag     1602
Leu Glu Lys Ala Ser Arg Gln Asp Arg Glu Leu Leu Ala Arg Leu Glu
488                 493                 498                 503

aag gag cta aag aag gtg agc gac gtc gcc ggc gag aca cag ggc agc     1650
Lys Glu Leu Lys Lys Val Ser Asp Val Ala Gly Glu Thr Gln Gly Ser
504                 509                 514                 519

ctg agt gtg gcc cag gat gag ctg gtg acc ttc agt gag gag ctg gcc     1698
Leu Ser Val Ala Gln Asp Glu Leu Val Thr Phe Ser Glu Glu Leu Ala
520                 525                 530                 535

aat ctc tac cac cac gtg tgc atg tgc aac aat gag aca ccc aac cgt     1746
Asn Leu Tyr His His Val Cys Met Cys Asn Asn Glu Thr Pro Asn Arg
536                 541                 546                 551

gtc atg ctg gac tac tac cgc gag ggc cag ggc ggg gcc ggc cgc acc     1794
Val Met Leu Asp Tyr Tyr Arg Glu Gly Gln Gly Gly Ala Gly Arg Thr
552                 557                 562                 567

agt ccc ggg ggc cgc acc agc ccc gag gcg cgt ggc cgg cgc tca ccc     1842
Ser Pro Gly Gly Arg Thr Ser Pro Glu Ala Arg Gly Arg Arg Ser Pro
568                 573                 578                 583

atc ctc cta ccc aag ggg ctg ctg gct cct gag gcg ggc cga gca gat     1890
Ile Leu Leu Pro Lys Gly Leu Leu Ala Pro Glu Ala Gly Arg Ala Asp
584                 589                 594                 599

ggt ggg acg ggg gac agc agc ccc tcg cct ggc tcc tca ctg cca tca     1938
Gly Gly Thr Gly Asp Ser Ser Pro Ser Pro Gly Ser Ser Leu Pro Ser
600                 605                 610                 615

ccc ctg agt gac cca cgc cgg gag ccc atg aac atc tac aac ctg atc     1986
Pro Leu Ser Asp Pro Arg Arg Glu Pro Met Asn Ile Tyr Asn Leu Ile
616                 621                 626                 631
```

```
gct atc atc cgt gac cag atc aag cac ctg cag gca gcc gtg gac cgc     2034
Ala Ile Ile Arg Asp Gln Ile Lys His Leu Gln Ala Ala Val Asp Arg
632                 637                 642                 647

acc acg gag ctg tca cgc cag cgc att gcc tct cag gag ctg ggc ccc     2082
Thr Thr Glu Leu Ser Arg Gln Arg Ile Ala Ser Gln Glu Leu Gly Pro
648                 653                 658                 663

gcc gtg gac aag gac aag gaa gcg ctt atg gag gag atc ctc aag ctg     2130
Ala Val Asp Lys Asp Lys Glu Ala Leu Met Glu Glu Ile Leu Lys Leu
664                 669                 674                 679

aag tcg ctg ctc agc acc aag cgg gag cag atc acc acg ctg cgc act     2178
Lys Ser Leu Leu Ser Thr Lys Arg Glu Gln Ile Thr Thr Leu Arg Thr
680                 685                 690                 695

gtg ctc aag gcc aac aag cag acg gcc gag gtg gcc ctt gcc aac ctg     2226
Val Leu Lys Ala Asn Lys Gln Thr Ala Glu Val Ala Leu Ala Asn Leu
696                 701                 706                 711

aag agc aag tat gag aat gag aag gcc atg gtt acc gag acc atg atg     2274
Lys Ser Lys Tyr Glu Asn Glu Lys Ala Met Val Thr Glu Thr Met Met
712                 717                 722                 727

aag ctg cgc aat gag ctc aag gcc ctc aag gag gac gca gcc acc ttc     2322
Lys Leu Arg Asn Glu Leu Lys Ala Leu Lys Glu Asp Ala Ala Thr Phe
728                 733                 738                 743

tcc tcg ctg cgt gct atg ttt gcc acc agg tgt gac gag tac att aca     2370
Ser Ser Leu Arg Ala Met Phe Ala Thr Arg Cys Asp Glu Tyr Ile Thr
744                 749                 754                 759

cag ctg gat gag atg cag cgg cag ctg gcg gct gct gag gac gag aag     2418
Gln Leu Asp Glu Met Gln Arg Gln Leu Ala Ala Ala Glu Asp Glu Lys
760                 765                 770                 775

aag acg ctg aac tcg ctg ctg cgc atg gcc atc cag cag aag ctg gcg     2466
Lys Thr Leu Asn Ser Leu Leu Arg Met Ala Ile Gln Gln Lys Leu Ala
776                 781                 786                 791

ctg acc cag cgg ctg gag ctg ctc gag ctg gac cat gag cag acc cgg     2514
Leu Thr Gln Arg Leu Glu Leu Leu Glu Leu Asp His Glu Gln Thr Arg
792                 797                 802                 807

cgt ggc cgt gcc aaa gcc gcc ccg aag acc aag cca gcc aca ccg agc     2562
Arg Gly Arg Ala Lys Ala Ala Pro Lys Thr Lys Pro Ala Thr Pro Ser
808                 813                 818                 823

gta agt cac acc tgt gcc tgt gcc agc gac agg gcc gag ggc acc ggg     2610
Val Ser His Thr Cys Ala Cys Ala Ser Asp Arg Ala Glu Gly Thr Gly
824                 829                 834                 839

ctg gcc aac cag gtg ttc tgc agc gag aag cac agc att tac tgt gat     2658
Leu Ala Asn Gln Val Phe Cys Ser Glu Lys His Ser Ile Tyr Cys Asp
840                 845                 850                 855
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tag gggc tgtggggcgc cgcacgctgc agctaacatc tgcttcacct caactaaccc 2715
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856

agcagcagcg ggacggcggt gctaggtcaa tcttaacgtg actaatgcac agagggtagg 2775

agtctagccg aggcgccatg gggcgttgca tcagcaggac acttgtgaga gctttgtgtc 2835

gcttctcact cctcaaagcc ccctcaggag cacccagtcc tcagctgctc tcttaggtgg 2895

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gctccgcgaa agtggctgca agccggccgc ccactgtcag ggttgggggg acagagaaag 180

tgatgtgcgc cttctaaagc ctcgcccagc gccgccgaag cagcttcacc tctccaactt 240

tctcccaccg actgcttgtc ttgaccctgc cctccaccct ccccagagcc acttcgggtg 300

cgcgctcttg ggtaaagggg gggtcaccgg ctgtctggg atg gct tcc aat ttt 354
Met Ala Ser Asn Phe
1

aat gac ata gtg aag caa ggg tac gtg agg atc cgg agc aga cgc ctc 402
Asn Asp Ile Val Lys Gln Gly Tyr Val Arg Ile Arg Ser Arg Arg Leu
6 11 16 21

ggg att tat cag cga tgc tgg tta gta ttc aag aaa gct tca agc aaa 450
Gly Ile Tyr Gln Arg Cys Trp Leu Val Phe Lys Lys Ala Ser Ser Lys
22 27 32 37

ggt cca aaa aga ctg gag aaa ttt tct gat gaa cgt gct gca tat ttc 498
Gly Pro Lys Arg Leu Glu Lys Phe Ser Asp Glu Arg Ala Ala Tyr Phe
38 43 48 53

agg tgt tat cat aag gtt aca gaa ctc aat aat gtg aag aac gta gct 546
Arg Cys Tyr His Lys Val Thr Glu Leu Asn Asn Val Lys Asn Val Ala

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 54                  59                  64                  69

cga ttg cca aaa agc acc aag aaa cat gcc ata ggg att tat ttc aat      594
Arg Leu Pro Lys Ser Thr Lys Lys His Ala Ile Gly Ile Tyr Phe Asn
 70                  75                  80                  85

gac gat acc tcc aag act ttt gct tgc gaa tca gat ctt gag gct gat      642
Asp Asp Thr Ser Lys Thr Phe Ala Cys Glu Ser Asp Leu Glu Ala Asp
 86                  91                  96                 101

gag tgg tgc aaa gta ctc cag atg gag tgt gta gga aca cgg atc aat      690
Glu Trp Cys Lys Val Leu Gln Met Glu Cys Val Gly Thr Arg Ile Asn
102                 107                 112                 117

gac atc agc ctt gga gag cct gac tta ctg gcc act ggg gtt gag aga      738
Asp Ile Ser Leu Gly Glu Pro Asp Leu Leu Ala Thr Gly Val Glu Arg
118                 123                 128                 133

gaa cag agt gag aga ttc aat gtg tat ttg atg cca tct cct aac tta      786
Glu Gln Ser Glu Arg Phe Asn Val Tyr Leu Met Pro Ser Pro Asn Leu
134                 139                 144                 149

gat gta cat ggc gaa tgt gcc ttg cag att aca tat gag tat atc tgt      834
Asp Val His Gly Glu Cys Ala Leu Gln Ile Thr Tyr Glu Tyr Ile Cys
150                 155                 160                 165

ctt tgg gac gtc cag aat ccc aga gtc aaa ctc atc tct tgg ccg cta      882
Leu Trp Asp Val Gln Asn Pro Arg Val Lys Leu Ile Ser Trp Pro Leu
166                 171                 176                 181

agc gcc ctg cgg cgg tat gga cgt gat act acg tgg ttc act ttt gag      930
Ser Ala Leu Arg Arg Tyr Gly Arg Asp Thr Thr Trp Phe Thr Phe Glu
182                 187                 192                 197

gca ggg agg atg tgt gag act ggt gaa ggg ctg ttt atc ttt cag acc      978
Ala Gly Arg Met Cys Glu Thr Gly Glu Gly Leu Phe Ile Phe Gln Thr
198                 203                 208                 213

cga gac ggg gag gcc atc tat cag aaa gtc cac tct gct gcc ttg gcc     1026
Arg Asp Gly Glu Ala Ile Tyr Gln Lys Val His Ser Ala Ala Leu Ala
214                 219                 224                 229

ata gcc gag cag cac gag cgc ttg cta cag agt gtg aaa aac tcg atg     1074
Ile Ala Glu Gln His Glu Arg Leu Leu Gln Ser Val Lys Asn Ser Met
230                 235                 240                 245

ctc cag atg aag atg agt gag cgg gcc gcc tcg ctg agc acc atg gtg     1122
Leu Gln Met Lys Met Ser Glu Arg Ala Ala Ser Leu Ser Thr Met Val
246                 251                 256                 261

ccc ctg cct cgc agc gcc tac tgg cag cac atc aca cgg cag cac agc     1170
Pro Leu Pro Arg Ser Ala Tyr Trp Gln His Ile Thr Arg Gln His Ser
262                 267                 272                 277

acg gga cag ctc tac cgc ttg caa gat gtt tcc agc cct ctg aag ctt     1218
Thr Gly Gln Leu Tyr Arg Leu Gln Asp Val Ser Ser Pro Leu Lys Leu
278                 283                 288                 293
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cat cga aca gag act ttt cca gcc tac aga tct gag cac tga cagtaac     1267
His Arg Thr Glu Thr Phe Pro Ala Tyr Arg Ser Glu His  *
294                 299                 304

tgccaagaat tgttaacaca cttgtgatgt gtcagccaca gattcaccca ggaggtcaca   1327

gaatgacagc aagggaaatg acgaccaaga gaagaagctt aaagtcctgg ctaattgtgt   1387

ggtcattgga aaactctgca atacaataat tttctttatt ttctttttct tttttaaatt   1447

cttagtgtaa ttgaaacgtg ctctatagat attgactctg tgttccctct tttacagctg   1507

gacagaaaga agtcaatgtc acgaaatgat tttctattgt agatactttg tcccttgcac   1567

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tcctcagtta ttattactgt ggttctgatt aactactgga aattatattt gattatatca   1747

ccaattagtt aaatcagtgc ttcgactcac tcttatctgt tctgttcaaa actatttgtt   1807

caaagaaccc attagtgttg tttacagggt tacagtttct ctcacatgct ttcctcaccc   1867

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aataaaagat cattcttcac ccac                                         1951
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ccgggcaggt gaactctcca cggggtctag ggcccgcgaa agggttcgga accgagtcag    180

cgcgccttgc gggcaggatt cacgccgctg tgacccggag gtcctcaggg ggcgaagccc    240

cggcctaggc ctcgcggag atg ccc agc tgc ggt gct tgt act tgc ggc gcg      292
                     Met Pro Ser Cys Gly Ala Cys Thr Cys Gly Ala
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gcg gcc gtc cgg ctc atc acc tcc tca ctc gcc tcc gcg cag aga ggt      340
Ala Ala Val Arg Leu Ile Thr Ser Ser Leu Ala Ser Ala Gln Arg Gly
 12                  17                  22                  27

att tct ggt ggt cgc att cat atg tca gtt tta gga agg ctt ggg aca      388
Ile Ser Gly Gly Arg Ile His Met Ser Val Leu Gly Arg Leu Gly Thr
 28                  33                  38                  43

ttt gaa act cag att ctg caa aga gct cct ctt aga tcc ttt aca gaa      436
Phe Glu Thr Gln Ile Leu Gln Arg Ala Pro Leu Arg Ser Phe Thr Glu
 44                  49                  54                  59

aca cca gca tac ttt gcc tca aaa gat ggg ata agt aaa gat ggt tct      484
Thr Pro Ala Tyr Phe Ala Ser Lys Asp Gly Ile Ser Lys Asp Gly Ser
 60                  65                  70                  75

gga gat gga aat aag aaa tca gca agt gag gga agt agt aag aaa tca      532
Gly Asp Gly Asn Lys Lys Ser Ala Ser Glu Gly Ser Ser Lys Lys Ser
 76                  81                  86                  91

ggc tct ggg aat tct ggg aaa ggt gga aac cag ctg cgc tgt cct aaa      580
Gly Ser Gly Asn Ser Gly Lys Gly Gly Asn Gln Leu Arg Cys Pro Lys
 92                  97                 102                 107

tgt ggc gac ttg tgc aca cat gta gag acc ttt gta tca tcc acc cgt      628
Cys Gly Asp Leu Cys Thr His Val Glu Thr Phe Val Ser Ser Thr Arg
108                 113                 118                 123

ttt gtc aag tgt gaa aag tgt cat cat ttt ttt gtt gtg cta tct gaa      676
Phe Val Lys Cys Glu Lys Cys His His Phe Phe Val Val Leu Ser Glu
124                 129                 134                 139

gca gac tca aag aaa agc ata att aaa gaa ccc gaa tca gca gca gaa      724
Ala Asp Ser Lys Lys Ser Ile Ile Lys Glu Pro Glu Ser Ala Ala Glu
140                 145                 150                 155

gct gta aaa ttg gca ttc caa cag aaa cca cca cct ccc cct aag aag      772
Ala Val Lys Leu Ala Phe Gln Gln Lys Pro Pro Pro Pro Pro Lys Lys
156                 161                 166                 171

att tat aac tac ctc gac aag tat gtt gtt ggc cag tca ttt gct aag      820
Ile Tyr Asn Tyr Leu Asp Lys Tyr Val Val Gly Gln Ser Phe Ala Lys
172                 177                 182                 187

aag gtg ctt tca gtt gct gtg tac aat cat tat aag aga ata tat aat      868
Lys Val Leu Ser Val Ala Val Tyr Asn His Tyr Lys Arg Ile Tyr Asn
188                 193                 198                 203

aat atc cca gct aat ctg aga cag caa gca gag gtt gag aag cag aca      916
Asn Ile Pro Ala Asn Leu Arg Gln Gln Ala Glu Val Glu Lys Gln Thr
204                 209                 214                 219

tca tta aca cca aga gag tta gaa ata aga aga cgg gag gat gag tac      964
Ser Leu Thr Pro Arg Glu Leu Glu Ile Arg Arg Arg Glu Asp Glu Tyr
220                 225                 230                 235
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US 2005/0260186 A1

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aga ttt aca aaa ttg ctt cag att gct gga att agc cca cat ggt aat      1012
Arg Phe Thr Lys Leu Leu Gln Ile Ala Gly Ile Ser Pro His Gly Asn
236                 241                 246                 251

gct tta gga gca tca atg cag caa cag gta aat caa caa ata cct cag      1060
Ala Leu Gly Ala Ser Met Gln Gln Gln Val Asn Gln Gln Ile Pro Gln
252                 257                 262                 267

gaa aaa cga gga ggg gaa gta ttg gat tct tct cat gat gac ata aaa      1108
Glu Lys Arg Gly Gly Glu Val Leu Asp Ser Ser His Asp Asp Ile Lys
268                 273                 278                 283

ctt gaa aaa agt aat att ttg ctg ctt gga cca act ggg tca ggt aaa      1156
Leu Glu Lys Ser Asn Ile Leu Leu Leu Gly Pro Thr Gly Ser Gly Lys
284                 289                 294                 299

act ctg ctg gca caa acc cta gct aaa tgc ctt gat gtc cct ttt gct      1204
Thr Leu Leu Ala Gln Thr Leu Ala Lys Cys Leu Asp Val Pro Phe Ala
300                 305                 310                 315

atc tgt gac tgt aca act ttg act cag gct gga tat gta ggc gaa gat      1252
Ile Cys Asp Cys Thr Thr Leu Thr Gln Ala Gly Tyr Val Gly Glu Asp
316                 321                 326                 331

att gaa tct gtg att gca aaa cta ctc caa gat gcc aat tat aat gtg      1300
Ile Glu Ser Val Ile Ala Lys Leu Leu Gln Asp Ala Asn Tyr Asn Val
332                 337                 342                 347

gaa aaa gca caa caa gga att gtc ttt ctg gat gaa gta gat aag att      1348
Glu Lys Ala Gln Gln Gly Ile Val Phe Leu Asp Glu Val Asp Lys Ile
348                 353                 358                 363

ggc agt gtg cca ggc att cat caa tta cgg gat gta ggt gga gaa ggc      1396
Gly Ser Val Pro Gly Ile His Gln Leu Arg Asp Val Gly Gly Glu Gly
364                 369                 374                 379

gtt cag caa ggc tta tta aaa cta cta gaa ggc aca ata gtc aat gtt      1444
Val Gln Gln Gly Leu Leu Lys Leu Leu Glu Gly Thr Ile Val Asn Val
380                 385                 390                 395

cca gaa aag aat tcc cga aag ctc cgt gga gaa aca gtt caa gtt gat      1492
Pro Glu Lys Asn Ser Arg Lys Leu Arg Gly Glu Thr Val Gln Val Asp
396                 401                 406                 411

aca aca aac atc ctg ttt gtg gca tct ggt gct ttc aat ggt tta gac      1540
Thr Thr Asn Ile Leu Phe Val Ala Ser Gly Ala Phe Asn Gly Leu Asp
412                 417                 422                 427

aga atc atc agc agg agg aaa aat gaa aag tat ctt gga ttt gga aca      1588
Arg Ile Ile Ser Arg Arg Lys Asn Glu Lys Tyr Leu Gly Phe Gly Thr
428                 433                 438                 443

cca tct aat ctg gga aaa ggc aga agg gct gca gct gct gca gac ctt      1636
Pro Ser Asn Leu Gly Lys Gly Arg Arg Ala Ala Ala Ala Asp Leu
444                 449                 454                 459
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gct aat cga agt ggg gaa tcg aat act cac caa gac att gaa gaa aaa     1684
Ala Asn Arg Ser Gly Glu Ser Asn Thr His Gln Asp Ile Glu Glu Lys
460                 465                 470                 475

gat cgg tta ttg cgt cat gtg gaa gcc aga gat ctg att gag ttt ggc     1732
Asp Arg Leu Leu Arg His Val Glu Ala Arg Asp Leu Ile Glu Phe Gly
476                 481                 486                 491

atg att cct gag ttt gtg gga cgg ttg cct gtg gtg gtt cca ttg cat     1780
Met Ile Pro Glu Phe Val Gly Arg Leu Pro Val Val Val Pro Leu His
492                 497                 502                 507

agc cta gat gag aaa aca ctt gta caa ata tta act gag cca cga aat     1828
Ser Leu Asp Glu Lys Thr Leu Val Gln Ile Leu Thr Glu Pro Arg Asn
508                 513                 518                 523

gct gtt att cct cag tac cag gcc tta ttc agc atg gat aag tgt gaa     1876
Ala Val Ile Pro Gln Tyr Gln Ala Leu Phe Ser Met Asp Lys Cys Glu
524                 529                 534                 539

ctg aat gtt act gag gat gct ttg aaa gct ata gcc aga ttg gca cta     1924
Leu Asn Val Thr Glu Asp Ala Leu Lys Ala Ile Ala Arg Leu Ala Leu
540                 545                 550                 555

gaa cga aaa aca ggt gca cga ggc ctt cgg tcc ata atg gaa aag ctg     1972
Glu Arg Lys Thr Gly Ala Arg Gly Leu Arg Ser Ile Met Glu Lys Leu
556                 561                 566                 571

tta cta gaa cca atg ttt gaa gtc cct aat tct gat atc gta tgt gtg     2020
Leu Leu Glu Pro Met Phe Glu Val Pro Asn Ser Asp Ile Val Cys Val
572                 577                 582                 587

gag gtt gac aaa gaa gta gta gaa gga aaa aag gaa cca gga tac atc     2068
Glu Val Asp Lys Glu Val Val Glu Gly Lys Lys Glu Pro Gly Tyr Ile
588                 593                 598                 603

cgg gct cca aca aaa gaa tcc tct gaa gag gag tat gac tct gga gtt     2116
Arg Ala Pro Thr Lys Glu Ser Ser Glu Glu Glu Tyr Asp Ser Gly Val
604                 609                 614                 619

gaa gaa gaa gga tgg ccc cgc caa gca gat gct gca aac agc taa act     2164
Glu Glu Glu Gly Trp Pro Arg Gln Ala Asp Ala Ala Asn Ser  *
620                 625                 630

gtcatattgc tgtcttgtat atacagcttt tccttctttt gtttaggatc ataattgtct   2224

ctacagtctg atattaaagg cattggatct atcttggata tcatacatgg tcagagaagc   2284

ctttaggaga agaatcagat catgtatata attgtaacat cacattgatt ttacggaaga   2344

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aaattgaata ttgagatacc attctttagt gttacctttt ttacccacat gtgtttctga   2584
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aaatattgga attttattca tcttaaaaat tggaccaggt aggccgggcg tggtggctcg 2644

cgcctgtaat cccagcactt tgggggccg aggcgggtgg atcacgaggt caggagttca 2704

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cggccgcgaa ttcggatcct cgagagatct ctttttttgg gtttggtggg gtatcttcat 2884

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Met Glu Leu Pro Ser Gly Pro Gly Pro
1 5

gac cgg ttt ttt gac tcg cac cgg ctt ccg ggg gac tgc ttc cta ctg 160
Asp Arg Phe Phe Asp Ser His Arg Leu Pro Gly Asp Cys Phe Leu Leu
10 15 20 25

ctc ggg ctg ttg ctc tac ccc cca gtc ggg ttc tgc ctc ctg gtc ctg 208
Leu Gly Leu Leu Leu Tyr Pro Pro Val Gly Phe Cys Leu Leu Val Leu
26 31 36 41

cgc ctt ttt ttc gga atc cac gtt ttc ctg gtc agc tgc ccg ctg cca 256
Arg Leu Phe Phe Gly Ile His Val Phe Leu Val Ser Cys Pro Leu Pro
42 47 52 57

aac agc gtc ctt cga aaa ttc gta ggg cgg acc atg tgt gcg ggg cta 304
Asn Ser Val Leu Arg Lys Phe Val Gly Arg Thr Met Cys Ala Gly Leu
58 63 68 73

ggg ctc ggg gcc cgg cag gag gac tcc gga ctc cgg gat cac agg gtc 352
Gly Leu Gly Ala Arg Gln Glu Asp Ser Gly Leu Arg Asp His Arg Val
74 79 84 89

agg gtc ctc att tcc aac cat gtg aca cct ttc gac cac aac ata gtc 400
Arg Val Leu Ile Ser Asn His Val Thr Pro Phe Asp His Asn Ile Val
90 95 100 105

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aat ttg ctt acc acc tgt agc acc cct cta ctc aat agt ccc ccc agc      448
Asn Leu Leu Thr Thr Cys Ser Thr Pro Leu Leu Asn Ser Pro Pro Ser
106                 111                 116                 121

ttt gtg tgc tgg tct cgg ggc ttc atg gag atg aat ggg cgg ggg gag      496
Phe Val Cys Trp Ser Arg Gly Phe Met Glu Met Asn Gly Arg Gly Glu
122                 127                 132                 137

ttg gtg gag tca ctc aag aga ttc tgt gct tcc acg agg ctt ccc ccc      544
Leu Val Glu Ser Leu Lys Arg Phe Cys Ala Ser Thr Arg Leu Pro Pro
138                 143                 148                 153

act cct ctg ctg cta ttc cct gag gaa gag gcc acc aat ggc cgg gag      592
Thr Pro Leu Leu Leu Phe Pro Glu Glu Glu Ala Thr Asn Gly Arg Glu
154                 159                 164                 169

ggg ctc ctg cgc ttc agt tcc tgg cca ttt tct atc caa gat gtg gta      640
Gly Leu Leu Arg Phe Ser Ser Trp Pro Phe Ser Ile Gln Asp Val Val
170                 175                 180                 185

caa cct ctt acc ctg caa gtt cag aga ccc ctg gtc tct gtg acg gtg      688
Gln Pro Leu Thr Leu Gln Val Gln Arg Pro Leu Val Ser Val Thr Val
186                 191                 196                 201

tca gat gcc tcc tgg gtc tca gaa ctg ctg tgg tca ctt ttc gtc cct      736
Ser Asp Ala Ser Trp Val Ser Glu Leu Leu Trp Ser Leu Phe Val Pro
202                 207                 212                 217

ttc acg gtg tat caa tgg ctt cgt cct gtt cat cgc caa cta ggg gaa      784
Phe Thr Val Tyr Gln Trp Leu Arg Pro Val His Arg Gln Leu Gly Glu
218                 223                 228                 233

gcg aat gag gag ttt gca ctc cgt gta caa cag ctg gtg gcc aag gaa      832
Ala Asn Glu Glu Phe Ala Leu Arg Val Gln Gln Leu Val Ala Lys Glu
234                 239                 244                 249

ttg ggc cag aca ggg aca cgg ctc act cca gct gac aaa gca gag cac      880
Leu Gly Gln Thr Gly Thr Arg Leu Thr Pro Ala Asp Lys Ala Glu His
250                 255                 260                 265

atg aag cga caa aga cac ccc aga ttg cgc ccc cag tca gcc cag tct      928
Met Lys Arg Gln Arg His Pro Arg Leu Arg Pro Gln Ser Ala Gln Ser
266                 271                 276                 281

tct ttc cct ccc tcc cct ggt cct tct cct gat gtg caa ctg gca act      976
Ser Phe Pro Pro Ser Pro Gly Pro Ser Pro Asp Val Gln Leu Ala Thr
282                 287                 292                 297

ctg gct cag aga gtc aag gaa gtt ttg ccc cat gtg cca ttg ggt gtc     1024
Leu Ala Gln Arg Val Lys Glu Val Leu Pro His Val Pro Leu Gly Val
298                 303                 308                 313

atc cag aga gac ctg gcc aag act ggc tgt gta gac ttg act atc act     1072
Ile Gln Arg Asp Leu Ala Lys Thr Gly Cys Val Asp Leu Thr Ile Thr
314                 319                 324                 329
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aat ctg ctt gag ggg gcc gta gct ttc atg cct gaa gac atc acc aag     1120
Asn Leu Leu Glu Gly Ala Val Ala Phe Met Pro Glu Asp Ile Thr Lys
330                 335                 340                 345

gga act cag tcc cta ccc aca gcc tct gcc tcc aag ttt ccc agc tct     1168
Gly Thr Gln Ser Leu Pro Thr Ala Ser Ala Ser Lys Phe Pro Ser Ser
346                 351                 356                 361

ggc ccg gtg acc cct cag cca aca gcc cta aca ttt gcc aag tct tcc     1216
Gly Pro Val Thr Pro Gln Pro Thr Ala Leu Thr Phe Ala Lys Ser Ser
362                 367                 372                 377

tgg gcc cgg cag gag agc ctg cag gag cgc aag caa gca cta tat gaa     1264
Trp Ala Arg Gln Glu Ser Leu Gln Glu Arg Lys Gln Ala Leu Tyr Glu
378                 383                 388                 393

tac gca aga agg aga ttc aca gag aga cga gcc cag gag gct gac tga     1312
Tyr Ala Arg Arg Arg Phe Thr Glu Arg Arg Ala Gln Glu Ala Asp  *
394                 399                 404                 409

gctcaaagga acaggatggc acccagagcc gcaggacgga gactgggggc agccctcacc   1372

caactcacaa caggctggat gggtgggtgg taaaaaggga aggatgaggc tcccccaatg   1432

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tattttaaaa agctttgtat ttcgtcatag aaaagttcat ccccccagaa tgaaaatgag     180

gacatttgag aaggtgattt aaggtgtgga catttgagaa ggtgtcctat caaattagta     240

aaccaaagga aaagtactga atagattaat ccaaaacact tacttttttt taaacgaaga     300

ggatttcacc ttgacagaaa aacaactttt attcaatatg tatttcctga aattaaagag     360

acaagtacag actgaaagga aaatagattc gtaaataagc tacgtcaact ctatcctgct     420

gaggatagct cagtgatgtt aaatccttta caaatccctg gttgtcttcc tacagacaag     480

actgcttttt gatgggactg atattaagag aaataggacc tttggggcat tcaactcctt     540
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gataaaactt aaaagtatcg gcatgagtgg cttaacagag gaaataaaga agttttcaac    600

taaatccaaa agtgcggtca ttttctttac tgctgttatt ttaaaaacct cttcataacc    660

attgaaaaag aatcgacaac tattttaaaa gattaaagaa aggcag   atg tct gca     715
                                                     Met Ser Ala
                                                       1

aat aat tcc cct cca tca gcc cag aag tct gta tta ccc aca gct att      763
Asn Asn Ser Pro Pro Ser Ala Gln Lys Ser Val Leu Pro Thr Ala Ile
  4                   9                  14                  19

cct gct gtg ctt cca gct gct tct ccg tgt tca agt cct aag acg gga      811
Pro Ala Val Leu Pro Ala Ala Ser Pro Cys Ser Ser Pro Lys Thr Gly
 20                  25                  30                  35

ctc tct gcc cga ctc tct aat gga agc ttc agt gca cca tca ctc acc      859
Leu Ser Ala Arg Leu Ser Asn Gly Ser Phe Ser Ala Pro Ser Leu Thr
 36                  41                  46                  51

aac tcc aga ggc tca gtg cat aca gtt tca ttt cta ctg caa att ggc      907
Asn Ser Arg Gly Ser Val His Thr Val Ser Phe Leu Leu Gln Ile Gly
 52                  57                  62                  67

ctc aca cgg gag agt gtt acc att gaa gcc cag gaa ctg tct tta tct      955
Leu Thr Arg Glu Ser Val Thr Ile Glu Ala Gln Glu Leu Ser Leu Ser
 68                  73                  78                  83

gct gtc aag gat ctt gtg tgc tcc ata gtt tat caa aag ttt cca gag     1003
Ala Val Lys Asp Leu Val Cys Ser Ile Val Tyr Gln Lys Phe Pro Glu
 84                  89                  94                  99

tgt gga ttc ttt ggc atg tat gac aaa att ctt ctc ttt cgc cat gac     1051
Cys Gly Phe Phe Gly Met Tyr Asp Lys Ile Leu Leu Phe Arg His Asp
100                 105                 110                 115

atg aac tca gaa aac att ttg cag ctg att acc tca gca gat gaa ata     1099
Met Asn Ser Glu Asn Ile Leu Gln Leu Ile Thr Ser Ala Asp Glu Ile
116                 121                 126                 131

cat gaa gga gac cta gtg gaa gtg gtt ctt tca gct tta gcc aca gta     1147
His Glu Gly Asp Leu Val Glu Val Val Leu Ser Ala Leu Ala Thr Val
132                 137                 142                 147

gaa gac ttc cag att cgt cca cat act ctc tat gta cat tct tac aaa     1195
Glu Asp Phe Gln Ile Arg Pro His Thr Leu Tyr Val His Ser Tyr Lys
148                 153                 158                 163

gct cct act ttc tgt gat tac tgt ggt gag atg ctg tgg gga ttg gta     1243
Ala Pro Thr Phe Cys Asp Tyr Cys Gly Glu Met Leu Trp Gly Leu Val
164                 169                 174                 179

cgt caa gga ctg aaa tgt gaa ggc tgt gga tta aat tac cat aaa cga     1291
Arg Gln Gly Leu Lys Cys Glu Gly Cys Gly Leu Asn Tyr His Lys Arg
180                 185                 190                 195

tgt gcc ttc aag att cca aat aac tgt agt gga gta aga aag aga cgt     1339
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Cys Ala Phe Lys Ile Pro Asn Asn Cys Ser Gly Val Arg Lys Arg Arg
196                 201                 206                 211

ctg tca aat gta tct tta cca gga ccc ggc ctc tca gtt cca aga ccc     1387
Leu Ser Asn Val Ser Leu Pro Gly Pro Gly Leu Ser Val Pro Arg Pro
212                 217                 222                 227

cta cag cct gaa tat gta gcc ctt ccc agt gaa gag tca cat gtc cac     1435
Leu Gln Pro Glu Tyr Val Ala Leu Pro Ser Glu Glu Ser His Val His
228                 233                 238                 243

cag gaa cca agt aag aga att cct tct tgg agt ggt cgc cca atc tgg     1483
Gln Glu Pro Ser Lys Arg Ile Pro Ser Trp Ser Gly Arg Pro Ile Trp
244                 249                 254                 259

atg gaa aag atg gta atg tgc aga gtg aaa gtt cca cac aca ttt gct     1531
Met Glu Lys Met Val Met Cys Arg Val Lys Val Pro His Thr Phe Ala
260                 265                 270                 275

gtt cac tct tac acc cgt ccc acg ata tgt cag tac tgc aag cgg tta     1579
Val His Ser Tyr Thr Arg Pro Thr Ile Cys Gln Tyr Cys Lys Arg Leu
276                 281                 286                 291

ctg aaa ggc ctc ttt cgc caa gga atg cag tgt aaa gat tgc aaa ttc     1627
Leu Lys Gly Leu Phe Arg Gln Gly Met Gln Cys Lys Asp Cys Lys Phe
292                 297                 302                 307

aac tgc cat aaa cgc tgt gca tca aaa gta cca aga gac tgc ctt gga     1675
Asn Cys His Lys Arg Cys Ala Ser Lys Val Pro Arg Asp Cys Leu Gly
308                 313                 318                 323

gag gtt act ttc aat gga gaa cct tcc agt ctg gga aca gat aca gat     1723
Glu Val Thr Phe Asn Gly Glu Pro Ser Ser Leu Gly Thr Asp Thr Asp
324                 329                 334                 339

ata cca atg gat att gac aat aat gac ata aat agt gat agt agt cgg     1771
Ile Pro Met Asp Ile Asp Asn Asn Asp Ile Asn Ser Asp Ser Ser Arg
340                 345                 350                 355

ggt ttg gat gac aca gaa gag cca tca ccc cca gaa gat aag atg ttc     1819
Gly Leu Asp Asp Thr Glu Glu Pro Ser Pro Pro Glu Asp Lys Met Phe
356                 361                 366                 371

ttc ttg gat cca tct gat ctc gat gtg gaa aga gat gaa gaa gcc gtt     1867
Phe Leu Asp Pro Ser Asp Leu Asp Val Glu Arg Asp Glu Glu Ala Val
372                 377                 382                 387

aaa aca atc agt cca tca aca agc aat aat att ccg cta atg agg gtt     1915
Lys Thr Ile Ser Pro Ser Thr Ser Asn Asn Ile Pro Leu Met Arg Val
388                 393                 398                 403

gta caa tcc atc aag cac aca aag agg aag agc agc aca atg gtg aag     1963
Val Gln Ser Ile Lys His Thr Lys Arg Lys Ser Ser Thr Met Val Lys
404                 409                 414                 419

gaa ggg tgg atg gtc cat tac acc agc agg gat aac ctg aga aag agg     2011
Glu Gly Trp Met Val His Tyr Thr Ser Arg Asp Asn Leu Arg Lys Arg
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US 2006/0246520 A1

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420                 425                 430                 435

cat tat tgg aga ctt gac agc aaa tgt cta aca tta ttt cag aat gaa     2059
His Tyr Trp Arg Leu Asp Ser Lys Cys Leu Thr Leu Phe Gln Asn Glu
436                 441                 446                 451

tct gga tca aag tat tat aag gaa att cca ctt tca gaa att ctc cgc     2107
Ser Gly Ser Lys Tyr Tyr Lys Glu Ile Pro Leu Ser Glu Ile Leu Arg
452                 457                 462                 467

ata tct tca cca cga gat ttc aca aac att tca caa ggc agc aat cca     2155
Ile Ser Ser Pro Arg Asp Phe Thr Asn Ile Ser Gln Gly Ser Asn Pro
468                 473                 478                 483

cac tgt ttt gaa atc att act gat act atg gta tac ttc gtt ggt gag     2203
His Cys Phe Glu Ile Ile Thr Asp Thr Met Val Tyr Phe Val Gly Glu
484                 489                 494                 499

aac aat ggg gac agc tct cat aat cct gtt ctt gct gcc act gga gtt     2251
Asn Asn Gly Asp Ser Ser His Asn Pro Val Leu Ala Ala Thr Gly Val
500                 505                 510                 515

gga ctt gat gta gca cag agc tgg gaa aaa gca att cgc caa gcc ctc     2299
Gly Leu Asp Val Ala Gln Ser Trp Glu Lys Ala Ile Arg Gln Ala Leu
516                 521                 526                 531

atg cct gtt act cct caa gca agt gtt tgc act tct cca ggg caa ggg     2347
Met Pro Val Thr Pro Gln Ala Ser Val Cys Thr Ser Pro Gly Gln Gly
532                 537                 542                 547

aaa gat cac aaa gat ttg tct aca agt atc tct gta tct aat tgt cag     2395
Lys Asp His Lys Asp Leu Ser Thr Ser Ile Ser Val Ser Asn Cys Gln
548                 553                 558                 563

att cag gag aat gtg gat atc agt act gtt tac cag atc ttt gca gat     2443
Ile Gln Glu Asn Val Asp Ile Ser Thr Val Tyr Gln Ile Phe Ala Asp
564                 569                 574                 579

gag gtg ctt ggt tca ggc cag ttt ggc atc gtt tat gga gga aaa cat     2491
Glu Val Leu Gly Ser Gly Gln Phe Gly Ile Val Tyr Gly Gly Lys His
580                 585                 590                 595

aga aag act ggg agg gat gtg gct att aaa gta att gat aag atg aga     2539
Arg Lys Thr Gly Arg Asp Val Ala Ile Lys Val Ile Asp Lys Met Arg
596                 601                 606                 611

ttc ccc aca aaa caa gaa agt caa ctc cgt aat gaa gtg gct att tta     2587
Phe Pro Thr Lys Gln Glu Ser Gln Leu Arg Asn Glu Val Ala Ile Leu
612                 617                 622                 627

cag aat ttg cac cat cct ggg att gta aac ctg gaa tgt atg ttt gaa     2635
Gln Asn Leu His His Pro Gly Ile Val Asn Leu Glu Cys Met Phe Glu
628                 633                 638                 643

acc cca gaa cga gtc ttt gta gta atg gaa aag ctg cat gga gat atg     2683
Thr Pro Glu Arg Val Phe Val Val Met Glu Lys Leu His Gly Asp Met
644                 649                 654                 659
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ttg gaa atg att cta tcc agt gag aaa agt cgg ctt cca gaa cga att     2731
Leu Glu Met Ile Leu Ser Ser Glu Lys Ser Arg Leu Pro Glu Arg Ile
660                 665                 670                 675

act aaa ttc atg gtc aca cag ata ctt gtt gct ttg agg aat ctg cat     2779
Thr Lys Phe Met Val Thr Gln Ile Leu Val Ala Leu Arg Asn Leu His
676                 681                 686                 691

ttt aag aat att gtg cac tgt gat tta aag cca gaa aat gtg ctg ctt     2827
Phe Lys Asn Ile Val His Cys Asp Leu Lys Pro Glu Asn Val Leu Leu
692                 697                 702                 707

gca tca gca gag cca ttt cct cag gtg aag ctg tgt gac ttt gga ttt     2875
Ala Ser Ala Glu Pro Phe Pro Gln Val Lys Leu Cys Asp Phe Gly Phe
708                 713                 718                 723

gca cgc atc att ggt gaa aag tca ttc agg aga tct gtg gta gga act     2923
Ala Arg Ile Ile Gly Glu Lys Ser Phe Arg Arg Ser Val Val Gly Thr
724                 729                 734                 739

cca gca tac tta gcc cct gaa gtt ctc cgg agc aaa ggt tac aac cgt     2971
Pro Ala Tyr Leu Ala Pro Glu Val Leu Arg Ser Lys Gly Tyr Asn Arg
740                 745                 750                 755

tcc cta gat atg tgg tca gtg gga gtt atc atc tat gtg agc ctc agt     3019
Ser Leu Asp Met Trp Ser Val Gly Val Ile Ile Tyr Val Ser Leu Ser
756                 761                 766                 771

ggc aca ttt cct ttt aat gag gat gaa gat ata aat gac caa atc caa     3067
Gly Thr Phe Pro Phe Asn Glu Asp Glu Asp Ile Asn Asp Gln Ile Gln
772                 777                 782                 787

aat gct gca ttt atg tac cca cca aat cca tgg aga gaa att tct ggt     3115
Asn Ala Ala Phe Met Tyr Pro Pro Asn Pro Trp Arg Glu Ile Ser Gly
788                 793                 798                 803

gaa gca att gat ctg ata aac aat ctg ctt caa gtg aag atg aga aaa     3163
Glu Ala Ile Asp Leu Ile Asn Asn Leu Leu Gln Val Lys Met Arg Lys
804                 809                 814                 819

cgt tac agt gtt gac aaa tct ctt agt cat ccc tgg cta cag gac tat     3211
Arg Tyr Ser Val Asp Lys Ser Leu Ser His Pro Trp Leu Gln Asp Tyr
820                 825                 830                 835

cag act tgg ctt gac ctt aga gaa ttt gaa act cgc att gga gaa cgt     3259
Gln Thr Trp Leu Asp Leu Arg Glu Phe Glu Thr Arg Ile Gly Glu Arg
836                 841                 846                 851

tac att aca cat gaa agt gat gat gct cgc tgg gaa ata cat gca tac     3307
Tyr Ile Thr His Glu Ser Asp Asp Ala Arg Trp Glu Ile His Ala Tyr
852                 857                 862                 867

aca cat aac ctt gta tac cca aag cac ttc att atg gct cct aat cca     3355
Thr His Asn Leu Val Tyr Pro Lys His Phe Ile Met Ala Pro Asn Pro
868                 873                 878                 883
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Asp Asp Met Glu Glu Asp Pro  *
884                 889

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gctgcaaaga tatgaagaaa tatgataacg aataagtgac accagtactg tagttcataa   3529

tgagtaggta caggcgggaa actgaataat aagaagtcat aatggaatca aggtgaagct   3589

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                                                Met Thr Thr Ser
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Arg Cys Ser His Leu Pro Glu Val Leu Pro Asp Cys Thr Ser Ser Ala
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Ala Pro Val Val Lys Thr Val Glu Asp Cys Gly Ser Leu Val Asn Gly
 21                  26                  31                  36

cag ccg cag tat gtc atg caa gtt tca gcc aag gac ggg cag ctg ctg      440
Gln Pro Gln Tyr Val Met Gln Val Ser Ala Lys Asp Gly Gln Leu Leu
 37                  42                  47                  52

tca aca gta gtg cgg act ctt gcc acc cag agc ccc ttc aat gac cgg      488
Ser Thr Val Val Arg Thr Leu Ala Thr Gln Ser Pro Phe Asn Asp Arg
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ccg atg tgc agg atc tgc cac gag ggc agc agc caa gag gac ttg ctc      536
Pro Met Cys Arg Ile Cys His Glu Gly Ser Ser Gln Glu Asp Leu Leu
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tct cca tgt gaa tgt aca ggg acc ttg ggg aca att cat cgg agc tgc      584
Ser Pro Cys Glu Cys Thr Gly Thr Leu Gly Thr Ile His Arg Ser Cys
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Leu Glu His Trp Leu Ser Ser Ser Asn Thr Ser Tyr Cys Glu Leu Cys
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His Phe Arg Phe Ala Val Glu Arg Lys Pro Arg Pro Leu Val Glu Trp
117                 122                 127                 132

ctg aga aac cct ggc ccc cag cat gag aag cgg act ctg ttt ggc gac      728
Leu Arg Asn Pro Gly Pro Gln His Glu Lys Arg Thr Leu Phe Gly Asp
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Leu Cys Leu Arg Gly Ala Val Asp His Leu His Phe Ser Ser Arg Leu
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gaa gcc gtc gga ctg att gca ctc act gtc gca ctc ttc act att tac      872
Glu Ala Val Gly Leu Ile Ala Leu Thr Val Ala Leu Phe Thr Ile Tyr
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Glu Trp Arg Arg Thr Asn Gln Arg Val Ile Leu Leu Ile Pro Lys Ser
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gtc aat gta cct tct aac cag ccg tcc ttg ctg ggc ctc cat tcg gtc     1016
Val Asn Val Pro Ser Asn Gln Pro Ser Leu Leu Gly Leu His Ser Val
229                 234                 239                 244

aag agg aac tca aag gag aca gtt gtt tga t gtttgtatgg ttggttggtt     1067
Lys Arg Asn Ser Lys Glu Thr Val Val  *
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Phe Tyr Glu Glu Tyr Gln Thr Thr Leu Gly Ala Ser Ile Leu Ser Lys
33 38 43 48

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Glu Ala Leu Asp Ile Trp Arg Gly Asp Val Leu Ala Lys Ile Val Pro
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113 118 123 128

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Ala Asp Arg Lys Tyr Gln Ser Ile Leu Glu Asn His Leu Thr Glu Ser
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Ile Leu Cys Ala Ile Cys Pro Asn Pro Lys Leu Val Ile Thr Gly Gly
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Thr Ser Thr Val Val Cys Val Trp Glu Met Gly Thr Ser Lys Glu Lys
 29                  34                  39                  44

gcc aag acc gtc acc ctc aaa cag gcc tta ctg ggc cac act gat acc      793
Ala Lys Thr Val Thr Leu Lys Gln Ala Leu Leu Gly His Thr Asp Thr
 45                  50                  55                  60

gtc acc tgc gcc aca gca tca tta gcc tat cac ata att gtc agt ggg      841
Val Thr Cys Ala Thr Ala Ser Leu Ala Tyr His Ile Ile Val Ser Gly
 61                  66                  71                  76

tcc cgt gat cga acc tgt atc att tgg gat ttg aac aaa ctg tca ttt      889
Ser Arg Asp Arg Thr Cys Ile Ile Trp Asp Leu Asn Lys Leu Ser Phe
 77                  82                  87                  92

cta acc cag ctt cga ggg cat cga gct cca gtt tct gct ctt tgt atc      937
Leu Thr Gln Leu Arg Gly His Arg Ala Pro Val Ser Ala Leu Cys Ile
 93                  98                 103                 108

aat gaa tta aca ggg gac att gtg tcc tgc gct ggc aca tat atc cat      985
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Val Trp Ser Ile Asn Gly Asn Pro Ile Val Ser Val Asn Thr Phe Thr
125                 130                 135                 140

ggt agg agc cag cag atc atc tgc tgc tgc atg tcg gag atg aac gaa     1081
Gly Arg Ser Gln Gln Ile Ile Cys Cys Cys Met Ser Glu Met Asn Glu
141                 146                 151                 156

tgg gac acg cag aac gtc ata gtg aca gga cac tca gat gga gtg gtt     1129
Trp Asp Thr Gln Asn Val Ile Val Thr Gly His Ser Asp Gly Val Val
157                 162                 167                 172

cgg ttt tgg aga atg gaa ttt ttg caa gtt cct gaa aca cca gct cct     1177
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205                 210                 215                 220

gag cag agc atc agc cag gac cct aag gac act cca agc caa ccc agc     1321
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237                 242                 247                 252

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269                 274                 279                 284

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Asn Pro Ile Glu Val Arg Asn Tyr Ser Arg Leu Lys Pro Gly Tyr Arg
301                 306                 311                 316

tgg gaa cgg cag ctg gtg ttc agg agt aag ctg act atg cac aca gcc     1609
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317                 322                 327                 332

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Phe Asp Arg Lys Asp Asn Ala His Pro Ala Glu Val Thr Ala Leu Gly
333                 338                 343                 348

atc tcc aag gat cac agt agg atc ctc gtt ggt gac agt cga ggc cga     1705
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349                 354                 359                 364

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His Trp Val Lys Asp Glu Gly Gly Asp Ser Cys Ser Gly Cys Ser Val
381                 386                 391                 396

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Arg Phe Ser Leu Thr Glu Arg Arg His His Cys Arg Asn Cys Gly Gln
397                 402                 407                 412
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429 434 439 444

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acacttccat ttctaaaagt tcaaatatac ttgttaataa aaggattatc ggcattaata 3914

ctttaattta aagaaaagtt gtgttctgtt ttcctttctg tgtcttactc cccccacact 3974

ctccctcccc catcaccatc ttcaattcta ataaataatg ctgatgttca acagttgcag 4034

aaattgtgct attatgtaac tgtgggcctt gcccctgtct ggccctctag atgatttgta 4094

gcagtgttat tctacacttt ttaaaagaag cgtcctcctt ttgtccatga atcatgttta 4154

ccccataccc agtggcagag gtgttcttta aagacttgaa tatatgaatg tgtgtgtgta 4214

gttacttaaa ggttattcct ctttgtaata ggaaactata tgggatgaac acttttaaac 4274

tttccgacac aacttccatt actaactttc taacagaact tccataacta gaaggtggaa 4334

accaaaaccc tcatggtagt atttcctctg gcagctggtg ctgtgggcaa ctgttttgtt 4394

caatcgggtt tcttttcttt ttgcctctaa tgcagaaatc aacagaatca ctcacacata 4454

caagtacact cacatacata aactaattat ttctctggat atctttctgt gttccatgta 4514

aatttattta ccaacatcta ttgtcaacat gtacatctac cttagtatgg tctgcattct 4574

ttttctgaga gtacctcata gggctcctgc ctgatctttg tagtttgttc attcatccat 4634

ccacctgttc atttgttcat ccatgtattc taacatttct atgtagtgtg caactctaat 4694

gtcatgcttt tgaagaagag aatagctgcc catagcagcc atccgtctgg ataatagcaa 4754

aacactctag ataagttatt ttgcactttc ttatgtataa agttggtaga aacttatttt 4814

tgctttgtat catttaaata cattttgttt tggtaaatga actgtgtata aaatatttat 4874

gccgttaaaa ctgtttttag aaagtatttt taatttcagc aagtttggtt acttgttgca 4934

tgactcttaa cacagctgac tttttgtgtc agtgcaatgt atatttttg tcctgttatt 4994

aacttgtaag ccctagtaat ggccaattat ttgtacagca acagaagtaa attgaagata 5054

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ctggctaaga ctggattgat tgtggacttt tatactatat tgcagaaacc aatatctgtt   5114

tcttggtggt tatgtaaaag acctgaagaa ttactatcta gtgtgcagtc tgtgatatct   5174

gaatgttcat tgtatatttg tctctgatgc aaaaaggtag agtaacacaa ttacaataca   5234

tgattaaatg caatagtcca ggtacttaag taatttttt ttcatttcaa ataaatacct   5294

atttaccacc aaaaaaaaaa at                                           5316
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<210> 109
<211> 1263
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<213> Homo sapiens

<220>
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<222> (207)..(1253)

<400> 109

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gaaaaggcgc tccgtcatgg ggatccagac ggtaagaccc tcattcagta tcctccactg    120

ggggacccct ccccatctgg ttctggccac tcagcatttg gccctcgagg ccaagaattc    180

ggcacgagag gaaaaggcgc tccgtc atg ggg atc cag acg agc ccc gtc ctg      233
                                Met Gly Ile Gln Thr Ser Pro Val Leu
                                  1               5

ctg gcc tcc ctg ggg gtg ggg ctg gtc act ctg ctc ggc ctg gct gtg      281
Leu Ala Ser Leu Gly Val Gly Leu Val Thr Leu Leu Gly Leu Ala Val
 10                  15                  20                  25

ggc tcc tac ttg gtt cgg agg tcc cgc cgg cct cag gtc act ctc ctg      329
Gly Ser Tyr Leu Val Arg Arg Ser Arg Arg Pro Gln Val Thr Leu Leu
 26                  31                  36                  41

ggt cgg ctt gtc agg tgg tgg agg aaa agg cgc tcc gtc atg ggg atc      377
Gly Arg Leu Val Arg Trp Trp Arg Lys Arg Arg Ser Val Met Gly Ile
 42                  47                  52                  57

cag acg agc ccc gtc ctg ctg gcc tcc ctg ggg gtg ggg ctg gtc act      425
Gln Thr Ser Pro Val Leu Leu Ala Ser Leu Gly Val Gly Leu Val Thr
 58                  63                  68                  73

ctg ctc ggc ctg gct gtg ggc tcc tac ttg gtt cgg agg tcc cgc cgg      473
Leu Leu Gly Leu Ala Val Gly Ser Tyr Leu Val Arg Arg Ser Arg Arg
 74                  79                  84                  89

cct cag gtc act ctc ctg gac ccc aat gaa aag tac ctg cta cga ctg      521
Pro Gln Val Thr Leu Leu Asp Pro Asn Glu Lys Tyr Leu Leu Arg Leu
 90                  95                 100                 105
```

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cta gac aag acg act gtg agc cac aac acc aag agg ttc cgc ttt gcc      569
Leu Asp Lys Thr Thr Val Ser His Asn Thr Lys Arg Phe Arg Phe Ala
106                 111                 116                 121

ctg ccc acc gcc cac cac act ctg ggg ctg cct gtg ggc aaa cat atc      617
Leu Pro Thr Ala His His Thr Leu Gly Leu Pro Val Gly Lys His Ile
122                 127                 132                 137

tac ctc tcc acc cga att gat ggc agc ctg gtc atc agg cca tac act      665
Tyr Leu Ser Thr Arg Ile Asp Gly Ser Leu Val Ile Arg Pro Tyr Thr
138                 143                 148                 153

cct gtc acc agt gat gag gat caa ggc tat gtg gat ctt gtc atc aag      713
Pro Val Thr Ser Asp Glu Asp Gln Gly Tyr Val Asp Leu Val Ile Lys
154                 159                 164                 169

gtc tac ctg aag ggt gtg cac ccc aaa ttt cct gag gga ggg aag atg      761
Val Tyr Leu Lys Gly Val His Pro Lys Phe Pro Glu Gly Gly Lys Met
170                 175                 180                 185

tct cag tac ctg gat agc ctg aag gtt ggg gat gtg gtg gag ttt cgg      809
Ser Gln Tyr Leu Asp Ser Leu Lys Val Gly Asp Val Val Glu Phe Arg
186                 191                 196                 201

ggg cca agc ggg ttg ctc act tac act gga aaa ggg cat ttt aac att      857
Gly Pro Ser Gly Leu Leu Thr Tyr Thr Gly Lys Gly His Phe Asn Ile
202                 207                 212                 217

cag ccc aac aag aaa tct cca cca gaa ccc cga gtg gcg aag aaa ctg      905
Gln Pro Asn Lys Lys Ser Pro Pro Glu Pro Arg Val Ala Lys Lys Leu
218                 223                 228                 233

gga atg att gcc ggc ggg aca gga atc acc cca atg cta cag ctg atc      953
Gly Met Ile Ala Gly Gly Thr Gly Ile Thr Pro Met Leu Gln Leu Ile
234                 239                 244                 249

cgg gcc atc ctg aaa gtc cct gaa gat cca acc cag tgc ttt ctg ctt     1001
Arg Ala Ile Leu Lys Val Pro Glu Asp Pro Thr Gln Cys Phe Leu Leu
250                 255                 260                 265

ttt gcc aac cag aca gaa aag gat atc atc ttg cgg gag gac tta gag     1049
Phe Ala Asn Gln Thr Glu Lys Asp Ile Ile Leu Arg Glu Asp Leu Glu
266                 271                 276                 281

gaa ctg cag gcc cgc tat ccc aat cgc ttt aag ctc tgg ttc act ctg     1097
Glu Leu Gln Ala Arg Tyr Pro Asn Arg Phe Lys Leu Trp Phe Thr Leu
282                 287                 292                 297

gat cat ccc cca aaa ggt atc ctt ccc att ttt gga cat ccc act atc     1145
Asp His Pro Pro Lys Gly Ile Leu Pro Ile Phe Gly His Pro Thr Ile
298                 303                 308                 313

ccc tca tcg tca aaa tca aag cct tgc ccc ttt gtg aat tct ggc ttc     1193
Pro Ser Ser Ser Lys Ser Lys Pro Cys Pro Phe Val Asn Ser Gly Phe
314                 319                 324                 329
```

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att gaa atc aac ctt gcc tca cac tgc caa ctc gga agt ttg agt gca     1241
Ile Glu Ile Asn Leu Ala Ser His Cys Gln Leu Gly Ser Leu Ser Ala
330                 335                 340                 345

cag acc cag tga aaaaaaaaaa                                      1263
Gln Thr Gln  *
346
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<210> 110
<211> 2075
<212> DNA
<213> Homo sapiens

<220>
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<222> (147)..(2075)

<400> 110

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ggtgcagacg ggatctgccg gatccccagg ctcgtatttt tatccaaaag aaggacctgg     60

aggaggatga gagcgttact gctgcacacc taaagtcaag ggggagaagc ccgaggaaga    120

ttgaccagtt ttgtaattct agcaac atg gtc cat gga tca gtg aca ttc agg      173
                              Met Val His Gly Ser Val Thr Phe Arg
                                1               5

gat gtg gcc att gac ttc tct cag gag gag tgg gag tgc ctg cag cct      221
Asp Val Ala Ile Asp Phe Ser Gln Glu Glu Trp Glu Cys Leu Gln Pro
 10                  15                  20                  25

gat cag agg acc ttg tac agg gat gtg atg ttg gag aac tac agc cac      269
Asp Gln Arg Thr Leu Tyr Arg Asp Val Met Leu Glu Asn Tyr Ser His
 26                  31                  36                  41

ctg atc tca ctg gca gga agt tcc att tct aaa cca gat gta att acg      317
Leu Ile Ser Leu Ala Gly Ser Ser Ile Ser Lys Pro Asp Val Ile Thr
 42                  47                  52                  57

tta cta gag caa gag aaa gag ccc tgg atg gtt gta agg aaa gaa aca      365
Leu Leu Glu Gln Glu Lys Glu Pro Trp Met Val Val Arg Lys Glu Thr
 58                  63                  68                  73

agc aga cgg tat cca gat ttg gag tta aaa tat gga cct gag aaa gta      413
Ser Arg Arg Tyr Pro Asp Leu Glu Leu Lys Tyr Gly Pro Glu Lys Val
 74                  79                  84                  89

tct cca gaa aat gat acc tct gaa gta aat tta ccc aaa cag gtt ata      461
Ser Pro Glu Asn Asp Thr Ser Glu Val Asn Leu Pro Lys Gln Val Ile
 90                  95                 100                 105

aag caa ata agt aca act ctt ggc att gag gcc ttt tat ttt aga aat      509
Lys Gln Ile Ser Thr Thr Leu Gly Ile Glu Ala Phe Tyr Phe Arg Asn
106                 111                 116                 121
```

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gac tca gaa tat aga caa ttt gag gga cta cag gga tat caa gaa gga      557
Asp Ser Glu Tyr Arg Gln Phe Glu Gly Leu Gln Gly Tyr Gln Glu Gly
122                 127                 132                 137

aat atc aat caa aag atg atc agc tat gaa aaa ctg cct act cat act      605
Asn Ile Asn Gln Lys Met Ile Ser Tyr Glu Lys Leu Pro Thr His Thr
138                 143                 148                 153

cct cat gct tct ctt att tgc aat aca cat aaa ccg tat gaa tgt aag      653
Pro His Ala Ser Leu Ile Cys Asn Thr His Lys Pro Tyr Glu Cys Lys
154                 159                 164                 169

gaa tgt ggg aaa tac ttt agt cgt agt gca aat ctt att cag cat cag      701
Glu Cys Gly Lys Tyr Phe Ser Arg Ser Ala Asn Leu Ile Gln His Gln
170                 175                 180                 185

agt att cat act gga gag aaa ccc ttt gaa tgt aag gag tgt ggg aaa      749
Ser Ile His Thr Gly Glu Lys Pro Phe Glu Cys Lys Glu Cys Gly Lys
186                 191                 196                 201

gcc ttt cga ctt cac ata caa ttt act cga cat cag aaa ttt cat act      797
Ala Phe Arg Leu His Ile Gln Phe Thr Arg His Gln Lys Phe His Thr
202                 207                 212                 217

ggt gag aaa cct ttt gaa tgt aac gaa tgt gga aag gcc ttt agt ctt      845
Gly Glu Lys Pro Phe Glu Cys Asn Glu Cys Gly Lys Ala Phe Ser Leu
218                 223                 228                 233

ctt acc ctg ctt aat cgc cat aag aac att cac aca ggt gag aaa ctg      893
Leu Thr Leu Leu Asn Arg His Lys Asn Ile His Thr Gly Glu Lys Leu
234                 239                 244                 249

ttt gaa tgt aag gaa tgt ggg aag tcc ttt aat cgt agc tca aac ctt      941
Phe Glu Cys Lys Glu Cys Gly Lys Ser Phe Asn Arg Ser Ser Asn Leu
250                 255                 260                 265

gtt caa cat cag agt att cat tct ggt gta aaa cca tat gaa tgt aag      989
Val Gln His Gln Ser Ile His Ser Gly Val Lys Pro Tyr Glu Cys Lys
266                 271                 276                 281

gag tgt ggg aaa ggc ttt aat cgt ggt gca cac ctt att cag cat cag     1037
Glu Cys Gly Lys Gly Phe Asn Arg Gly Ala His Leu Ile Gln His Gln
282                 287                 292                 297

aaa att cat tcc aat gag aaa ccc ttt gta tgt aag gaa tgt ggg atg     1085
Lys Ile His Ser Asn Glu Lys Pro Phe Val Cys Lys Glu Cys Gly Met
298                 303                 308                 313

gcc ttt cga tat cat tac caa ctt att gaa cat tgc caa att cat act     1133
Ala Phe Arg Tyr His Tyr Gln Leu Ile Glu His Cys Gln Ile His Thr
314                 319                 324                 329

ggt gag aaa ccc ttt gaa tgt aaa gaa tgt gga aag gcg ttt act ctt     1181
Gly Glu Lys Pro Phe Glu Cys Lys Glu Cys Gly Lys Ala Phe Thr Leu
330                 335                 340                 345
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ctg aca aag ctt gtt cga cat cag aag att cat act ggt gag aaa ccc     1229
Leu Thr Lys Leu Val Arg His Gln Lys Ile His Thr Gly Glu Lys Pro
346                 351                 356                 361

ttt gaa tgc agg gaa tgt ggg aag gcc ttt agt ctt ctc aac cag ctt     1277
Phe Glu Cys Arg Glu Cys Gly Lys Ala Phe Ser Leu Leu Asn Gln Leu
362                 367                 372                 377

aat cgc cat aag aac att cac aca ggt gaa aaa ccg ttt gaa tgt aag     1325
Asn Arg His Lys Asn Ile His Thr Gly Glu Lys Pro Phe Glu Cys Lys
378                 383                 388                 393

gaa tgt ggg aag tcc ttt aat cgt agc tca aac ctt gtt caa cat cag     1373
Glu Cys Gly Lys Ser Phe Asn Arg Ser Ser Asn Leu Val Gln His Gln
394                 399                 404                 409

agt att cat gct ggt ata aaa cca tat gaa tgt aag gag tgt ggg aaa     1421
Ser Ile His Ala Gly Ile Lys Pro Tyr Glu Cys Lys Glu Cys Gly Lys
410                 415                 420                 425

ggc ttt aat cgt ggt gca cac ctt att cag cat cag aaa att cat tcc     1469
Gly Phe Asn Arg Gly Ala His Leu Ile Gln His Gln Lys Ile His Ser
426                 431                 436                 441

aat gag aaa cct ttt gta tgt agg gaa tgt gag atg gcc ttt aga tat     1517
Asn Glu Lys Pro Phe Val Cys Arg Glu Cys Glu Met Ala Phe Arg Tyr
442                 447                 452                 457

cat tgc caa ctt att gaa cat tct cga att cat act ggt gac aag cca     1565
His Cys Gln Leu Ile Glu His Ser Arg Ile His Thr Gly Asp Lys Pro
458                 463                 468                 473

ttt gaa tgt caa gac tgt ggg aag gcc ttc aat cgt ggc tca agc ctt     1613
Phe Glu Cys Gln Asp Cys Gly Lys Ala Phe Asn Arg Gly Ser Ser Leu
474                 479                 484                 489

gtt caa cat cag agt att cac act ggt gag aag ccc tat gaa tgt aag     1661
Val Gln His Gln Ser Ile His Thr Gly Glu Lys Pro Tyr Glu Cys Lys
490                 495                 500                 505

gag tgt ggg aag gct ttt aga ctt tac cta caa ctt tcc caa cat cag     1709
Glu Cys Gly Lys Ala Phe Arg Leu Tyr Leu Gln Leu Ser Gln His Gln
506                 511                 516                 521

aaa act cac aca ggt gaa aaa cca ttt gaa tgt aag gaa tgt ggg aaa     1757
Lys Thr His Thr Gly Glu Lys Pro Phe Glu Cys Lys Glu Cys Gly Lys
522                 527                 532                 537

ttc ttt cgt cgt ggt tca aat ctt aat caa cat cga agt att cat act     1805
Phe Phe Arg Arg Gly Ser Asn Leu Asn Gln His Arg Ser Ile His Thr
538                 543                 548                 553

gga aag aaa ccc ttt gaa tgt aag gaa tgt ggg aaa gcc ttt cga ctt     1853
Gly Lys Lys Pro Phe Glu Cys Lys Glu Cys Gly Lys Ala Phe Arg Leu
554                 559                 564                 569

cat atg cac ctt att cga cat cag aaa ttg cat act ggt gag aaa ccc     1901
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His Met His Leu Ile Arg His Gln Lys Leu His Thr Gly Glu Lys Pro
570                 575                 580                 585

ttt gaa tgt aag gag tgt ggg aaa gcc ttt cga ctt cat atg caa ctt     1949
Phe Glu Cys Lys Glu Cys Gly Lys Ala Phe Arg Leu His Met Gln Leu
586                 591                 596                 601

att cga cat cag aaa ttg cat act ggt gag aaa ccc ttt gaa tgt aag     1997
Ile Arg His Gln Lys Leu His Thr Gly Glu Lys Pro Phe Glu Cys Lys
602                 607                 612                 617

gaa tgt gga aag gtt ttt agt ctt ccc acc cag ctt aat cgc cat aag     2045
Glu Cys Gly Lys Val Phe Ser Leu Pro Thr Gln Leu Asn Arg His Lys
618                 623                 628                 633

aac att cac aca ggt gag aag gca tct tga                            2075
Asn Ile His Thr Gly Glu Lys Ala Ser  *
634                 639
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<212> DNA
<213> Homo sapiens

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<222> (238)..(2985)

<400> 111

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gcctccctgg aactggttca agaggggggag agaagagttt gcttgtgggt gtttcccttg    120

tcttatctgt gagtgagcat atgctagggt tgaatttatt ttgacgcttt cattttaaat    180

ttggaaccaa agtaagagtt taaagtgcaa cagaagagag tctgctgaac tttagac   237

atg agg gat cca ggg agg aag agc ctg gcc caa cta gag aat ctg tgc      285
Met Arg Asp Pro Gly Arg Lys Ser Leu Ala Gln Leu Glu Asn Leu Cys
  1               5                  10                  15

aaa cag ctg tat gaa acc aca gac aca acc act cga ctc cag gca gag      333
Lys Gln Leu Tyr Glu Thr Thr Asp Thr Thr Thr Arg Leu Gln Ala Glu
 17                  22                  27                  32

aaa gcc ttg gtt gaa ttt acc aac agc cct gat tgc ctg agc aag tgc      381
Lys Ala Leu Val Glu Phe Thr Asn Ser Pro Asp Cys Leu Ser Lys Cys
 33                  38                  43                  48

cag cta ctc ctc gaa aga gga agt tcc tct tac tcc cag tta ctg gca      429
Gln Leu Leu Leu Glu Arg Gly Ser Ser Ser Tyr Ser Gln Leu Leu Ala
 49                  54                  59                  64
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gct aca tgc ctt acc aag ctt gta tca cgc aca aac aac ccc cta cca      477
Ala Thr Cys Leu Thr Lys Leu Val Ser Arg Thr Asn Asn Pro Leu Pro
 65                  70                  75                  80

ttg gaa cag cga ata gat att cgg aac tat gtg ctc aac tac ctt gcc      525
Leu Glu Gln Arg Ile Asp Ile Arg Asn Tyr Val Leu Asn Tyr Leu Ala
 81                  86                  91                  96

act cgg ccg aag ttg gct act ttc gtg aca caa gca ctt att cag tta      573
Thr Arg Pro Lys Leu Ala Thr Phe Val Thr Gln Ala Leu Ile Gln Leu
 97                 102                 107                 112

tat gcc aga atc aca aaa ctg ggc tgg ttt gac tgt cag aag gat gac      621
Tyr Ala Arg Ile Thr Lys Leu Gly Trp Phe Asp Cys Gln Lys Asp Asp
113                 118                 123                 128

tat gtc ttc aga aat gca atc aca gac gtc aca agg ttt tta cag gat      669
Tyr Val Phe Arg Asn Ala Ile Thr Asp Val Thr Arg Phe Leu Gln Asp
129                 134                 139                 144

agt gtt gaa tac tgc atc att ggt gtc aca att tta tct cag cta acc      717
Ser Val Glu Tyr Cys Ile Ile Gly Val Thr Ile Leu Ser Gln Leu Thr
145                 150                 155                 160

aat gaa att aat caa gta agt gct aca gcc ttc ctc att gaa gca gac      765
Asn Glu Ile Asn Gln Val Ser Ala Thr Ala Phe Leu Ile Glu Ala Asp
161                 166                 171                 176

acc acc cat cct tta acc aag cac aga aaa ata gcc tct tct ttt cgc      813
Thr Thr His Pro Leu Thr Lys His Arg Lys Ile Ala Ser Ser Phe Arg
177                 182                 187                 192

gat tca tca tta ttt gat atc ttc aca ctt tcc tgc aat tta cta aaa      861
Asp Ser Ser Leu Phe Asp Ile Phe Thr Leu Ser Cys Asn Leu Leu Lys
193                 198                 203                 208

cag gct tca gga aag aat cta aac ttg aat gat gaa agt cag cat ggc      909
Gln Ala Ser Gly Lys Asn Leu Asn Leu Asn Asp Glu Ser Gln His Gly
209                 214                 219                 224

ttg ctc atg caa ctg ctc aag ctc act cat aac tgc ctc aac ttt gac      957
Leu Leu Met Gln Leu Leu Lys Leu Thr His Asn Cys Leu Asn Phe Asp
225                 230                 235                 240

ttc atc ggc act tcc act gat gag tcc tca gac gac ctg tgt aca gtg     1005
Phe Ile Gly Thr Ser Thr Asp Glu Ser Ser Asp Asp Leu Cys Thr Val
241                 246                 251                 256

cag att ccc acc agc tgg aga tca gcc ttc tta gat tct tca acc ttg     1053
Gln Ile Pro Thr Ser Trp Arg Ser Ala Phe Leu Asp Ser Ser Thr Leu
257                 262                 267                 272

cag ctg tcc acc att ggg cgt tgt gaa tat gag aag acg tgt gca ctc     1101
Gln Leu Ser Thr Ile Gly Arg Cys Glu Tyr Glu Lys Thr Cys Ala Leu
273                 278                 283                 288

ctc gtg cag ttg ttt gac cag tcg gcc cag tcg tac cag gag ctg cta     1149
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Leu Val Gln Leu Phe Asp Gln Ser Ala Gln Ser Tyr Gln Glu Leu Leu
289                 294                 299                 304

cag agc gcc agc gca agc cca atg gac att gca gtg cag gag gga agg     1197
Gln Ser Ala Ser Ala Ser Pro Met Asp Ile Ala Val Gln Glu Gly Arg
305                 310                 315                 320

ctg aca tgg ctg gtt tac att att gga gca gtg atc ggt ggc cgg gtt     1245
Leu Thr Trp Leu Val Tyr Ile Ile Gly Ala Val Ile Gly Gly Arg Val
321                 326                 331                 336

tct ttt gcc agc act gat gag caa gac gcc atg gat ggt gag ctt gtc     1293
Ser Phe Ala Ser Thr Asp Glu Gln Asp Ala Met Asp Gly Glu Leu Val
337                 342                 347                 352

tgt cgg gtg ctc cag ctg atg aac cta aca gat tct cgt ttg gcc cag     1341
Cys Arg Val Leu Gln Leu Met Asn Leu Thr Asp Ser Arg Leu Ala Gln
353                 358                 363                 368

gcg ggt aat gag aag cta gag ttg gcc atg ctg agc ttt ttt gaa cag     1389
Ala Gly Asn Glu Lys Leu Glu Leu Ala Met Leu Ser Phe Phe Glu Gln
369                 374                 379                 384

ttt cgt aag atc tac att ggg gac caa gtg cag aaa tcc tct aag ctg     1437
Phe Arg Lys Ile Tyr Ile Gly Asp Gln Val Gln Lys Ser Ser Lys Leu
385                 390                 395                 400

tac cgc cga ctc tca gaa gtt ctg ggc ttg aat gat gag acc atg gtc     1485
Tyr Arg Arg Leu Ser Glu Val Leu Gly Leu Asn Asp Glu Thr Met Val
401                 406                 411                 416

cta agc gtc ttc ata gga aaa atc atc acc aac ttg aag tac tgg ggc     1533
Leu Ser Val Phe Ile Gly Lys Ile Ile Thr Asn Leu Lys Tyr Trp Gly
417                 422                 427                 432

cgt tgt gaa cca atc acc tcc aag aca cta cag ctt ctc aat gac ctc     1581
Arg Cys Glu Pro Ile Thr Ser Lys Thr Leu Gln Leu Leu Asn Asp Leu
433                 438                 443                 448

tcc att ggg tac agt agc gta agg aag cta gtg aag ctt agt gcg gta     1629
Ser Ile Gly Tyr Ser Ser Val Arg Lys Leu Val Lys Leu Ser Ala Val
449                 454                 459                 464

cag ttc atg ctg aac aat cac acg agc gag cac ttt tca ttt ttg ggt     1677
Gln Phe Met Leu Asn Asn His Thr Ser Glu His Phe Ser Phe Leu Gly
465                 470                 475                 480

att aac aat cag tcc aac ctg aca gac atg cgg tgt cgg act acc ttc     1725
Ile Asn Asn Gln Ser Asn Leu Thr Asp Met Arg Cys Arg Thr Thr Phe
481                 486                 491                 496

tac aca gca ctt ggg cgt ctc ctc atg gtg gat tta gga gag gat gaa     1773
Tyr Thr Ala Leu Gly Arg Leu Leu Met Val Asp Leu Gly Glu Asp Glu
497                 502                 507                 512

gat cag tat gag cag ttc atg ctg cca ctc aca gca gca ttt gag gct     1821
Asp Gln Tyr Glu Gln Phe Met Leu Pro Leu Thr Ala Ala Phe Glu Ala
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Application No. 10/576,360

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513                 518                 523                 528

gtg gcc cag atg ttt agc acc aat agt ttc aac gag cag gag gca aag     1869
Val Ala Gln Met Phe Ser Thr Asn Ser Phe Asn Glu Gln Glu Ala Lys
529                 534                 539                 544

cga act cta gtt ggc cta gta aga gac ctg aga ggg atc gct ttc gct     1917
Arg Thr Leu Val Gly Leu Val Arg Asp Leu Arg Gly Ile Ala Phe Ala
545                 550                 555                 560

ttc aat gcc aag acc agc ttc atg atg ctc ttt gaa tgg ata tat cca     1965
Phe Asn Ala Lys Thr Ser Phe Met Met Leu Phe Glu Trp Ile Tyr Pro
561                 566                 571                 576

tcc tat atg cca att ctc caa cgg gca att gag ctc tgg tac cat gat     2013
Ser Tyr Met Pro Ile Leu Gln Arg Ala Ile Glu Leu Trp Tyr His Asp
577                 582                 587                 592

cca gcc tgt act aca cct gta ctc aag ttg atg gct gaa ttg gtt cat     2061
Pro Ala Cys Thr Thr Pro Val Leu Lys Leu Met Ala Glu Leu Val His
593                 598                 603                 608

aat agg tcc cag cga ctc cag ttt gat gtc tct tcc ccc aat ggc atc     2109
Asn Arg Ser Gln Arg Leu Gln Phe Asp Val Ser Ser Pro Asn Gly Ile
609                 614                 619                 624

tta ctc ttc cga gaa acc agc aag atg ata aca atg tat ggc aat cgc     2157
Leu Leu Phe Arg Glu Thr Ser Lys Met Ile Thr Met Tyr Gly Asn Arg
625                 630                 635                 640

atc ctg aca cta gga gag gtc cca aag gat cag gtc tat gct ctg aag     2205
Ile Leu Thr Leu Gly Glu Val Pro Lys Asp Gln Val Tyr Ala Leu Lys
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ctc aag ggc atc tcc atc tgc ttc tcc atg ctg aag gct gct ctc agt     2253
Leu Lys Gly Ile Ser Ile Cys Phe Ser Met Leu Lys Ala Ala Leu Ser
657                 662                 667                 672

ggg agt tac gtc aat ttc gga gtc ttt cgt ctc tat gga gac gat gcc     2301
Gly Ser Tyr Val Asn Phe Gly Val Phe Arg Leu Tyr Gly Asp Asp Ala
673                 678                 683                 688

ctg gac aat gct ctg cag acc ttc atc aag ctg ctc ctc tct att cct     2349
Leu Asp Asn Ala Leu Gln Thr Phe Ile Lys Leu Leu Leu Ser Ile Pro
689                 694                 699                 704

cac agt gat ctc ttg gat tac ccc aag ctc agc cag tct tat tat tca     2397
His Ser Asp Leu Leu Asp Tyr Pro Lys Leu Ser Gln Ser Tyr Tyr Ser
705                 710                 715                 720

cta ctg gaa gtc ctg acc cag gac cat atg aac ttt att gca agc ctg     2445
Leu Leu Glu Val Leu Thr Gln Asp His Met Asn Phe Ile Ala Ser Leu
721                 726                 731                 736

gaa cct cac gtc atc atg tat att ctc tct tcc att tct gaa gga ctt     2493
Glu Pro His Val Ile Met Tyr Ile Leu Ser Ser Ile Ser Glu Gly Leu
737                 742                 747                 752
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Thr Ala Leu Asp Thr Met Val Cys Thr Gly Cys Cys Ser Cys Leu Asp
753                 758                 763                 768

cac att gtg aca tac ctc ttc aag cag ctg tca cgt agc acc aag aag     2589
His Ile Val Thr Tyr Leu Phe Lys Gln Leu Ser Arg Ser Thr Lys Lys
769                 774                 779                 784

agg acc aca ccc ctg aac cag gag agc gac cgc ttt ctg cac atc atg     2637
Arg Thr Thr Pro Leu Asn Gln Glu Ser Asp Arg Phe Leu His Ile Met
785                 790                 795                 800

cag cag cat cca gag atg atc cag cag atg ctg tcc acg gtg ctg aac     2685
Gln Gln His Pro Glu Met Ile Gln Gln Met Leu Ser Thr Val Leu Asn
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atc atc atc ttt gaa gac tgt agg aac cag tgg tct atg tcc cga cca     2733
Ile Ile Ile Phe Glu Asp Cys Arg Asn Gln Trp Ser Met Ser Arg Pro
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Leu Leu Gly Leu Ile Leu Leu Asn Glu Lys Tyr Phe Ser Asp Leu Arg
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aac agt att gtg aac agc cag cca ccg gag aag cag cag gcc atg cac     2829
Asn Ser Ile Val Asn Ser Gln Pro Pro Glu Lys Gln Gln Ala Met His
849                 854                 859                 864

ctg tgt ttt gag aac ctg atg gaa ggc atc gag cga aat ctt ctt acg     2877
Leu Cys Phe Glu Asn Leu Met Glu Gly Ile Glu Arg Asn Leu Leu Thr
865                 870                 875                 880

aaa aac aga gac agg ttc acc cag aac ctg tca gca ttc cgt cga gaa     2925
Lys Asn Arg Asp Arg Phe Thr Gln Asn Leu Ser Ala Phe Arg Arg Glu
881                 886                 891                 896

gtc aac gac tca atg aag aat tcc act tat ggc gtg aat agc aat gac     2973
Val Asn Asp Ser Met Lys Asn Ser Thr Tyr Gly Val Asn Ser Asn Asp
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Met Met Ser  *
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gcagatcact tgagatcagg agttcgagac cagcctggtg ccttggcatc tccca atg 178
Met

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ggg tgg ctt tgc tct ggg ctc ctg ttc cct gtg agc tgc ctg gtc ctg      226
Gly Trp Leu Cys Ser Gly Leu Leu Phe Pro Val Ser Cys Leu Val Leu
  2                   7                  12                  17

ctg cag gtg gca agc tct ggg aac atg aag gtc ttg cag gag ccc acc      274
Leu Gln Val Ala Ser Ser Gly Asn Met Lys Val Leu Gln Glu Pro Thr
 18                  23                  28                  33

tgc gtc tcc gac tac atg agc atc tct act tgc gag tgg aag atg aat      322
Cys Val Ser Asp Tyr Met Ser Ile Ser Thr Cys Glu Trp Lys Met Asn
 34                  39                  44                  49

ggt ccc acc aat tgc agc acc gag ctc cgc ctg ttg tac cag ctg gtt      370
Gly Pro Thr Asn Cys Ser Thr Glu Leu Arg Leu Leu Tyr Gln Leu Val
 50                  55                  60                  65

ttt ctg ctc tcc gaa gcc cac acg tgt atc cct gag aac aac gga ggc      418
Phe Leu Leu Ser Glu Ala His Thr Cys Ile Pro Glu Asn Asn Gly Gly
 66                  71                  76                  81

gcg ggg tgc gtg tgc cac ctg ctc atg gat gac gtg gtc agt gcg gat      466
Ala Gly Cys Val Cys His Leu Leu Met Asp Asp Val Val Ser Ala Asp
 82                  87                  92                  97

aac tat aca ctg gac ctg tgg gct ggg cag cag ctg ctg tgg aag ggc      514
Asn Tyr Thr Leu Asp Leu Trp Ala Gly Gln Gln Leu Leu Trp Lys Gly
 98                 103                 108                 113

tcc ttc aag ccc agc gag cat gtg aaa ccc agg gcc cca gga aac ctg      562
Ser Phe Lys Pro Ser Glu His Val Lys Pro Arg Ala Pro Gly Asn Leu
114                 119                 124                 129

aca gtt cac acc aat gtc tcc gac act ctg ctg ctg acc tgg agc aac      610
Thr Val His Thr Asn Val Ser Asp Thr Leu Leu Leu Thr Trp Ser Asn
130                 135                 140                 145

ccg tat ccc cct gac aat tac ctg tat aat cat ctc acc tat gca gtc      658
Pro Tyr Pro Pro Asp Asn Tyr Leu Tyr Asn His Leu Thr Tyr Ala Val
146                 151                 156                 161

aac att tgg agt gaa aac gac ccg gca gat ttc aga atc tat aac gtg      706
Asn Ile Trp Ser Glu Asn Asp Pro Ala Asp Phe Arg Ile Tyr Asn Val
162                 167                 172                 177

acc tac cta gaa ccc tcc ctc cgc atc gca gcc agc acc ctg aag tct      754
Thr Tyr Leu Glu Pro Ser Leu Arg Ile Ala Ala Ser Thr Leu Lys Ser
178                 183                 188                 193

ggg att tcc tac agg gca cgg gtg agg gcc tgg gct cag tgc tat aac      802
Gly Ile Ser Tyr Arg Ala Arg Val Arg Ala Trp Ala Gln Cys Tyr Asn
194                 199                 204                 209

acc acc tgg agt gag tgg agc ccc agc acc aag tgg cac aac tcc tac      850
Thr Thr Trp Ser Glu Trp Ser Pro Ser Thr Lys Trp His Asn Ser Tyr
210                 215                 220                 225
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agg gag ccc ttc gag cag cac ctc ctg ctg ggc gtc agc gtt tcc tgc      898
Arg Glu Pro Phe Glu Gln His Leu Leu Leu Gly Val Ser Val Ser Cys
226                 231                 236                 241

att gtc atc ctg gcc gtc tgc ctg ttg tgc tat gtc agc atc acc aag      946
Ile Val Ile Leu Ala Val Cys Leu Leu Cys Tyr Val Ser Ile Thr Lys
242                 247                 252                 257

att aag aaa gaa tgg tgg gat cag att ccc aac cca gcc cgc agc cgc      994
Ile Lys Lys Glu Trp Trp Asp Gln Ile Pro Asn Pro Ala Arg Ser Arg
258                 263                 268                 273

ctc gtg gct ata ata atc cag gat gct cag ggg tca cag tgg gag aag     1042
Leu Val Ala Ile Ile Ile Gln Asp Ala Gln Gly Ser Gln Trp Glu Lys
274                 279                 284                 289

cgg tcc cga ggc cag gaa cca gcc aag tgc cca cac tgg aag aat tgt     1090
Arg Ser Arg Gly Gln Glu Pro Ala Lys Cys Pro His Trp Lys Asn Cys
290                 295                 300                 305

ctt acc aag ctc ttg ccc tgt ttt ctg gag cac aac atg aaa agg gat     1138
Leu Thr Lys Leu Leu Pro Cys Phe Leu Glu His Asn Met Lys Arg Asp
306                 311                 316                 321

gaa gat cct cac aag gct gcc aaa gag atg cct ttc cag ggc tct gga     1186
Glu Asp Pro His Lys Ala Ala Lys Glu Met Pro Phe Gln Gly Ser Gly
322                 327                 332                 337

aaa tca gca tgg tgc cca gtg gag atc agc aag aca gtc ctc tgg cca     1234
Lys Ser Ala Trp Cys Pro Val Glu Ile Ser Lys Thr Val Leu Trp Pro
338                 343                 348                 353

gag agc atc agc gtg gtg cga tgt gtg gag ttg ttt gag gcc ccg gtg     1282
Glu Ser Ile Ser Val Val Arg Cys Val Glu Leu Phe Glu Ala Pro Val
354                 359                 364                 369

gag tgt gag gag gag gag gag gta gag gaa gaa aaa ggg agc ttc tgt     1330
Glu Cys Glu Glu Glu Glu Glu Val Glu Glu Glu Lys Gly Ser Phe Cys
370                 375                 380                 385

gca tcg cct gag agc agc agg gat gac ttc cag gag gga agg gag ggc     1378
Ala Ser Pro Glu Ser Ser Arg Asp Asp Phe Gln Glu Gly Arg Glu Gly
386                 391                 396                 401

att gtg gcc cgg cta aca gag agc ctg ttc ctg gac ctg ctc gga gag     1426
Ile Val Ala Arg Leu Thr Glu Ser Leu Phe Leu Asp Leu Leu Gly Glu
402                 407                 412                 417

gag aat ggg ggc ttt tgc cag cag gac atg ggg gag tca tgc ctt ctt     1474
Glu Asn Gly Gly Phe Cys Gln Gln Asp Met Gly Glu Ser Cys Leu Leu
418                 423                 428                 433

cca cct tcg gga agt acg agt gct cac atg ccc tgg gat gag ttc cca     1522
Pro Pro Ser Gly Ser Thr Ser Ala His Met Pro Trp Asp Glu Phe Pro
434                 439                 444                 449
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agt gca ggg ccc aag gag gca cct ccc tgg ggc aag gag cag cct ctc     1570
Ser Ala Gly Pro Lys Glu Ala Pro Pro Trp Gly Lys Glu Gln Pro Leu
450                 455                 460                 465

cac ctg gag cca agt cct cct gcc agc ccg acc cag agt cca gac aac     1618
His Leu Glu Pro Ser Pro Pro Ala Ser Pro Thr Gln Ser Pro Asp Asn
466                 471                 476                 481

ctg act tgc aca gag acg ccc ctc gtc atc gca ggc aac cct gct tac     1666
Leu Thr Cys Thr Glu Thr Pro Leu Val Ile Ala Gly Asn Pro Ala Tyr
482                 487                 492                 497

cgc agc ttc agc aac tcc ctg agc cag tca ccg tgt ccc aga gag ctg     1714
Arg Ser Phe Ser Asn Ser Leu Ser Gln Ser Pro Cys Pro Arg Glu Leu
498                 503                 508                 513

ggt cca gac cca ctg ctg gcc aga cac ctg gag gaa gta gaa ccc gag     1762
Gly Pro Asp Pro Leu Leu Ala Arg His Leu Glu Glu Val Glu Pro Glu
514                 519                 524                 529

atg ccc tgt gtc ccc cag ctc tct gag cca acc act gtg ccc caa cct     1810
Met Pro Cys Val Pro Gln Leu Ser Glu Pro Thr Thr Val Pro Gln Pro
530                 535                 540                 545

gag cca gaa acc tgg gag cag atc ctc cgc cga aat gtc ctc cag cat     1858
Glu Pro Glu Thr Trp Glu Gln Ile Leu Arg Arg Asn Val Leu Gln His
546                 551                 556                 561

ggg gca gct gca gcc ccc gtc tcg gcc ccc acc agt ggc tat cag gag     1906
Gly Ala Ala Ala Ala Pro Val Ser Ala Pro Thr Ser Gly Tyr Gln Glu
562                 567                 572                 577

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Phe Val His Ala Val Glu Gln Gly Gly Thr Gln Ala Ser Ala Val Val
578                 583                 588                 593

ggc ttg ggt ccc cca gga gag gct ggt tac aag gcc ttc tca agc ctg     2002
Gly Leu Gly Pro Pro Gly Glu Ala Gly Tyr Lys Ala Phe Ser Ser Leu
594                 599                 604                 609

ctt gcc agc agt gct gtg tcc cca gag aaa tgt ggg ttt ggg gct agc     2050
Leu Ala Ser Ser Ala Val Ser Pro Glu Lys Cys Gly Phe Gly Ala Ser
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agt ggg gaa gag ggg tat aag cct ttc caa gac ctc att cct ggc tgc     2098
Ser Gly Glu Glu Gly Tyr Lys Pro Phe Gln Asp Leu Ile Pro Gly Cys
626                 631                 636                 641

cct ggg gac cct gcc cca gtc cct gtc ccc ttg ttc acc ttt gga ctg     2146
Pro Gly Asp Pro Ala Pro Val Pro Val Pro Leu Phe Thr Phe Gly Leu
642                 647                 652                 657

gac agg gag cca cct cgc agt ccg cag agc tca cat ctc cca agc agc     2194
Asp Arg Glu Pro Pro Arg Ser Pro Gln Ser Ser His Leu Pro Ser Ser
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tcc cca gag cac ctg ggt ctg gag ccg ggg gaa aag gta gag gac atg     2242
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Pro Lys Pro Pro Leu Pro Gln Glu Gln Ala Thr Asp Pro Leu Val Asp
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agc ctg ggc agt ggc att gtc tac tca gcc ctt acc tgc cac ctg tgc     2338
Ser Leu Gly Ser Gly Ile Val Tyr Ser Ala Leu Thr Cys His Leu Cys
706                 711                 716                 721

ggc cac ctg aaa cag tgt cat ggc cag gag gat ggt ggc cag acc cct     2386
Gly His Leu Lys Gln Cys His Gly Gln Glu Asp Gly Gly Gln Thr Pro
722                 727                 732                 737

gtc atg gcc agt cct tgc tgt ggc tgc tgc tgt gga gac agg tcc tcg     2434
Val Met Ala Ser Pro Cys Cys Gly Cys Cys Cys Gly Asp Arg Ser Ser
738                 743                 748                 753

ccc cct aca acc ccc ctg agg gcc cca gac ccc tct cca ggg ggg gtt     2482
Pro Pro Thr Thr Pro Leu Arg Ala Pro Asp Pro Ser Pro Gly Gly Val
754                 759                 764                 769

cca ctg gag gcc agt ctg tgt ccg gcc tcc ctg gca ccc tcg ggc atc     2530
Pro Leu Glu Ala Ser Leu Cys Pro Ala Ser Leu Ala Pro Ser Gly Ile
770                 775                 780                 785

tca gag aag agt aaa tcc tca tca tcc ttc cat cct gcc cct ggc aat     2578
Ser Glu Lys Ser Lys Ser Ser Ser Ser Phe His Pro Ala Pro Gly Asn
786                 791                 796                 801

gct cag agc tca agc cag acc ccc aaa atc gtg aac ttt gtc tcc gtg     2626
Ala Gln Ser Ser Ser Gln Thr Pro Lys Ile Val Asn Phe Val Ser Val
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gga ccc aca tac atg agg gtc tct tag gtgca tgtcctcttg ttgctgagtc     2678
Gly Pro Thr Tyr Met Arg Val Ser  *
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Tyr Ser Leu Met Lys Phe Phe Thr Gly Pro Met Ser Asp Phe Lys Asn
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Val Asp Glu Ser Val Gly Ser Lys Thr Arg Arg Ala Phe Leu Tyr Leu
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Leu Leu Lys His Lys Tyr Ser Phe Leu Val Gly Cys Ala Ser Ile Ser
105                 110                 115                 120

gat gtc ata gct cag gtt gtt ttt gta gcc att ttg ctt cac agt cac      555
Asp Val Ile Ala Gln Val Val Phe Val Ala Ile Leu Leu His Ser His
121                 126                 131                 136

ctg gaa tgc cgg gag ccc ctg ctc atc ccg atc ctc tcc ttg tac atg      603
Leu Glu Cys Arg Glu Pro Leu Leu Ile Pro Ile Leu Ser Leu Tyr Met
137                 142                 147                 152

ggc gca ctt gtg cgc tgc acc acc ctg tgc ctg ggc tac tac aag aac      651
Gly Ala Leu Val Arg Cys Thr Thr Leu Cys Leu Gly Tyr Tyr Lys Asn
153                 158                 163                 168

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Ile His Asp Ile Ile Pro Asp Arg Ser Gly Pro Glu Leu Gly Gly Asp
169                 174                 179                 184

gca aca ata aga aag atg ctg agc ttc tgg tgg cct ttg gct cta att      747
Ala Thr Ile Arg Lys Met Leu Ser Phe Trp Trp Pro Leu Ala Leu Ile
185                 190                 195                 200

ctg gcc aca cag aga atc agt cgg cct att gtc aac ctc ttt gtt tcc      795
Leu Ala Thr Gln Arg Ile Ser Arg Pro Ile Val Asn Leu Phe Val Ser
201                 206                 211                 216

cgg gac ctt ggt ggc agt tct gca gcc aca gag gca gtg gcg att ttg      843
Arg Asp Leu Gly Gly Ser Ser Ala Ala Thr Glu Ala Val Ala Ile Leu
217                 222                 227                 232

aca gcc aca tac cct gtg ggt cac atg cca tac ggc tgg ttg acg gaa      891
Thr Ala Thr Tyr Pro Val Gly His Met Pro Tyr Gly Trp Leu Thr Glu
233                 238                 243                 248

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249                 254                 259                 264

ctg gtg agc acg agc aac aca gtc acg gca gcc cac atc aag aag ttc      987
Leu Val Ser Thr Ser Asn Thr Val Thr Ala Ala His Ile Lys Lys Phe
265                 270                 275                 280

acc ttc gtc tgc atg gct ctg tca ctc acg ctc tgt ttc gtg atg ttt     1035
Thr Phe Val Cys Met Ala Leu Ser Leu Thr Leu Cys Phe Val Met Phe
281                 286                 291                 296

tgg aca ccc aac gtg tct gag aaa atc ttg ata gac atc atc gga gtg     1083
Trp Thr Pro Asn Val Ser Glu Lys Ile Leu Ile Asp Ile Ile Gly Val
297                 302                 307                 312

gac ttt gcc ttt gca gaa ctc tgt gtt gtt cct ttg cgg atc ttc tcc     1131
Asp Phe Ala Phe Ala Glu Leu Cys Val Val Pro Leu Arg Ile Phe Ser
313                 318                 323                 328
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atg aca ctg aag aaa acc ttc gtc ctt gcc ccc agc tct gtg ctg cgg     1227
Met Thr Leu Lys Lys Thr Phe Val Leu Ala Pro Ser Ser Val Leu Arg
345                 350                 355                 360

atc atc gtc ctc atc gcc agc ctc gtg gtc cta ccc tac ctg ggg gtg     1275
Ile Ile Val Leu Ile Ala Ser Leu Val Val Leu Pro Tyr Leu Gly Val
361                 366                 371                 376

cac ggt gcg acc ctg ggc gtg ggc tcc ctc ctg gcg ggc ttt gtg gga     1323
His Gly Ala Thr Leu Gly Val Gly Ser Leu Leu Ala Gly Phe Val Gly
377                 382                 387                 392

gaa tcc acc atg gtc gcc atc gct gcg tgc tat gtc tac cgg aag cag     1371
Glu Ser Thr Met Val Ala Ile Ala Ala Cys Tyr Val Tyr Arg Lys Gln
393                 398                 403                 408

aaa aag aag atg gag aat gag tcg gcc acg gag ggg gaa gac tct gcc     1419
Lys Lys Lys Met Glu Asn Glu Ser Ala Thr Glu Gly Glu Asp Ser Ala
409                 414                 419                 424

atg aca gac atg cct ccg aca gag gag gtg aca gac atc gtg gaa atg     1467
Met Thr Asp Met Pro Pro Thr Glu Glu Val Thr Asp Ile Val Glu Met
425                 430                 435                 440

aga gag gag aat gaa taa ggcacg ggacgccatg ggcactgcag ggacagtcag     1521
Arg Glu Glu Asn Glu  *
441                 446

tcaggatgac acttcggcat catctcttcc ctctcccatc gtattttgtt ccctttttt    1581

tgttttgttt tggtaatgaa agaggccttg atttaaaggt ttcgtgtcaa ttctctagca    1641

tactgggtat gctcacactg acgggggggac ctagtgaatg gtctttactg ttgctatgta   1701

aaaacaaacg aaacaactga cttcataccc ctgcctcacg aaaacccaaa agacacagct    1761

gcctcacggt tgacgttgtg tcctcctccc ctggacaatc tcctcttgga accaaaggac    1821

tgcagctgtg ccatcgcgcc tcggtcaccc tgcacagcag gccacagact ctcctgtccc    1881

ccttcatcgc tcttaagaat caacaggtta aaactcggct tcctttgatt tgcttcccag    1941

tcacatggcc gtacaaagag atggagcccc ggtggcctct taaatttccc ttccgccacg    2001

gagttcgaaa ccatctactc cacacatgca ggaggcgggt ggcacgctgc agcccggagt    2061

ccccgttcac actgaggaac ggagacctgt gaccacagca ggctgacaga tggacagaat    2121

ctcccgtaga aaggtttggt ttgaaatgcc ccgggggcag caaactgaca tggttgaatg    2181

atagcatttc actctgcgtt ctcctagatc tgagcaagct gtcagttctc acccccaccg    2241
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tgtatataca tgagctaact tttttaaatt gtcacaaaag cgcatctcca gattccagac 2301

cctgccgcat gacttttcct gaaggcttgc ttttccctcg cctttcctga aggtcgcatt 2361

agagcgagtc acatggagca tcctaacttt gcattttagt ttttacagtg aactgaagct 2421

ttaagtaagt ctcatccagc attctaatgc caggttgctg tagggtaact tttgaagtag 2481

atatattacc tggttctgct atccttagtc ataactctgc ggtacaggta attgagaatg 2541

tactacggta cttccctccc acaccatacg ataaagcaag acattttata acgataccag 2601

agtcactatg tggtcctccc tgaaataacg cattcgaaat ccatgcagtg cagtatattt 2661

ttctaagttt tggaaagcag gttttttcct ttaaaaaaat tatagacacg gttcactaaa 2721

ttgatttagt cagaattcct agactgaaag aacctaaaca aaaaaatatt ttaaagatat 2781

aaatatatgc tgtatatgtt atgtaattta ttttaggcta taatacattt cctattttcg 2841

cattttcaat aaaatgtctc taatacaata cggtgattgc ttgtgtgctc aacatacctg 2901

cagttgaaac gtattgtatc aatgaacatt gtaccttatt ggcagcagtt ttataaagtc 2961

cgtcatttgc atttgaatgt aaggctcagt aaatgacaga actatttttc attatgggta 3021

actgggggaa taaatgggtc actggagtag gaatagaagt gcaagctgga aaggcaaaaa 3081

tgagaaagaa aaaggcaggc cctttgtgtc taccgttttc agtgctgtgt gctcgtgc 3139

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<213> Homo sapiens

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<400> 114
cgttcctcgg cgccgccggg gccccagagg gcagcggcag caacagcagc agcagcagca 60

gcgggagtgg ag atg gcg gcg gcg gcg gct cag ggg ggc ggg ggc ggg 108
Met Ala Ala Ala Ala Ala Gln Gly Gly Gly Gly Gly
1 5 10

gag ccc cgt aga acc gag ggg gtc ggc ccg ggg gtc ccg ggg gag gtg 156
Glu Pro Arg Arg Thr Glu Gly Val Gly Pro Gly Val Pro Gly Glu Val
13 18 23 28

gag atg gtg aag ggg cag ccg ttc gac gtg ggc ccg cgc tac acg cag 204
Glu Met Val Lys Gly Gln Pro Phe Asp Val Gly Pro Arg Tyr Thr Gln
29 34 39 44

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ttg cag tac atc ggc gag ggc gcg tac ggc atg gtc agc tcg gcc tat      252
Leu Gln Tyr Ile Gly Glu Gly Ala Tyr Gly Met Val Ser Ser Ala Tyr
 45                  50                  55                  60

gac cac gtg cgc aag act cgc gtg gcc atc aag aag atc agc ccc ttc      300
Asp His Val Arg Lys Thr Arg Val Ala Ile Lys Lys Ile Ser Pro Phe
 61                  66                  71                  76

gaa cat cag acc tac tgc cag cgc acg ctc cgg gag atc cag atc ctg      348
Glu His Gln Thr Tyr Cys Gln Arg Thr Leu Arg Glu Ile Gln Ile Leu
 77                  82                  87                  92

ctg cgc ttc cgc cat gag aat gtc atc ggc atc cga gac att ctg cgg      396
Leu Arg Phe Arg His Glu Asn Val Ile Gly Ile Arg Asp Ile Leu Arg
 93                  98                 103                 108

gcg tcc acc ctg gaa gcc atg aga gat gtc tac att gtg cag gac ctg      444
Ala Ser Thr Leu Glu Ala Met Arg Asp Val Tyr Ile Val Gln Asp Leu
109                 114                 119                 124

atg gag act gac ctg tac aag ttg ctg aaa agc cag cag ctg agc aat      492
Met Glu Thr Asp Leu Tyr Lys Leu Leu Lys Ser Gln Gln Leu Ser Asn
125                 130                 135                 140

gac cat atc tgc tac ttc ctc tac cag atc ctg cgg ggc ctc aag tac      540
Asp His Ile Cys Tyr Phe Leu Tyr Gln Ile Leu Arg Gly Leu Lys Tyr
141                 146                 151                 156

atc cac tcc gcc aac gtg ctc cac cga gat cta aag ccc tcc aac ctg      588
Ile His Ser Ala Asn Val Leu His Arg Asp Leu Lys Pro Ser Asn Leu
157                 162                 167                 172

ctc atc aac acc acc tgc gac ctt aag att tgt gat ttc ggc ctg gcc      636
Leu Ile Asn Thr Thr Cys Asp Leu Lys Ile Cys Asp Phe Gly Leu Ala
173                 178                 183                 188

cgg att gcc gat cct gag cat gac cac acc ggc ttc ctg acg gag tat      684
Arg Ile Ala Asp Pro Glu His Asp His Thr Gly Phe Leu Thr Glu Tyr
189                 194                 199                 204

gtg gct acg cgc tgg tac cgg gcc cca gag atc atg ctg aac tcc aag      732
Val Ala Thr Arg Trp Tyr Arg Ala Pro Glu Ile Met Leu Asn Ser Lys
205                 210                 215                 220

ggc tat acc aag tcc atc gac atc tgg tct gtg ggc tgc att ctg gct      780
Gly Tyr Thr Lys Ser Ile Asp Ile Trp Ser Val Gly Cys Ile Leu Ala
221                 226                 231                 236

gag atg ctc tct aac cgg ccc atc ttc cct ggc aag cac tac ctg gat      828
Glu Met Leu Ser Asn Arg Pro Ile Phe Pro Gly Lys His Tyr Leu Asp
237                 242                 247                 252

cag ctc aac cac att ctg ggc atc ctg ggc tcc cca tcc cag gag gac      876
Gln Leu Asn His Ile Leu Gly Ile Leu Gly Ser Pro Ser Gln Glu Asp
253                 258                 263                 268

ctg aat tgt atc atc aac atg aag gcc cga aac tac cta cag tct ctg      924
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Leu Asn Cys Ile Ile Asn Met Lys Ala Arg Asn Tyr Leu Gln Ser Leu
269                 274                 279                 284

ccc tcc aag acc aag gtg gct tgg gcc aag ctt ttc ccc aag tca gac      972
Pro Ser Lys Thr Lys Val Ala Trp Ala Lys Leu Phe Pro Lys Ser Asp
285                 290                 295                 300

tcc aaa gcc ctt gac ctg ctg gac cgg atg tta acc ttt aac ccc aat     1020
Ser Lys Ala Leu Asp Leu Leu Asp Arg Met Leu Thr Phe Asn Pro Asn
301                 306                 311                 316

aaa cgg atc aca gtg gag gaa gcg ctg gct cac ccc tac ctg gag cag     1068
Lys Arg Ile Thr Val Glu Glu Ala Leu Ala His Pro Tyr Leu Glu Gln
317                 322                 327                 332

tac tat gac ccg acg gat gag cca gtg gcc gag gag ccc ttc acc ttc     1116
Tyr Tyr Asp Pro Thr Asp Glu Pro Val Ala Glu Glu Pro Phe Thr Phe
333                 338                 343                 348

gcc atg gag ctg gat gac cta cct aag gag cgg ctg aag gag ctc atc     1164
Ala Met Glu Leu Asp Asp Leu Pro Lys Glu Arg Leu Lys Glu Leu Ile
349                 354                 359                 364

ttc cag gag aca gca cgc ttc cag ccc gga gtg ctg gag gcc ccc tag     1212
Phe Gln Glu Thr Ala Arg Phe Gln Pro Gly Val Leu Glu Ala Pro  *
365                 370                 375                 380

ccccagacag acatctctgc accctggggc ctggacctgc ctcctgcctg cccctctccc   1272

gccagactgt tagaaaatgg acactgtgcc cagcccggac cttggcagcc caggccgggg   1332

tggagcatgg gcctggccac ctctctcctt tgctgaggcc tccagcttca ggcaggccaa   1392

ggccaaggcc ttctcctccc cacccgccct ccccacgggg cctcgggacc tcaggtggcc   1452

ccagttcaat ctcccgctgc tgctgctgct gcgcccttac cttccccagc gtcccagtct   1512

ctggcagttt tggaatggaa gggttctggc tgccccaacc tgctgaaggg cagaggtgga   1572

gggtgggggg cgctgagtag ggactcaggg ccatgcctgc ccccctcatc tcattcaaac   1632

cccaccctag tttccctgaa ggaacattcc ttagtctcaa gggctagcat ccctgaggag   1692

ccaggccggg ccgaatcccc tccctgtcaa agctgtcact tcgcgtgccc tcgctgcttc   1752

tgtgtgtggt gagcagaagt ggagctgggg ggcgtggaga gcccggcgcc cctgccacct   1812

ccctgacccg tctaatatat aaatatagag atgtgtctat ggctgaaaaa aaaaaaa      1869
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<222> (151)..(819)

<400> 115
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aggccaggtg tgtgcgtccg tcggtctttc cgtgcccacg ccggagacca gccccggagg 120

ccgcctgggc ctatccctgt gccaggcacc atg aag cag gag tct gca gcc 171
Met Lys Gln Glu Ser Ala Ala
1 5

ccg aac acc ccg ccc acc tcg cag tcc cct acg ccg tcc gct cag ttc 219
Pro Asn Thr Pro Pro Thr Ser Gln Ser Pro Thr Pro Ser Ala Gln Phe
8 13 18 23

ccc cga aac gac ggc gac cct caa gcg ctg tgg att ttc ggg tac ggc 267
Pro Arg Asn Asp Gly Asp Pro Gln Ala Leu Trp Ile Phe Gly Tyr Gly
24 29 34 39

tcc ctg gtg tgg agg ccc gac ttc gcc tac agc gac agc cgt gtg ggc 315
Ser Leu Val Trp Arg Pro Asp Phe Ala Tyr Ser Asp Ser Arg Val Gly
40 45 50 55

ttc gtg cgc ggc tac agc cgc cgt ttc tgg cag gga gac acc ttc cat 363
Phe Val Arg Gly Tyr Ser Arg Arg Phe Trp Gln Gly Asp Thr Phe His
56 61 66 71

cgg ggc agc gac aag atg cct ggc cgt gtg gtg acg ctc ctt gaa gat 411
Arg Gly Ser Asp Lys Met Pro Gly Arg Val Val Thr Leu Leu Glu Asp
72 77 82 87

cat gag ggc tgc act tgg ggc gtg gca tac caa gtg caa ggg gag cag 459
His Glu Gly Cys Thr Trp Gly Val Ala Tyr Gln Val Gln Gly Glu Gln
88 93 98 103

gta agc aag gcc ctg aag tac ctg aat gtg cga gag gca gtg ctt ggt 507
Val Ser Lys Ala Leu Lys Tyr Leu Asn Val Arg Glu Ala Val Leu Gly
104 109 114 119

ggc tac gat acc aag gag gtc acc ttc tat ccc caa gat gct cct gac 555
Gly Tyr Asp Thr Lys Glu Val Thr Phe Tyr Pro Gln Asp Ala Pro Asp
120 125 130 135

caa cca ctg aag gca ttg gcc tat gtg gcc acc cca cag aac cct ggt 603
Gln Pro Leu Lys Ala Leu Ala Tyr Val Ala Thr Pro Gln Asn Pro Gly
136 141 146 151

tac ctg ggc cct gcg cct gaa gag gcc att gcc acg cag atc ctg gcc 651
Tyr Leu Gly Pro Ala Pro Glu Glu Ala Ile Ala Thr Gln Ile Leu Ala
152 157 162 167

tgc cgg ggc ttc tcc ggc cac aac ctt gaa tac ttg ctg cgt gtg cgg 699
Cys Arg Gly Phe Ser Gly His Asn Leu Glu Tyr Leu Leu Arg Val Arg
168 173 178 183

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gac ttc atg cag ctc tgt ggg cct cag gcg cag gac gag cac ctg gca      747
Asp Phe Met Gln Leu Cys Gly Pro Gln Ala Gln Asp Glu His Leu Ala
184                 189                 194                 199

gcc atc gtg gac gct gtg ggc acc atg ttg ccc tgc ttc tgc ccc acc      795
Ala Ile Val Asp Ala Val Gly Thr Met Leu Pro Cys Phe Cys Pro Thr
200                 205                 210                 215

gag cag gct ctg gcg ctg gtg tga ggggctgagc ccctgcgggg agtgctcatg     849
Glu Gln Ala Leu Ala Leu Val  *
216                 221

ggacatcagg gccagacacc cactccagtg cacaagacag acttgcgacc gcttgagccc    909

actgagcaga tatggtgggt ggctggaggc ttctctttct cagtccctgc ctgtctgcca    969

gcctgcagct ctcctgcttg acactgactt actacttgaa actttattta ttgcaccatg   1029

ttggtgtggt gggcaggtgg agggcctgcc ctggacacag gggccctgct gagcagtggc   1089

cccatcctgg aacttgacca gattcccccc agtgctgctg ctaaccccac accacccagg   1149

cctccacctc cccagggagt ctccaagagc ctcgatcctc tgctcactca gcccagccat   1209

ccatagccct gggaattcca cctgccaagg atcccagcag gctggatgag ggatagtagg   1269

gcatgaggag aaggagccct gtaaggactg aggccccggc cagcccttct cctccaccag   1329

ttccccagag cagagctgga gctgatgcct ggacacagct gctgagcctg gcctgggcct   1389

cttacccact tggttgtttt cttgtccctc tgtctgtctg tctatctact tgtctgtctg   1449

ggccactcct gcctgtgtgt tggtctattc ctgggaagct catcactaca ggccctggca   1509

accttcccag tctgtcccat actgttaccc ataaaactat ctctttaaaa aaaaaaa      1566
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<211> 4626
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<221> CDS
<222> (111)..(2225)

<220>
<221> misc_feature
<222> (1)...(4626)
<223> n = a,t,c or g

<400> 116

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catcgaaatg catgatgtat ataactatct attcgatgat gaagataccc caccaaaccc     60

aaaaaaagag atctctcgag gatccgaatt cgcggacgcg tcgacctttt   atg aat     116
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                                                          Met Asn
                                                            1

gtc aag cta tta att caa gac ttg gag gat att gag cag agg gtg cct      164
Val Lys Leu Leu Ile Gln Asp Leu Glu Asp Ile Glu Gln Arg Val Pro
  3                   8                  13                  18

gtg atg gat gcc caa tac aag ata att aca aag aca gca cac ctc att      212
Val Met Asp Ala Gln Tyr Lys Ile Ile Thr Lys Thr Ala His Leu Ile
 19                  24                  29                  34

acc aaa gaa agc ccc caa gaa gaa gga aaa gaa atg ttt gcg acc atg      260
Thr Lys Glu Ser Pro Gln Glu Glu Gly Lys Glu Met Phe Ala Thr Met
 35                  40                  45                  50

tca aag ctc aaa gag cag cta acc aag gtc aaa gaa tgt tac tcc cca      308
Ser Lys Leu Lys Glu Gln Leu Thr Lys Val Lys Glu Cys Tyr Ser Pro
 51                  56                  61                  66

ctc ctt tat gag tct cag cag ctg ttg att ccg ttg gag gaa tta gaa      356
Leu Leu Tyr Glu Ser Gln Gln Leu Leu Ile Pro Leu Glu Glu Leu Glu
 67                  72                  77                  82

aag cag atg acg tcc ttt tat gac tca ctt ggg aaa atc aat gaa att      404
Lys Gln Met Thr Ser Phe Tyr Asp Ser Leu Gly Lys Ile Asn Glu Ile
 83                  88                  93                  98

atc aca gtt ctt gag cgt gag gca caa tcg agt gcc ctt ttt aaa caa      452
Ile Thr Val Leu Glu Arg Glu Ala Gln Ser Ser Ala Leu Phe Lys Gln
 99                 104                 109                 114

aaa cat cag gaa ctg tta gct tgt caa gaa aac tgt aag aaa acc ttg      500
Lys His Gln Glu Leu Leu Ala Cys Gln Glu Asn Cys Lys Lys Thr Leu
115                 120                 125                 130

aca ctt att gag aaa ggc agt caa agt gtt caa aag ttt gtg acc ttg      548
Thr Leu Ile Glu Lys Gly Ser Gln Ser Val Gln Lys Phe Val Thr Leu
131                 136                 141                 146

agc aac gtg tta aag cat ttt gat cag acg agg cta caa aga cag att      596
Ser Asn Val Leu Lys His Phe Asp Gln Thr Arg Leu Gln Arg Gln Ile
147                 152                 157                 162

gca gat att cat gtt gct ttt cag agt atg gta aag aaa act gga gat      644
Ala Asp Ile His Val Ala Phe Gln Ser Met Val Lys Lys Thr Gly Asp
163                 168                 173                 178

tgg aag aag cat gtg gaa acc aac agt cgc ttg atg aag aag ttt gag      692
Trp Lys Lys His Val Glu Thr Asn Ser Arg Leu Met Lys Lys Phe Glu
179                 184                 189                 194

gag tct cga gca gag ttg gag aag gta ctg cgg att gct cag gag ggc      740
Glu Ser Arg Ala Glu Leu Glu Lys Val Leu Arg Ile Ala Gln Glu Gly
195                 200                 205                 210

ctg gag gaa aag ggg gat cca gag gag ctc ctg cgg aga cac act gag      788
Leu Glu Glu Lys Gly Asp Pro Glu Glu Leu Leu Arg Arg His Thr Glu
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US 2005/0250705 A1

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211                 216                 221                 226

ttt ttc agt cag ctg gat cag agg gtg ctc aat gct ttc ctg aaa gct      836
Phe Phe Ser Gln Leu Asp Gln Arg Val Leu Asn Ala Phe Leu Lys Ala
227                 232                 237                 242

tgt gat gaa ctc acc gac atc ctt cca gag cag gag cag cag ggg ctg      884
Cys Asp Glu Leu Thr Asp Ile Leu Pro Glu Gln Glu Gln Gln Gly Leu
243                 248                 253                 258

cag gaa gct gtt cga aag ctc cac aaa caa tgg aag gat ctt caa gga      932
Gln Glu Ala Val Arg Lys Leu His Lys Gln Trp Lys Asp Leu Gln Gly
259                 264                 269                 274

gaa gcc cct tat cat ttg ctt cat ctg aag att gat gtg gag aag aat      980
Glu Ala Pro Tyr His Leu Leu His Leu Lys Ile Asp Val Glu Lys Asn
275                 280                 285                 290

agg ttc tta gcc tct gca gaa gaa tgc aga act gag ctg gat cga gag     1028
Arg Phe Leu Ala Ser Ala Glu Glu Cys Arg Thr Glu Leu Asp Arg Glu
291                 296                 301                 306

acc aag ctg atg ccc cag gaa ggc agt gaa aag ata att aaa gag cac     1076
Thr Lys Leu Met Pro Gln Glu Gly Ser Glu Lys Ile Ile Lys Glu His
307                 312                 317                 322

agg gtt ttc ttc agt gac aaa ggt cct cat cat ctc tgt gag aaa agg     1124
Arg Val Phe Phe Ser Asp Lys Gly Pro His His Leu Cys Glu Lys Arg
323                 328                 333                 338

tta cag ctc atc gag gaa ctc tgt gtg aaa ctc cca gtg cgg gac cca     1172
Leu Gln Leu Ile Glu Glu Leu Cys Val Lys Leu Pro Val Arg Asp Pro
339                 344                 349                 354

gta agg gac aca cct gga acc tgt cac gtg act ctc aaa gag ctc aga     1220
Val Arg Asp Thr Pro Gly Thr Cys His Val Thr Leu Lys Glu Leu Arg
355                 360                 365                 370

gct gcc att gac agc acc tac agg aag ctc atg gaa gac cca gac aag     1268
Ala Ala Ile Asp Ser Thr Tyr Arg Lys Leu Met Glu Asp Pro Asp Lys
371                 376                 381                 386

tgg aag gac tac act agc aga ttc tct gag ttc tca tct tgg ata tct     1316
Trp Lys Asp Tyr Thr Ser Arg Phe Ser Glu Phe Ser Ser Trp Ile Ser
387                 392                 397                 402

aca aat gag aca caa tta aag ggg atc aag ggt gag gcc atc gat act     1364
Thr Asn Glu Thr Gln Leu Lys Gly Ile Lys Gly Glu Ala Ile Asp Thr
403                 408                 413                 418

gcc aac cac gga gag gtt aaa cgt gcc gtt gaa gag atc aga aat ggt     1412
Ala Asn His Gly Glu Val Lys Arg Ala Val Glu Glu Ile Arg Asn Gly
419                 424                 429                 434

gtt acc aaa agg ggt gag acc ctc agc tgg ctg aaa tcc agg ctg aaa     1460
Val Thr Lys Arg Gly Glu Thr Leu Ser Trp Leu Lys Ser Arg Leu Lys
435                 440                 445                 450
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gtt ttg aca gaa gtt tct tct gag aat gaa gcc caa aag cag gga gat      1508
Val Leu Thr Glu Val Ser Ser Glu Asn Glu Ala Gln Lys Gln Gly Asp
451                 456                 461                 466

gag ctg gca aaa tta tcc agc tct ttc aag gct ctt gtg acg ctg ctg      1556
Glu Leu Ala Lys Leu Ser Ser Ser Phe Lys Ala Leu Val Thr Leu Leu
467                 472                 477                 482

tca gag gtt gaa aag atg cta agc aat ttt ggg gac tgt gtc cag tac      1604
Ser Glu Val Glu Lys Met Leu Ser Asn Phe Gly Asp Cys Val Gln Tyr
483                 488                 493                 498

aaa gaa ata gtc aaa aat tct ctc gaa gaa tta att tct ggc tct aaa      1652
Lys Glu Ile Val Lys Asn Ser Leu Glu Glu Leu Ile Ser Gly Ser Lys
499                 504                 509                 514

gaa gtc cag gaa caa gct gag aag atc ttg gat act gaa aat ctg ttt      1700
Glu Val Gln Glu Gln Ala Glu Lys Ile Leu Asp Thr Glu Asn Leu Phe
515                 520                 525                 530

gaa gca cag cag tta ctt ctt cat cac cag caa aag aca aag cgg atc      1748
Glu Ala Gln Gln Leu Leu Leu His His Gln Gln Lys Thr Lys Arg Ile
531                 536                 541                 546

tca gca aag aag aga gat gtg cag cag cag atc gcg cag gcg cag cag      1796
Ser Ala Lys Lys Arg Asp Val Gln Gln Gln Ile Ala Gln Ala Gln Gln
547                 552                 557                 562

gga gaa ggg ggg ctg cct gac cga ggc cac gag gag ctg cgg aag ctg      1844
Gly Glu Gly Gly Leu Pro Asp Arg Gly His Glu Glu Leu Arg Lys Leu
563                 568                 573                 578

gag agc aca ctg gat ggc ctg gag cgc agc cgg gag agg cag gaa cgc      1892
Glu Ser Thr Leu Asp Gly Leu Glu Arg Ser Arg Glu Arg Gln Glu Arg
579                 584                 589                 594

cgc atc cag gtc aca tta aga aaa tgg gag cga ttt gaa aca aac aaa      1940
Arg Ile Gln Val Thr Leu Arg Lys Trp Glu Arg Phe Glu Thr Asn Lys
595                 600                 605                 610

gaa aca gta gta aga tac ctt ttt caa aca ggt tcc agt cat gaa cgc      1988
Glu Thr Val Val Arg Tyr Leu Phe Gln Thr Gly Ser Ser His Glu Arg
611                 616                 621                 626

ttc ttg agt ttt agc agt ttg gaa agt tta tct tca gaa ctg gaa caa      2036
Phe Leu Ser Phe Ser Ser Leu Glu Ser Leu Ser Ser Glu Leu Glu Gln
627                 632                 637                 642

aca aag gag ttt tct aaa cgg aca gaa agt att gca gtc cag gct gag      2084
Thr Lys Glu Phe Ser Lys Arg Thr Glu Ser Ile Ala Val Gln Ala Glu
643                 648                 653                 658

aac ctt gta aag gaa gct tca gag ata ccg ctt ggg ccc caa aat aag      2132
Asn Leu Val Lys Glu Ala Ser Glu Ile Pro Leu Gly Pro Gln Asn Lys
659                 664                 669                 674
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cag ctg ctt caa cag cag gcc aag tca atc aaa gaa caa gtc aaa aaa     2180
Gln Leu Leu Gln Gln Gln Ala Lys Ser Ile Lys Glu Gln Val Lys Lys
675                 680                 685                 690

tta gaa gac acg ctt gaa gaa gag tat gtg att gac aag tcc taa act     2228
Leu Glu Asp Thr Leu Glu Glu Glu Tyr Val Ile Asp Lys Ser  *
691                 696                 701

ttcttctctg agataaagtt tcatacaatc tttcctgtac cttgtattca aaacactctt   2288

ttaaaatctc aaagtgtctg tgtatttcag catgttttga ggaaacaact cacagttcaa   2348

aagaaagtat cgctaataca ggaaacccaa aatctataac agagcccaaa aaatataaag   2408

gatgtgggtt ttgccatnct taaactgatc atgttcatga gaaagcccat atcctaacct   2468

attctgtggc cctttgtaca ttgtagaggg aaacttgaaa aagaactaat atttaaaata   2528

atttttttac tatattattc tgctgtcacc atttagagcg aaaaggagat attttgttag   2588

tgtagattcc aggcctaaat acacatcaca tagaccatat atctccaacc tgaagaagct   2648

cctggagctt gtttacagtg cctcggtatt caagttatcc tgactaatat gctctttcca   2708

gaaattaact ttaaaatatt ttatttttaa acttttaatg tttgtttatc tgaaaaaaaa   2768

aaactgcttg gcctattgat atcctgttat atacccaaaa tatacaaaaa agtttggagg   2828

ggaaaaacat atgaggatac agccaatatt attcaaaaca atatggctaa acatttctat   2888

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ttaaaattaa cattttacat ttgcctaaac tttaaaattt gatacatatt ttatttaaaa   3068

caaattatga cttgaaattt tgaggacttt atattacatt aaatattctc tatcaagtta   3128

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acagcattag gcacattcag ggtataaatt tgagactgca atattattta atttgacagt   3308

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aattaaaaat ctatagttga aattctgttc actaaatttg ttacaaataa aacctataag   3548

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gaccataaga catttatgaa aatggctgaa gtcacaaaga ttatacatcg caggattagc   3668

tctaataata gaaacagttc ttgcccggca gcatgggatt gagatcacga gctctgtctt   3728
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gattgataag atgcagttta taaaggtatt tctatagaaa gcatcactgc agtgtctctc 3788

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aaaacctgat aaactactca gaacaactgt gcaatttttt ttttagcgtg aatagtttca 4088

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catggacatg caaatcagcc aaattaaggt gacctgctca cacattatat ttataatcca 4388

tgtctagctt ttaagaacta ctttcttaca tttcatcaaa tgctgttcgg tcccaggaca 4448

agactttcat tgcaatgtga ctattaaaat taaattcata cattttatca agctaagagg 4508

tctggattaa tactgggcaa catttatagt tggaattatg tattcacatt gtctgacttg 4568

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ag atg gcg ttt gtg aag agt ggc tgg ttg ctg cga cag agt act att 167
Met Ala Phe Val Lys Ser Gly Trp Leu Leu Arg Gln Ser Thr Ile
1 5 10

ttg aag cgc tgg aag aag aac tgg ttt gat ctg tgg tcg gat ggt cac 215
Leu Lys Arg Trp Lys Lys Asn Trp Phe Asp Leu Trp Ser Asp Gly His
16 21 26 31

ctg atc tat tat gat gac cag act cgg cag aat atc gag gat aag gtc 263

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Leu Ile Tyr Tyr Asp Asp Gln Thr Arg Gln Asn Ile Glu Asp Lys Val
 32                  37                  42                  47

cac atg cca atg gac tgc atc aac atc cgc acg ggg cag gaa tgt cgg      311
His Met Pro Met Asp Cys Ile Asn Ile Arg Thr Gly Gln Glu Cys Arg
 48                  53                  58                  63

gat act cag ccc ccg gat gga aag tca aaa gac tgc atg ctc cag att      359
Asp Thr Gln Pro Pro Asp Gly Lys Ser Lys Asp Cys Met Leu Gln Ile
 64                  69                  74                  79

gtt tgt cga gat ggg aaa aca att agt ctt tgt gca gaa agc aca gat      407
Val Cys Arg Asp Gly Lys Thr Ile Ser Leu Cys Ala Glu Ser Thr Asp
 80                  85                  90                  95

gat tgc ttg gcc tgg aaa ttt aca ctc caa gat tct agg aca aac aca      455
Asp Cys Leu Ala Trp Lys Phe Thr Leu Gln Asp Ser Arg Thr Asn Thr
 96                 101                 106                 111

gcg tat gtg ggc tct gca gtc atg acc gat gag aca tcc gtg gtt tcc      503
Ala Tyr Val Gly Ser Ala Val Met Thr Asp Glu Thr Ser Val Val Ser
112                 117                 122                 127

tca cct cca cca tac acg gcc tat gct gca ccg gcc cct gag gta tat      551
Ser Pro Pro Pro Tyr Thr Ala Tyr Ala Ala Pro Ala Pro Glu Val Tyr
128                 133                 138                 143

ggc tat ggg cca tac ggt ggt gcg tac ccg cca gga act caa gtt gtc      599
Gly Tyr Gly Pro Tyr Gly Gly Ala Tyr Pro Pro Gly Thr Gln Val Val
144                 149                 154                 159

tac gct gcg aat ggg cag gcg tat gcc gtg ccc tac cag tac cca tat      647
Tyr Ala Ala Asn Gly Gln Ala Tyr Ala Val Pro Tyr Gln Tyr Pro Tyr
160                 165                 170                 175

gca gga ctt tat gga cag cag cct gct aac caa gtc atc att cga gag      695
Ala Gly Leu Tyr Gly Gln Gln Pro Ala Asn Gln Val Ile Ile Arg Glu
176                 181                 186                 191

cgc tat cga gac aac gac agc gac ctg gca ctg ggc atg ctg gca gga      743
Arg Tyr Arg Asp Asn Asp Ser Asp Leu Ala Leu Gly Met Leu Ala Gly
192                 197                 202                 207

gca gcc acg ggc atg gcc tta ggg tct cta ttt tgg gtc ttc tag ggg      791
Ala Ala Thr Gly Met Ala Leu Gly Ser Leu Phe Trp Val Phe  *
208                 213                 218

cctcaaggtc ttgatgtgca tagcttctga taaccctgtg tgcaataata tgatttgcag    851

ggcatttctg tttgtgacaa aagtttttaa taatagtttt aatcattcct ttgaaagtag    911

tgatgtcata attgtactaa tccacataag taccacagag aagggtttga actgtgctat    971

tttgttcaaa tgttgactct ccgggggcac tggctcattc caagactgtt cttgtgcaac   1031

tctcagaata ccttatttga gcatacctgt tttgaaaggc attttctttt tagagttagg   1091
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gaccagaact ggttgcatgt tactttagga gttgtgggtt ggtaagctcc caggtacttc 1271

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ctttaaaact tgagccaccg cgcccggccg gtcattcatt cttggcaaca agcatttatt 1571

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gccagacaac acccccctcct tcctcaccct gtctcctgca ttctcctgaa accttcatcc 120

acaca atg cct ccc aac ctc act ggc tac tac cgc ttt gtc tcg cag 167
Met Pro Pro Asn Leu Thr Gly Tyr Tyr Arg Phe Val Ser Gln
1 5 10

aag aac atg gag gac tac ctg caa gcc cta aac atc agc ttg gct gtg 215
Lys Asn Met Glu Asp Tyr Leu Gln Ala Leu Asn Ile Ser Leu Ala Val
15 20 25 30

cgg aag atc gcg ctg ctg ctg aag ccg gac aag gag atc gaa cac cag 263
Arg Lys Ile Ala Leu Leu Leu Lys Pro Asp Lys Glu Ile Glu His Gln
31 36 41 46

ggc aac cac atg acg gtg agg acg ctc agc acc ttc cga aac tac act 311
Gly Asn His Met Thr Val Arg Thr Leu Ser Thr Phe Arg Asn Tyr Thr
47 52 57 62

gtg cag ttt gat gtg gga gtg gag ttt gag gag gac ctc agg agc gtg 359
Val Gln Phe Asp Val Gly Val Glu Phe Glu Glu Asp Leu Arg Ser Val
63 68 73 78

gac gga cga aaa tgc cag acc ata gta acc tgg gag gag gag cac ctg 407
Asp Gly Arg Lys Cys Gln Thr Ile Val Thr Trp Glu Glu Glu His Leu

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 79                  84                  89                  94

gtg tgt gtg cag aaa ggg gag gtc ccc aac cgg ggc tgg aga cac tgg      455
Val Cys Val Gln Lys Gly Glu Val Pro Asn Arg Gly Trp Arg His Trp
 95                 100                 105                 110

ctg gag gga gag atg ctg tat ctg gaa ctg act gca agg gat gca gtg      503
Leu Glu Gly Glu Met Leu Tyr Leu Glu Leu Thr Ala Arg Asp Ala Val
111                 116                 121                 126

tgc gag cag gtc ttc agg aag gtc aga tag c cggagaggag ccaagatccc      554
Cys Glu Gln Val Phe Arg Lys Val Arg  *
127                 132

tccagacagc accagctcac agacgctctt gttgtgcccc cttcaagccc agattgtgcc    614

aggtcagctg tcccttcctc tggccacctt tcctccctct gggtccctcc tcacccctcc    674

ccgtgttaat ctgtaacttg cagcccccag gccaaagtcc tttctcacac tccactgccc    734

aatagtgacc tcacttccag gtcaaggtct ggcgtcccaa atgaaagaag caggcaaagg    794

gaaggagccc ctgagaacaa ccaatctccg ctctctcctg tccatttgac ctcttctttt    854

ccttctaaga aagaactaag ctttgggcat ttggcgatta gtgaaaattc tatcctgatg    914

gacttctgga aaactgtgac tggggttcaa gagtttaaac aggggctact ggcagagtct    974

ttttgtccat ttctttgtcc ttattcttga gaaagtctca tgtgctcaac aaaaccaggc   1034

ccaagacaca gccccccaca cacagggttc aacggactcc acggttctga catctgaagg   1094

catctggcca tttgatactt ccatcctatg tgttgggaat gagggatgga atggggtaag   1154

acctatgtcc agtgcttggg gaggcgggga gcttctaaat ggtgacctgt cctccgtacg   1214

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accgctggca gcctgaagag agtcgctggc cgtggtcgcc gctaggtagg atatatctgc    120

atcttgaaag gaagataaaa caaaagcctt ctttggaata gatggatttt tgtcactttc    180
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tgtgtgaact aaagtgattc aatgtctctt ttggattgct tctgcacttc aagaacacaa    240

gttgaatcac tcagacctga aaaacagtct gaaaccagta tccatcaata cttggttgat    300

gagccaaccc tttcctggtc acgtccatcc actagagcca gtgaagtact atgttccacc    360

aacgtttctc actatgagct ccaagtagaa ataggaagag gatttgacaa cttgacttct    420

gtccatcttg cacggcatac tcccacgggg aaccactggt aactataaaa attacaaatc    480

tggaaaactg caatgaagaa cgcctgaaag ctttacagaa agccgtgatt ctatcccact    540

ttttccggca tcccaatatt acaacttatt ggacagtttt cactgttggc agctggcttt    600

gggttatttc tccattt   atg gcc tat ggt tca gca agt caa ctc ttg agg      650
                     Met Ala Tyr Gly Ser Ala Ser Gln Leu Leu Arg
                       1               5

acc tat ttt cct gaa gga atg agt gaa act tta ata aga aac att ctc      698
Thr Tyr Phe Pro Glu Gly Met Ser Glu Thr Leu Ile Arg Asn Ile Leu
 12                  17                  22                  27

ttt gga gcc gtg aga ggg ttg aac tat ctg cac caa aat ggc tgt att      746
Phe Gly Ala Val Arg Gly Leu Asn Tyr Leu His Gln Asn Gly Cys Ile
 28                  33                  38                  43

cac agg agt att aaa gcc agc cat atc ctc att tct ggt gat ggc cta      794
His Arg Ser Ile Lys Ala Ser His Ile Leu Ile Ser Gly Asp Gly Leu
 44                  49                  54                  59

gtg acc ctc tct ggc ctt tcc cat ctg cat agt ttg gtt aag cat gga      842
Val Thr Leu Ser Gly Leu Ser His Leu His Ser Leu Val Lys His Gly
 60                  65                  70                  75

cag agg cat agg gct gtg tat gat ttc cca cag ttc agc aca tca gtg      890
Gln Arg His Arg Ala Val Tyr Asp Phe Pro Gln Phe Ser Thr Ser Val
 76                  81                  86                  91

cag ccg tgg ctg agt cca gaa cta ctg aga cag gat tta cat ggg tat      938
Gln Pro Trp Leu Ser Pro Glu Leu Leu Arg Gln Asp Leu His Gly Tyr
 92                  97                 102                 107

aat gtg aag tca gat att tac agt gtt ggg att aca gca tgt gaa tta      986
Asn Val Lys Ser Asp Ile Tyr Ser Val Gly Ile Thr Ala Cys Glu Leu
108                 113                 118                 123

gcc agt ggg cag gtg cct ttc cag gac atg cat aga act cag atg ctg     1034
Ala Ser Gly Gln Val Pro Phe Gln Asp Met His Arg Thr Gln Met Leu
124                 129                 134                 139

tta cag aaa ctg aaa ggt cct cct tat agc cca ttg gat atc agt att     1082
Leu Gln Lys Leu Lys Gly Pro Pro Tyr Ser Pro Leu Asp Ile Ser Ile
140                 145                 150                 155

ttc cct caa tca gaa tcc aga atg aaa aat tcc cag tca ggt gta gac     1130
Phe Pro Gln Ser Glu Ser Arg Met Lys Asn Ser Gln Ser Gly Val Asp
156                 161                 166                 171
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tct ggg att gga gaa agt gtg ctt gtc tcc agt gga act cac aca gta      1178
Ser Gly Ile Gly Glu Ser Val Leu Val Ser Ser Gly Thr His Thr Val
172                 177                 182                 187

aat agt gac cga tta cac aca cca tcc tca aaa act ttc tct cct gcc      1226
Asn Ser Asp Arg Leu His Thr Pro Ser Ser Lys Thr Phe Ser Pro Ala
188                 193                 198                 203

ttc ttt agc ttg gta cag ctc tgt ttg caa caa gat cct gag aaa agg      1274
Phe Phe Ser Leu Val Gln Leu Cys Leu Gln Gln Asp Pro Glu Lys Arg
204                 209                 214                 219

cca tca gca agc agt tta ttg tcc cat gtt ttc ttc aaa cag atg aaa      1322
Pro Ser Ala Ser Ser Leu Leu Ser His Val Phe Phe Lys Gln Met Lys
220                 225                 230                 235

gaa gaa agc cag gat tca ata ctt tca ctg ttg cct cct gct tat aac      1370
Glu Glu Ser Gln Asp Ser Ile Leu Ser Leu Leu Pro Pro Ala Tyr Asn
236                 241                 246                 251

aag cca tca ata tca ttg cct cca gtg tta cct tgg act gag cca gaa      1418
Lys Pro Ser Ile Ser Leu Pro Pro Val Leu Pro Trp Thr Glu Pro Glu
252                 257                 262                 267

tgt gat ttt cct gat gaa aaa gac tca tac tgg gaa ttc tag ggctgcc      1467
Cys Asp Phe Pro Asp Glu Lys Asp Ser Tyr Trp Glu Phe  *
268                 273                 278

aaatcatttt atgtcctata tacttgacac tttctccttg ctgcttttc ttctgtattt    1527

ctaggtacaa ataccagaat tatacttgaa aatacagttg gtgcactgga gaatctatta    1587

tttaaaacca ctctgttcaa aggggcacca gtttgtagtc cctctgtttc gcacagagta    1647

ctatgacaag gaaacatcag aattactaat ctagctagtg tcatttattc tggaattttt    1707

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ttcagtattt tgctgtccct tgggaatggg ccctcagagg acagtgcttc caagtacatc    1827

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ttacatcaga ccctttttctg gtagagggaa aatgtttgtg ctttcccttt ttcttctgtt    1947

aatacttatg gtaacaccta actgagcctc actcacatta aatgattcac ttgaaatata    2007

tacagaaatt gtaatttgct ttttttttaaa aaaggggggct aaagtaacac tttcctactt    2067

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<400> 120

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tta cag ctg ccg cgg ctc ccc gag ctg ttc gaa act ggt aga cag tta      100
Leu Gln Leu Pro Arg Leu Pro Glu Leu Phe Glu Thr Gly Arg Gln Leu
  7                  12                  17                  22

ctg gac gaa gta gaa gtg gcg act gaa ccc gcc ggt tcc cgg ata gtc      148
Leu Asp Glu Val Glu Val Ala Thr Glu Pro Ala Gly Ser Arg Ile Val
 23                  28                  33                  38

cag gag aag gtg ttc aag ggc ttg gac ctc ctt gag aag gct gcc gaa      196
Gln Glu Lys Val Phe Lys Gly Leu Asp Leu Leu Glu Lys Ala Ala Glu
 39                  44                  49                  54

atg tta tcg cag ctc gac ttg ttc agc cga aat gaa gat ttg gaa gag      244
Met Leu Ser Gln Leu Asp Leu Phe Ser Arg Asn Glu Asp Leu Glu Glu
 55                  60                  65                  70

att gct tcc acc gac ctg aag tac ctt ttg gtg cca gcg ttt caa gga      292
Ile Ala Ser Thr Asp Leu Lys Tyr Leu Leu Val Pro Ala Phe Gln Gly
 71                  76                  81                  86

gcc ctc acc atg aaa caa gtc aac ccc agc aag cgt cta gat cat ttg      340
Ala Leu Thr Met Lys Gln Val Asn Pro Ser Lys Arg Leu Asp His Leu
 87                  92                  97                 102

cag cgg gct cga gaa cac ttt ata aac tac tta act cag tgc cat tgc      388
Gln Arg Ala Arg Glu His Phe Ile Asn Tyr Leu Thr Gln Cys His Cys
103                 108                 113                 118

tat cat gtg gca gag ttt gag ctg ccc aaa acc atg aac aac tct gct      436
Tyr His Val Ala Glu Phe Glu Leu Pro Lys Thr Met Asn Asn Ser Ala
119                 124                 129                 134

gaa aat cac act gcc aat tcc tcc atg gct tat cct agt ctc gtt gct      484
Glu Asn His Thr Ala Asn Ser Ser Met Ala Tyr Pro Ser Leu Val Ala
135                 140                 145                 150

atg gca tct caa aga cag gct aaa ata cag aga tac aag cag aag aag      532
Met Ala Ser Gln Arg Gln Ala Lys Ile Gln Arg Tyr Lys Gln Lys Lys
151                 156                 161                 166

gag ttg gag cat agg ttg tct gca atg aaa tct gct gtg gaa agt ggt      580
Glu Leu Glu His Arg Leu Ser Ala Met Lys Ser Ala Val Glu Ser Gly
167                 172                 177                 182
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caa gca gat gat gag cgt gtt cgt gaa tat tat ctt ctt cac ctt cag      628
Gln Ala Asp Asp Glu Arg Val Arg Glu Tyr Tyr Leu Leu His Leu Gln
183                 188                 193                 198

agg tgg att gat atc agc tta gaa gag att gag agc att gac cag gaa      676
Arg Trp Ile Asp Ile Ser Leu Glu Glu Ile Glu Ser Ile Asp Gln Glu
199                 204                 209                 214

ata aag atc ctg aga gaa aga gac tct tca aga gag gca tca act tct      724
Ile Lys Ile Leu Arg Glu Arg Asp Ser Ser Arg Glu Ala Ser Thr Ser
215                 220                 225                 230

aac tca tct cgc cag gag agg cct cca gtg aaa ccc ttc att ctc act      772
Asn Ser Ser Arg Gln Glu Arg Pro Pro Val Lys Pro Phe Ile Leu Thr
231                 236                 241                 246

cgg aac atg gct caa gcc aaa gta ttt gga gct ggt tat cca agt ctg      820
Arg Asn Met Ala Gln Ala Lys Val Phe Gly Ala Gly Tyr Pro Ser Leu
247                 252                 257                 262

cca act atg acg gtg agt gac tgg tat gag caa cat cgg aaa tat gga      868
Pro Thr Met Thr Val Ser Asp Trp Tyr Glu Gln His Arg Lys Tyr Gly
263                 268                 273                 278

gca tta ccg gat cag gga ata gcc aag gca gca cca gag gaa ttc aga      916
Ala Leu Pro Asp Gln Gly Ile Ala Lys Ala Ala Pro Glu Glu Phe Arg
279                 284                 289                 294

aaa gca gct cag caa cag gaa gaa caa gaa gaa aag gag gaa gag gat      964
Lys Ala Ala Gln Gln Gln Glu Glu Gln Glu Glu Lys Glu Glu Glu Asp
295                 300                 305                 310

gat gaa caa aca ctc cac aga gcc cgg gag tgg gat gac tgg aag gac     1012
Asp Glu Gln Thr Leu His Arg Ala Arg Glu Trp Asp Asp Trp Lys Asp
311                 316                 321                 326

acc cat cct agg ggc tat ggg aac cga cag aac atg ggc tga tcttccc     1061
Thr His Pro Arg Gly Tyr Gly Asn Arg Gln Asn Met Gly  *
327                 332                 337

acaacaccac aggactgcag ggtgcacaac tcccctgcca aggaaaacca tgcagtcctc   1121

ccctccctgg tctcctgctt cagctctgta caacgagggc aaagatgcta aatcttgctt   1181

tgcattcagt aaagtgtcaa gtgattaagt gtgtatttgt accctagatg atatgaacca   1241

gcagtcttgt tttggcatca tcctcatcat gttgtattcc agcttcttaa gtggaaggaa   1301

aagagtgctg agaaatggct ctgtataatc tatggctatc cgaattctct gaaaaaataa   1361

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agtccactgt gtttcgtgca cacacagcca cagtgaggag tgtccacttc tgcagtgatg 180

gccagtcctt cgtgacagcc tctgacgaca agacagtcaa agtgtgggca actcatcgcc 240

agaaattcct gttctccctg agccagcata tcaactgggt ccgctgtgcc aagttctccc 300

ccgacgggcg gctcatcgtg tctgccagtg atgacaagac tgttaagctg tgggacaaga 360

gcagccggga atgtgtccac tcgtattgtg agcatggcgg ctttgtcacc tatgtggact 420

tccaccccag tgggacgtgc attgccgctg ccggc atg gac aac aca gtg aag 473
Met Asp Asn Thr Val Lys
1

gtg tgg gac gtg cgg act cac cgg ctg ctg cag cat tat cag ttg cac 521
Val Trp Asp Val Arg Thr His Arg Leu Leu Gln His Tyr Gln Leu His
7 12 17 22

agt gca gca gtg aac ggg ctc tct ttc cac ccg tcg gga aac tac ctg 569
Ser Ala Ala Val Asn Gly Leu Ser Phe His Pro Ser Gly Asn Tyr Leu
23 28 33 38

atc aca gcc tcc agt gac tca acc ctg aag atc ctg gac ctg atg gag 617
Ile Thr Ala Ser Ser Asp Ser Thr Leu Lys Ile Leu Asp Leu Met Glu
39 44 49 54

ggc cgg ctg ctc tac aca ctc cac ggg cat cag gga cca gcc acc act 665
Gly Arg Leu Leu Tyr Thr Leu His Gly His Gln Gly Pro Ala Thr Thr
55 60 65 70

gtt gcc ttt tca aga acg ggg gag tat ttt gct tct gga ggc tct gat 713
Val Ala Phe Ser Arg Thr Gly Glu Tyr Phe Ala Ser Gly Gly Ser Asp
71 76 81 86

gaa caa gtg atg gtt tgg aag agt aac ttt gat att gtt gat cat gga 761
Glu Gln Val Met Val Trp Lys Ser Asn Phe Asp Ile Val Asp His Gly
87 92 97 102

gaa gtc acg aaa gtg ccg agg ccc cca gcc aca ctg gcc agc tcc atg 809
Glu Val Thr Lys Val Pro Arg Pro Pro Ala Thr Leu Ala Ser Ser Met
103 108 113 118

ggg aat ctg aca gtc tcc att ctg gag cag cgg ttg aca ctg aca gaa 857
Gly Asn Leu Thr Val Ser Ile Leu Glu Gln Arg Leu Thr Leu Thr Glu
119 124 129 134

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gac aag ctg aag cag tgt ctg gag aac cag cag cta atc atg cag aga      905
Asp Lys Leu Lys Gln Cys Leu Glu Asn Gln Gln Leu Ile Met Gln Arg
135                 140                 145                 150

gca aca cca tga tca ggggagcagg aatcaggagc tcggtggatt tgcaggtggc      960
Ala Thr Pro  *
151

aggccaggga tttgtaccat gggacttggg taaataaagg ggactgaact ctgtgggaat   1020

cacatccata ctggagccct ggatttttgc agttctgccc tccaccttgc tatctgcacc   1080

aggaggctct ccacctggca gccagaggtc ccccagtggg ccgggctcac acacaaatga   1140

tgcttcagac ccgaatgaga ggaccacatt ttgcttaatg taaaggagcc acttgaaaat   1200

gtctgctcct tcggggtcct gagattgtgg ctccccctct ggaggaggtg gctccacgat   1260

gccttgattt tcactcatca tttggacatg tgactggctt ttcctacctc tgccatggtg   1320

tagaaattga ttgcacagga atctcaaaat taaacctgaa ttcaatgcaa aaaaaaaa     1378
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GGCCGAATTC GCGGCCGCGT CGACCCACGC GTCCG

<210> 122
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<213> Homo sapiens

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<222> (456)..(1061)

<400> 122

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ctagtccagt gtggtggaat tccaagactg tccgcatctg ggtacccaat gtcaaaggtg     120

agtccactgt gtttcgtgca cacacagcca cagtgaggag tgtccacttc tgcagtgatg     180

gccagtcctt cgtgacagcc tctgacgaca agacagtcaa agtgtgggca actcatcgcc     240

agaaattcct gttctccctg agccagcata tcaactgggt ccgctgtgcc aagttctccc     300

ccgacgggcg gctcatcgtg tctgccagtg atgacaagac tgttaagctg tgggacaaga     360

gcagccggga atgtgtccac tcgtattgtg agcatggcgg ctttgtcacc tatgtggact     420

tccaccccag tgggacgtgc attgccgctg ccggc   atg gac aac aca gtg aag      473
                                          Met Asp Asn Thr Val Lys
                                            1

gtg tgg gac gtg cgg act cac cgg ctg ctg cag cat tat cag ttg cac      521
Val Trp Asp Val Arg Thr His Arg Leu Leu Gln His Tyr Gln Leu His
  7                  12                  17                  22
```

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agt gca gca gtg aac ggg ctc tct ttc cac ccg tcg gga aac tac ctg      569
Ser Ala Ala Val Asn Gly Leu Ser Phe His Pro Ser Gly Asn Tyr Leu
 23                  28                  33                  38

atc aca gcc tcc agt gac tca acc ctg aag atc ctg gac ctg atg gag      617
Ile Thr Ala Ser Ser Asp Ser Thr Leu Lys Ile Leu Asp Leu Met Glu
 39                  44                  49                  54

ggc cgg ctg ctc tac aca ctc cac ggg cat cag gga cca gcc acc act      665
Gly Arg Leu Leu Tyr Thr Leu His Gly His Gln Gly Pro Ala Thr Thr
 55                  60                  65                  70

gtt gcc ttt tca aga acg ggg gag tat ttt gct tct gga ggc tct gat      713
Val Ala Phe Ser Arg Thr Gly Glu Tyr Phe Ala Ser Gly Gly Ser Asp
 71                  76                  81                  86

gaa caa gtg atg gtt tgg aag agt aac ttt gat att gtt gat cat gga      761
Glu Gln Val Met Val Trp Lys Ser Asn Phe Asp Ile Val Asp His Gly
 87                  92                  97                 102

gaa gtc acg aaa gtg ccg agg ccc cca gcc aca ctg gcc agc tcc atg      809
Glu Val Thr Lys Val Pro Arg Pro Pro Ala Thr Leu Ala Ser Ser Met
103                 108                 113                 118

ggg aat ctg cca gaa gtg gac ttc cct gtc ccc cca ggc aga ggc agg      857
Gly Asn Leu Pro Glu Val Asp Phe Pro Val Pro Pro Gly Arg Gly Arg
119                 124                 129                 134

agt gtg gag tct gtg cag agc cag ccc cag gag ccc gtg agt gtg ccc      905
Ser Val Glu Ser Val Gln Ser Gln Pro Gln Glu Pro Val Ser Val Pro
135                 140                 145                 150

cag aca ctg act agc acg ctg gag cac att gtg ggc cag ctg gat gtc      953
Gln Thr Leu Thr Ser Thr Leu Glu His Ile Val Gly Gln Leu Asp Val
151                 156                 161                 166

ctc act cag aca gtc tcc att ctg gag cag cgg ttg aca ctg aca gaa     1001
Leu Thr Gln Thr Val Ser Ile Leu Glu Gln Arg Leu Thr Leu Thr Glu
167                 172                 177                 182

gac aag ctg aag cag tgt ctg gag aac cag cag cta atc atg cag aga     1049
Asp Lys Leu Lys Gln Cys Leu Glu Asn Gln Gln Leu Ile Met Gln Arg
183                 188                 193                 198

gca aca cca tga tca ggggagcagg aatcaggagc tcggtggatt tgcaggtggc     1104
Ala Thr Pro  *
199

aggccaggga tttgtaccat gggacttggg taaataaagg ggactgaact ctgtgggaat   1164

cacatccata ctggagccct ggatttttgc agttctgccc tccaccttgc tatctgcacc   1224

aggaggctct ccacctggca gccagaggtc ccccagtggg ccgggctcac acacaaatga   1284

tgcttcagac ccgaatgaga ggaccacatt ttgcttaatg taaaggagcc acttgaaaat   1344
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gtctgctcct tcggggtcct gagattgtgg ctccccctct ggaggaggtg gctccacgat 1404

gccttgattt tcactcatca tttggacatg tgactggctt ttcctacctc tgccatggtg 1464

tagaaattga ttgcacagga atctcaaaat taaacctgaa ttcaatgcaa aaaaaaaa 1522

<210> 123
<211> 2089
<212> DNA
<213> Homo sapiens

<220>
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<222> (398)..(2005)

<220>
<221> misc_feature
<222> (1)...(2089)
<223> n = a,t,c or g

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atttggccct cgaggccaag aattcggcac gagggtaagg aacagttaat aagaaaatgt 60

gccttgctaa ctgtgcacat tacaacaaag agctggcagc tcctgaagga aaagggcttg 120

tgccgctgcc gttcaaactt gtcagtcaac tcatgccagc agcctcagcg tctgcctccc 180

cagcacaccc tcattacatg tgtctgtctg gcctgatctg tgcatctgct cggagacgct 240

cctgacaagt cgggaatttc tctatttctc cactggtgca aagagcggat ttctccctgc 300

ttctcttctg tcacccccgc tcctctcccc caggaggctc cttgatttat ggtagctttg 360

gacttgcttc cccgtctgac tgtccttgac ttctaga atg gaa gaa gct gag ctg 415
Met Glu Glu Ala Glu Leu
1

gtg aag gga aga ctc cag gcc atc aca gat aaa aga aaa ata cag gaa 463
Val Lys Gly Arg Leu Gln Ala Ile Thr Asp Lys Arg Lys Ile Gln Glu
7 12 17 22

gaa atc tca cag aag cgt ctg aaa ata gag gaa gac aaa cta aag cac 511
Glu Ile Ser Gln Lys Arg Leu Lys Ile Glu Glu Asp Lys Leu Lys His
23 28 33 38

cag cat ttg aag aaa aag gcc ttg agg gag aaa tgg ctt cta gat gga 559
Gln His Leu Lys Lys Lys Ala Leu Arg Glu Lys Trp Leu Leu Asp Gly
39 44 49 54

atc agc agc gga aaa gaa cag gaa gag atg aag aag caa aat caa caa 607
Ile Ser Ser Gly Lys Glu Gln Glu Glu Met Lys Lys Gln Asn Gln Gln
55 60 65 70

gac cag cac cag atc cag gtt cta gaa caa agt atc ctc agg ctt gag 655

```
Asp Gln His Gln Ile Gln Val Leu Glu Gln Ser Ile Leu Arg Leu Glu
 71                  76                  81                  86

aaa gag atc caa gat ctt gaa aaa gct gaa ctg caa atc tca acg aag      703
Lys Glu Ile Gln Asp Leu Glu Lys Ala Glu Leu Gln Ile Ser Thr Lys
 87                  92                  97                 102

gaa gag gcc att tta aag aaa cta aag tca att gag cgg aca aca gaa      751
Glu Glu Ala Ile Leu Lys Lys Leu Lys Ser Ile Glu Arg Thr Thr Glu
103                 108                 113                 118

gac att ata aga tct gtg aaa gtg gaa aga gaa gaa aga gca gaa gag      799
Asp Ile Ile Arg Ser Val Lys Val Glu Arg Glu Glu Arg Ala Glu Glu
119                 124                 129                 134

tca att gag gac atc tat gct aat atc cct gac ctt cca aag tcc tac      847
Ser Ile Glu Asp Ile Tyr Ala Asn Ile Pro Asp Leu Pro Lys Ser Tyr
135                 140                 145                 150

ata cct tct agg tta agg aag gag ata aat gaa gaa aaa gaa gat gat      895
Ile Pro Ser Arg Leu Arg Lys Glu Ile Asn Glu Glu Lys Glu Asp Asp
151                 156                 161                 166

gaa caa aat agg aaa gct tta tat gcc atg gaa att aaa gtt gaa aaa      943
Glu Gln Asn Arg Lys Ala Leu Tyr Ala Met Glu Ile Lys Val Glu Lys
167                 172                 177                 182

gac ttg aag act gga gaa agt aca gtt ctg tct tca ata cct ctg cca      991
Asp Leu Lys Thr Gly Glu Ser Thr Val Leu Ser Ser Ile Pro Leu Pro
183                 188                 193                 198

tca gat gac ttt aaa ggt aca gga ata aaa gtt tat gat gat ggg caa     1039
Ser Asp Asp Phe Lys Gly Thr Gly Ile Lys Val Tyr Asp Asp Gly Gln
199                 204                 209                 214

aag tca gtg tat gca gta agt tct aat cac agt gca gca tac aat ggc     1087
Lys Ser Val Tyr Ala Val Ser Ser Asn His Ser Ala Ala Tyr Asn Gly
215                 220                 225                 230

acc gat ggc ctg gca cca gtt gaa gta gag gaa ctt cta aga caa gcc     1135
Thr Asp Gly Leu Ala Pro Val Glu Val Glu Glu Leu Leu Arg Gln Ala
231                 236                 241                 246

tca gag aga aac tct aaa tcc cca aca gag tat cat gag cct gta tat     1183
Ser Glu Arg Asn Ser Lys Ser Pro Thr Glu Tyr His Glu Pro Val Tyr
247                 252                 257                 262

gcc aat ccc ttt tac agg cct aca acc cca cag aga gaa acg gtg acc     1231
Ala Asn Pro Phe Tyr Arg Pro Thr Thr Pro Gln Arg Glu Thr Val Thr
263                 268                 273                 278

cct gga cca aac ttt caa gaa agg ata aag att aaa act aat gga ctg     1279
Pro Gly Pro Asn Phe Gln Glu Arg Ile Lys Ile Lys Thr Asn Gly Leu
279                 284                 289                 294

ggt att ggt gta aat gaa tcc ata cac aat atg ggc aat ggt ctt tca     1327
Gly Ile Gly Val Asn Glu Ser Ile His Asn Met Gly Asn Gly Leu Ser
```

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295                 300                 305                 310

gag gaa agg gga aac aac ttc aat cac atc agt ccc att ccg cca gtg     1375
Glu Glu Arg Gly Asn Asn Phe Asn His Ile Ser Pro Ile Pro Pro Val
311                 316                 321                 326

cct cat ccc cga tca gtg att caa caa gca gaa gag aag ctt cac acc     1423
Pro His Pro Arg Ser Val Ile Gln Gln Ala Glu Glu Lys Leu His Thr
327                 332                 337                 342

ccg caa aaa agg cta atg act cct tgg gaa gaa tcg aat gtc atg cag     1471
Pro Gln Lys Arg Leu Met Thr Pro Trp Glu Glu Ser Asn Val Met Gln
343                 348                 353                 358

gac aaa gat gca ccc tct cca aag cca agg ctg agc ccc aga gag aca     1519
Asp Lys Asp Ala Pro Ser Pro Lys Pro Arg Leu Ser Pro Arg Glu Thr
359                 364                 369                 374

ata ttt ggg aaa tct gaa cac cag aat tct tca ccc act tgt cag gag     1567
Ile Phe Gly Lys Ser Glu His Gln Asn Ser Ser Pro Thr Cys Gln Glu
375                 380                 385                 390

gac gag gaa gat gtc aga tat aat atc gtt cat tcc ctg cct cca gac     1615
Asp Glu Glu Asp Val Arg Tyr Asn Ile Val His Ser Leu Pro Pro Asp
391                 396                 401                 406

ata aat gat aca gaa ccg gtg aca atg att ttc atg ggg tat cag cag     1663
Ile Asn Asp Thr Glu Pro Val Thr Met Ile Phe Met Gly Tyr Gln Gln
407                 412                 417                 422

gca gaa gac agt gaa gaa gat aag aag ttt ctg aca gga tat gat ggg     1711
Ala Glu Asp Ser Glu Glu Asp Lys Lys Phe Leu Thr Gly Tyr Asp Gly
423                 428                 433                 438

atc atc cat gct gag ctg gtt gtg att gat gat gag gag gag gag gat     1759
Ile Ile His Ala Glu Leu Val Val Ile Asp Asp Glu Glu Glu Glu Asp
439                 444                 449                 454

gaa gga gaa gca gag aaa ccg tcc tac cac ccc ata gct ccc cat agt     1807
Glu Gly Glu Ala Glu Lys Pro Ser Tyr His Pro Ile Ala Pro His Ser
455                 460                 465                 470

cag gtg tac cag cca gcc aaa cca aca cca ctt cct aga aaa aga tca     1855
Gln Val Tyr Gln Pro Ala Lys Pro Thr Pro Leu Pro Arg Lys Arg Ser
471                 476                 481                 486

gaa gct agt cct cat gaa aac aca aat cat aaa tcc ccc cac aaa aat     1903
Glu Ala Ser Pro His Glu Asn Thr Asn His Lys Ser Pro His Lys Asn
487                 492                 497                 502

tcc ata tct ctg gaa aga gca aga agg aaa gct ttg ggc agc cct ggt     1951
Ser Ile Ser Leu Glu Arg Ala Arg Arg Lys Ala Leu Gly Ser Pro Gly
503                 508                 513                 518

tcc acc att ccc cat ttt tgt tgc ttc agg aca att ggg agt tgg ggg     1999
Ser Thr Ile Pro His Phe Cys Cys Phe Arg Thr Ile Gly Ser Trp Gly
519                 524                 529                 534
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```
ctt tag ggatccatcc tttaacagtt ttttagggtt gaggattggg ccagttnggg      2055
Leu  *
535

ggaaaaggtg ttttttnggg tttnttcccc cccg                              2089
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<210> 124
<211> 1866
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (162)..(1421)

<400> 124

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ggaattcgcc gggttccgtg tgtctatgtc aatgtgtctg tccttcactc ctccattgtc     60

tgccgccact gctgctgctg ctgctgctgc cgctgctgct gcacgaatcg ccgcagcccc    120

cagccttgcg cgtcgtcgct acctcctcgg acagaaattt t    atg aat aag cat      173
                                                 Met Asn Lys His
                                                   1

cag aag cca gtg cta aca ggc cag cgg ttc aaa act cgg aaa agg gat      221
Gln Lys Pro Val Leu Thr Gly Gln Arg Phe Lys Thr Arg Lys Arg Asp
  5                  10                  15                  20

gaa aaa gag aaa ttc gaa ccc aca gtc ttc agg gat aca ctt gtc cag      269
Glu Lys Glu Lys Phe Glu Pro Thr Val Phe Arg Asp Thr Leu Val Gln
 21                  26                  31                  36

ggg ctt aat gag gct ggt gat gac ctt gaa gct gta gcc aaa ttt ctg      317
Gly Leu Asn Glu Ala Gly Asp Asp Leu Glu Ala Val Ala Lys Phe Leu
 37                  42                  47                  52

gac tct aca ggc tca aga tta gat tat cgt cgc tat gca gac aca ctc      365
Asp Ser Thr Gly Ser Arg Leu Asp Tyr Arg Arg Tyr Ala Asp Thr Leu
 53                  58                  63                  68

ttc gat atc ctg gtg gct ggc agt atg ctt gcc cct gga gga acg cgc      413
Phe Asp Ile Leu Val Ala Gly Ser Met Leu Ala Pro Gly Gly Thr Arg
 69                  74                  79                  84

ata gat gat ggt gac aag acc aag atg acc aac cac tgt gtg ttt tca      461
Ile Asp Asp Gly Asp Lys Thr Lys Met Thr Asn His Cys Val Phe Ser
 85                  90                  95                 100

gca aat gaa gat cat gaa acc atc cga aac tat gct cag gtc ttc aat      509
Ala Asn Glu Asp His Glu Thr Ile Arg Asn Tyr Ala Gln Val Phe Asn
101                 106                 111                 116

aaa ctc atc agg aga tat aag tat ttg gag aag gca ttt gaa gat gaa      557
```

```
Lys Leu Ile Arg Arg Tyr Lys Tyr Leu Glu Lys Ala Phe Glu Asp Glu
117                 122                 127                 132

atg aaa aag ctt ctc ctc ttc ctt aaa gcc ttt tcc gaa aca gag cag      605
Met Lys Lys Leu Leu Leu Phe Leu Lys Ala Phe Ser Glu Thr Glu Gln
133                 138                 143                 148

aca aag ttg gcg atg ctg tcg ggg att ctg ctg ggc aat ggc acc ctg      653
Thr Lys Leu Ala Met Leu Ser Gly Ile Leu Leu Gly Asn Gly Thr Leu
149                 154                 159                 164

ccc gcc acc atc ctc acc agt ctc ttc acc gac agc tta gtc aaa gaa      701
Pro Ala Thr Ile Leu Thr Ser Leu Phe Thr Asp Ser Leu Val Lys Glu
165                 170                 175                 180

ggc att gcg gcc tca ttt gct gtc aag ctt ttc aaa gca tgg atg gca      749
Gly Ile Ala Ala Ser Phe Ala Val Lys Leu Phe Lys Ala Trp Met Ala
181                 186                 191                 196

gaa aaa gat gcc aac tct gtt acc tcg tct ttg aga aaa gcc aac tta      797
Glu Lys Asp Ala Asn Ser Val Thr Ser Ser Leu Arg Lys Ala Asn Leu
197                 202                 207                 212

gac aag agg ctg ctt gaa ctc ttt cca gtt aac aga cag agt gtg gat      845
Asp Lys Arg Leu Leu Glu Leu Phe Pro Val Asn Arg Gln Ser Val Asp
213                 218                 223                 228

cat ttt gct aaa tac ttc act gac gca ggt ctt aag gag ctt tcc gac      893
His Phe Ala Lys Tyr Phe Thr Asp Ala Gly Leu Lys Glu Leu Ser Asp
229                 234                 239                 244

ttc ctc cga gtc cag cag tcc ctg ggc acc agg aag gaa ctg cag aag      941
Phe Leu Arg Val Gln Gln Ser Leu Gly Thr Arg Lys Glu Leu Gln Lys
245                 250                 255                 260

gag ctc cag gag cgt ctt tct cag gaa tgc ccg atc aag gag gtg gtg      989
Glu Leu Gln Glu Arg Leu Ser Gln Glu Cys Pro Ile Lys Glu Val Val
261                 266                 271                 276

ctt tat gtc aaa gaa gaa atg aag agg aat gat ctt cca gaa aca gca     1037
Leu Tyr Val Lys Glu Glu Met Lys Arg Asn Asp Leu Pro Glu Thr Ala
277                 282                 287                 292

gtg att ggt ctt ctg tgg aca tgt ata atg aac gct gtt gag tgg aac     1085
Val Ile Gly Leu Leu Trp Thr Cys Ile Met Asn Ala Val Glu Trp Asn
293                 298                 303                 308

aag aag gaa gaa ctt gtt gca gag cag gct ctg aag cac ctg aag caa     1133
Lys Lys Glu Glu Leu Val Ala Glu Gln Ala Leu Lys His Leu Lys Gln
309                 314                 319                 324

tat gct ccc ctg ctg gcc gtg ttc agc tcc caa ggc cag tca gag ctg     1181
Tyr Ala Pro Leu Leu Ala Val Phe Ser Ser Gln Gly Gln Ser Glu Leu
325                 330                 335                 340

atc ctc ctc cag aag gtt cag gaa tac tgc tac gac aac atc cat ttc     1229
Ile Leu Leu Gln Lys Val Gln Glu Tyr Cys Tyr Asp Asn Ile His Phe
```

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341                 346                 351                 356

atg aaa gcc ttt cag aag att gtg gtt ctc ttt tat aaa gct gat gtt     1277
Met Lys Ala Phe Gln Lys Ile Val Val Leu Phe Tyr Lys Ala Asp Val
357                 362                 367                 372

ctg agc gaa gaa gca ata ctg aaa tgg tat aag gaa gca cat gtt gct     1325
Leu Ser Glu Glu Ala Ile Leu Lys Trp Tyr Lys Glu Ala His Val Ala
373                 378                 383                 388

aaa ggc aaa agt gtt ttt ctt gac cag atg aag aaa ttt gtt gag tgg     1373
Lys Gly Lys Ser Val Phe Leu Asp Gln Met Lys Lys Phe Val Glu Trp
389                 394                 399                 404

tta caa aat gca gaa gaa gaa tcc gaa tcg gaa ggt gag gaa aat taa     1421
Leu Gln Asn Ala Glu Glu Glu Ser Glu Ser Glu Gly Glu Glu Asn  *
405                 410                 415                 420

atggctcaac aagcacaata cctaggttac cacacaccac tttttgattg ggaatgctga   1481

accatttgag aagagaaact tggcttctgt tttcgcaaaa aaaaaaaaaa ataggatagg   1541

cttcccttgt gcagagggag aaatggtttt gtttttgttt tgtttttaaa tggagccctg   1601

aggcatcagc tattaaactt gggactctac ctctcactcc ctatatgcta acttaaagcc   1661

attcaacaag gagtcaagta gatttgaaat taaaaactca acagactcct ccttttttaa   1721

ctgtattttt cagggactgt gtggtgaccg ccccccctggt gtttattaca ggccccttttg  1781

gtagttgggg atctgctcat gtatgtgatt tgacaaacca gttttttaaa ataaatggct   1841

ttttaaaaat ttggaaaaaa aaaaa                                         1866
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<210> 125
<211> 1606
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (298)..(816)

<220>
<221> misc_feature
<222> (1)...(1606)
<223> n = a,t,c or g

<400> 125

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atttggccct cgaggccaag aattcggcac gagatacata cctcctattt acatgtccct     60

cctcccacta ttatgtcacc tttctaaaca ccgcaattgg gagatgagac aatgcgcagg    120

aacgaagaac tgttctggtg aagaggaccc aggggcagtg agaggggggct agggacaaaa   180
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ggtgaatggg gagctggttc aggttagaag aatgggtgca tgtgaggggc atttggagaa    240

tgcgagctgg gggagggaga gtggctgagc ctgtaggcac agtagacaca tgtagta   297

atg acg ggg atg tgt tat gcc cca cac cag gtg ttg tcc tac atc aat      345
Met Thr Gly Met Cys Tyr Ala Pro His Gln Val Leu Ser Tyr Ile Asn
  1               5                  10                  15

ggg gtc aca aca agc aaa cct gga gta tcc ttg gtc tac tcc atg ccc      393
Gly Val Thr Thr Ser Lys Pro Gly Val Ser Leu Val Tyr Ser Met Pro
 17                  22                  27                  32

tcc cgg aac ctg tcc ctg cgg ctg gag ggt ctc cag gag aaa gac tct      441
Ser Arg Asn Leu Ser Leu Arg Leu Glu Gly Leu Gln Glu Lys Asp Ser
 33                  38                  43                  48

ggc ccc tac agc tgc tcc gtg aat gtg caa gac aaa caa ggc aaa tct      489
Gly Pro Tyr Ser Cys Ser Val Asn Val Gln Asp Lys Gln Gly Lys Ser
 49                  54                  59                  64

agg ggc cac agc atc aaa acc tta gaa ctc aat gta ctg gtt cct cca      537
Arg Gly His Ser Ile Lys Thr Leu Glu Leu Asn Val Leu Val Pro Pro
 65                  70                  75                  80

gct cct cca tcc tgc cgt ctc cag ggt gtg ccc cat gtg ggg gca aac      585
Ala Pro Pro Ser Cys Arg Leu Gln Gly Val Pro His Val Gly Ala Asn
 81                  86                  91                  96

gtg acc ctg agc tgc cag tct cca agg agt aag ccc gct gtc caa tac      633
Val Thr Leu Ser Cys Gln Ser Pro Arg Ser Lys Pro Ala Val Gln Tyr
 97                 102                 107                 112

cag tgg gat cgg cag ctt cca tcc ttc cag act ttc ttt gca cca gca      681
Gln Trp Asp Arg Gln Leu Pro Ser Phe Gln Thr Phe Phe Ala Pro Ala
113                 118                 123                 128

tta gat gtc atc cgt ggg tct tta agc ctc acc aac ctt tcg tct tcc      729
Leu Asp Val Ile Arg Gly Ser Leu Ser Leu Thr Asn Leu Ser Ser Ser
129                 134                 139                 144

atg gct gga gtc tat gtc tgc aag gcc cac aat gag gtg ggc act gcc      777
Met Ala Gly Val Tyr Val Cys Lys Ala His Asn Glu Val Gly Thr Ala
145                 150                 155                 160

aat tgt aat gtg acg ctg gaa gtg agc aca ggt cag tga gggggcctgg       826
Asn Cys Asn Val Thr Leu Glu Val Ser Thr Gly Gln  *
161                 166                 171

agctgcagtg gttgctggag ctgttgtggg taccctggtt ggactggggt tgctggctgg    886

gctggtcctc ttgtaccacc gccggggcaa ggccctggag gagccagcca atgatatcaa    946

ggaggatgcc attgctcccc ggaccctgcc ctggcccaag agctcagaca caatctccaa   1006

gaatgggacc ctttcctctg tcacctccgc acgagccctc cggccacccc atggccctcc   1066
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caggcctggt gcattgaccc ccacgcccag tctctccagc caggccctgc cctcaccaag 1126

actgcccacg acagatgggg cccaccctca accaatatcc cccatccctg gtggggtttc 1186

ttcctctggc ttgagccgca tgggtgctgt gcctgtgatg gtgcctgccc agagtcaagc 1246

tggctctctg gtatgatgac cccaccactc attggctaaa ggatttgggg tctctccttc 1306

ctataggggt cacctctagc acagagggcc ttgagtcatg gggaaaggag ttcacactcc 1366

tgacccttag tactctgccc ccacctctct ttactgtggg ggaaaccatc ttcagtaagg 1426

accttaagtg tccagggaga cagaagggag aagagggaag ttggatcttt ggaatttggg 1486

gagggagcct tccaccccac ccttgantcc tccttattga aggccagctg gttgaantta 1546

ggntatttca ccaagagttg agggggggcag agattttcca ttcattgagt tttnccaggg 1606

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agggatcttt aaaaagggcc ccccccttttt ttttttttttt ttttttttttt ttttttttta 120

agggttgtcg tgcaggtaga ggaaatgaga gtgattacag aaaactggaa gaa atg 176
Met
1

cac caa aga ttc ctg gtt tca gag cgt tca aaa gat gat ctt cag cta 224
His Gln Arg Phe Leu Val Ser Glu Arg Ser Lys Asp Asp Leu Gln Leu
2 7 12 17

aga ctt acg aga gca gaa aat aga ata aaa caa ctt gaa act gac tcc 272
Arg Leu Thr Arg Ala Glu Asn Arg Ile Lys Gln Leu Glu Thr Asp Ser
18 23 28 33

tca gaa gaa ata tca cgt tac caa gaa atg att cag aaa ctt caa aat 320
Ser Glu Glu Ile Ser Arg Tyr Gln Glu Met Ile Gln Lys Leu Gln Asn
34 39 44 49

gta ttg gag tct gag aga gag aac tgt ggg ctt gtc agt gaa caa agg 368
Val Leu Glu Ser Glu Arg Glu Asn Cys Gly Leu Val Ser Glu Gln Arg
50 55 60 65

cta aaa ctt cag caa gaa aat aaa cag tta cgg aaa gag act gag agt 416
Leu Lys Leu Gln Gln Glu Asn Lys Gln Leu Arg Lys Glu Thr Glu Ser

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 66                  71                  76                  81

tta agg aag att gcc ctg gag gct caa aaa aaa gcc aaa gta aag atc      464
Leu Arg Lys Ile Ala Leu Glu Ala Gln Lys Lys Ala Lys Val Lys Ile
 82                  87                  92                  97

agt aca atg gaa cat gaa ttt tca ata aag gaa cgt gga ttt gaa gtt      512
Ser Thr Met Glu His Glu Phe Ser Ile Lys Glu Arg Gly Phe Glu Val
 98                 103                 108                 113

caa ttg aga gag atg gaa gac agt aat aga aat tcc att gtt gaa ctg      560
Gln Leu Arg Glu Met Glu Asp Ser Asn Arg Asn Ser Ile Val Glu Leu
114                 119                 124                 129

agg cat ctc cta gcg act caa cag aag gca gcc aat agg tgg aaa gaa      608
Arg His Leu Leu Ala Thr Gln Gln Lys Ala Ala Asn Arg Trp Lys Glu
130                 135                 140                 145

gaa acg aag aaa ctt act gaa agt gca gaa att aga atc aat aat cta      656
Glu Thr Lys Lys Leu Thr Glu Ser Ala Glu Ile Arg Ile Asn Asn Leu
146                 151                 156                 161

aag agt gag ctg agt cga cag aaa ctt cat acc caa gag ctg ctt tct      704
Lys Ser Glu Leu Ser Arg Gln Lys Leu His Thr Gln Glu Leu Leu Ser
162                 167                 172                 177

cag ctg gaa atg gca aat gaa aag gta gct gag aat gaa aag cta att      752
Gln Leu Glu Met Ala Asn Glu Lys Val Ala Glu Asn Glu Lys Leu Ile
178                 183                 188                 193

cta gag cat caa gaa aaa gcc aac aga ctt caa agg cgt cta agt cag      800
Leu Glu His Gln Glu Lys Ala Asn Arg Leu Gln Arg Arg Leu Ser Gln
194                 199                 204                 209

gca gaa gag aga gct gct tca gct tcc cag cag ctc agt gtg att aca      848
Ala Glu Glu Arg Ala Ala Ser Ala Ser Gln Gln Leu Ser Val Ile Thr
210                 215                 220                 225

gtg cag aga aga aaa gca gcc tcc ctg atg aat ctg gaa aat att taa      896
Val Gln Arg Arg Lys Ala Ala Ser Leu Met Asn Leu Glu Asn Ile  *
226                 231                 236                 241

aaatattcat agttcactca cagaacttta gagttgggaa agcagttgga ctagaagtg     955
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<213> Homo sapiens

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tcctacccac atttgccaaa atacgaaccc cttattattt atcagcctaa cccatctcga     120

gacttgaaga atcttatcta tcccaaccca ccacacccta ttaccacttt gaatgtgtcc     180

tcttatggat ggctctggga ttccttggtt tctgatgaaa aatcagctgt tactcttatt     240

gagggttcct catatggg  atg aac tgc ttc tct ttt gcc cgc ttt tgg aat      291
                     Met Asn Cys Phe Ser Phe Ala Arg Phe Trp Asn
                       1               5

tgt ttc ttt gtc ttt gac agt ctg ata aca atg ttt cta ggt gta aac      339
Cys Phe Phe Val Phe Asp Ser Leu Ile Thr Met Phe Leu Gly Val Asn
 12                  17                  22                  27

ctc tat tct gat tct gga tct gac tca gat tct gat caa gag aat gct      387
Leu Tyr Ser Asp Ser Gly Ser Asp Ser Asp Ser Asp Gln Glu Asn Ala
 28                  33                  38                  43

gcc tct ggc agt aat gcc tct gga agt gaa agt gat cag gat gaa aga      435
Ala Ser Gly Ser Asn Ala Ser Gly Ser Glu Ser Asp Gln Asp Glu Arg
 44                  49                  54                  59

ggt gat tca gga caa cca agt aat aag gaa ctg ttt gga gat gac agt      483
Gly Asp Ser Gly Gln Pro Ser Asn Lys Glu Leu Phe Gly Asp Asp Ser
 60                  65                  70                  75

gag gac gag gga gct tca cat cat agt ggt agt gat aat cac tct gaa      531
Glu Asp Glu Gly Ala Ser His His Ser Gly Ser Asp Asn His Ser Glu
 76                  81                  86                  91

aga tca gac aat aga tca gaa gct tct gag cgt tct gac cat gag gac      579
Arg Ser Asp Asn Arg Ser Glu Ala Ser Glu Arg Ser Asp His Glu Asp
 92                  97                 102                 107

aat gac ccc tca gat gta gat cag cac agt gga tca gaa gcc cct aat      627
Asn Asp Pro Ser Asp Val Asp Gln His Ser Gly Ser Glu Ala Pro Asn
108                 113                 118                 123

gat gat gaa gac gaa ggt cat aga tcg gat gga ggg agc cat cat tca      675
Asp Asp Glu Asp Glu Gly His Arg Ser Asp Gly Gly Ser His His Ser
124                 129                 134                 139

gaa gca gaa ggt tct gaa aaa gca cat tca gat gat gaa aaa tgg ggc      723
Glu Ala Glu Gly Ser Glu Lys Ala His Ser Asp Asp Glu Lys Trp Gly
140                 145                 150                 155

aga gaa gat aaa agt gac cag tca gat gat gaa aag ata caa aat tct      771
Arg Glu Asp Lys Ser Asp Gln Ser Asp Asp Glu Lys Ile Gln Asn Ser
156                 161                 166                 171

gat gat gag gag agg gca caa gga tct gat gaa gat aag ctg cag aat      819
Asp Asp Glu Glu Arg Ala Gln Gly Ser Asp Glu Asp Lys Leu Gln Asn
172                 177                 182                 187

tct gac gat gat gag aaa atg cag aac aca gat gat gag gag agg cct      867
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Ser Asp Asp Asp Glu Lys Met Gln Asn Thr Asp Asp Glu Glu Arg Pro
188                 193                 198                 203

cag ctt tcc gat gat gag aga caa cag cta tct gag gag gaa aag gct      915
Gln Leu Ser Asp Asp Glu Arg Gln Gln Leu Ser Glu Glu Glu Lys Ala
204                 209                 214                 219

aat tct gat gat gaa cgg ccg gta gct tct gat aat gat gat gag aaa      963
Asn Ser Asp Asp Glu Arg Pro Val Ala Ser Asp Asn Asp Asp Glu Lys
220                 225                 230                 235

cag aat tct gat gat gaa gaa caa cca cag ctg tct gat gaa gag aaa     1011
Gln Asn Ser Asp Asp Glu Glu Gln Pro Gln Leu Ser Asp Glu Glu Lys
236                 241                 246                 251

atg caa aat tct gat gat gaa agg cca cag gcc tca gat gaa gaa cac     1059
Met Gln Asn Ser Asp Asp Glu Arg Pro Gln Ala Ser Asp Glu Glu His
252                 257                 262                 267

agg cat tca gat gat gaa gag gaa cag gat cat aaa tca gaa tct gca     1107
Arg His Ser Asp Asp Glu Glu Glu Gln Asp His Lys Ser Glu Ser Ala
268                 273                 278                 283

aga ggc agt gat agt gaa gat gaa gtt tta cga atg aaa cgc aag aat     1155
Arg Gly Ser Asp Ser Glu Asp Glu Val Leu Arg Met Lys Arg Lys Asn
284                 289                 294                 299

gcg att gca tct gat tca gaa gcg gat agt gac act gag gtg cca aaa     1203
Ala Ile Ala Ser Asp Ser Glu Ala Asp Ser Asp Thr Glu Val Pro Lys
300                 305                 310                 315

gat aat agt gga acc atg gat tta ttt gga ggt gca gat gat atc tct     1251
Asp Asn Ser Gly Thr Met Asp Leu Phe Gly Gly Ala Asp Asp Ile Ser
316                 321                 326                 331

tca ggg agt gat gga gaa gac aaa cca cct act cca gga cag cct gtt     1299
Ser Gly Ser Asp Gly Glu Asp Lys Pro Pro Thr Pro Gly Gln Pro Val
332                 337                 342                 347

gat gaa aat gga ttg cct cag gat caa cag gaa gag gag cca att cct     1347
Asp Glu Asn Gly Leu Pro Gln Asp Gln Gln Glu Glu Glu Pro Ile Pro
348                 353                 358                 363

gag acc aga ata gaa gta gaa ata ccc aaa gta aac act gat tta gga     1395
Glu Thr Arg Ile Glu Val Glu Ile Pro Lys Val Asn Thr Asp Leu Gly
364                 369                 374                 379

aac gac tta tat ttt gtt aaa ctg ccc aac ttt ctc agt gta gag ccc     1443
Asn Asp Leu Tyr Phe Val Lys Leu Pro Asn Phe Leu Ser Val Glu Pro
380                 385                 390                 395

aga cct ttt gat cct cag tat tat gaa gat gaa ttt gaa gat gaa gaa     1491
Arg Pro Phe Asp Pro Gln Tyr Tyr Glu Asp Glu Phe Glu Asp Glu Glu
396                 401                 406                 411

atg ctg gat gaa gaa ggt aga acc agg tta aaa tta aag gta gaa aat     1539
Met Leu Asp Glu Glu Gly Arg Thr Arg Leu Lys Leu Lys Val Glu Asn
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412                 417                 422                 427

act ata aga tgg agg ata cgc cga gat gaa gaa gga aat gaa att aaa     1587
Thr Ile Arg Trp Arg Ile Arg Arg Asp Glu Glu Gly Asn Glu Ile Lys
428                 433                 438                 443

gaa agc aat gct cgg ata gtc aag tgg tca gat gga agc atg tcc ctg     1635
Glu Ser Asn Ala Arg Ile Val Lys Trp Ser Asp Gly Ser Met Ser Leu
444                 449                 454                 459

cat tta ggc aat gaa gtg ttt gat gtg tac aaa gcc cca ctg cag ggc     1683
His Leu Gly Asn Glu Val Phe Asp Val Tyr Lys Ala Pro Leu Gln Gly
460                 465                 470                 475

gac cac aat cat ctt ttt ata aga caa ggt act ggt cta cag gga caa     1731
Asp His Asn His Leu Phe Ile Arg Gln Gly Thr Gly Leu Gln Gly Gln
476                 481                 486                 491

gca gtc ttt aaa acg aaa ctc acc ttc aga cct cac tct acg gac agt     1779
Ala Val Phe Lys Thr Lys Leu Thr Phe Arg Pro His Ser Thr Asp Ser
492                 497                 502                 507

gcc aca cat aga aag atg act ctg tca ctt gca gat agg tgt tca aag     1827
Ala Thr His Arg Lys Met Thr Leu Ser Leu Ala Asp Arg Cys Ser Lys
508                 513                 518                 523

aca cag aag att aga atc ttg cca atg gct ggt cgt gat cct gaa tgc     1875
Thr Gln Lys Ile Arg Ile Leu Pro Met Ala Gly Arg Asp Pro Glu Cys
524                 529                 534                 539

caa cgc aca gaa atg att aag aaa gaa gaa gaa cgt ttg agg gct tcc     1923
Gln Arg Thr Glu Met Ile Lys Lys Glu Glu Glu Arg Leu Arg Ala Ser
540                 545                 550                 555

ata cgt agg gaa tct cag cag cgc cga atg aga gag aaa cag cac cag     1971
Ile Arg Arg Glu Ser Gln Gln Arg Arg Met Arg Glu Lys Gln His Gln
556                 561                 566                 571

cgg ggg ctg agc gcc agt tac ctg gaa cct gat cga tac gat gag gag     2019
Arg Gly Leu Ser Ala Ser Tyr Leu Glu Pro Asp Arg Tyr Asp Glu Glu
572                 577                 582                 587

gag gaa ggc gag gag tcc atc agc ttg gct gcc att aaa aac cga tat     2067
Glu Glu Gly Glu Glu Ser Ile Ser Leu Ala Ala Ile Lys Asn Arg Tyr
588                 593                 598                 603

aaa ggg ggc att cga gag gaa cga gcc aga atc tat tca tca gac agt     2115
Lys Gly Gly Ile Arg Glu Glu Arg Ala Arg Ile Tyr Ser Ser Asp Ser
604                 609                 614                 619

gat gag gga tca gaa gaa gat aaa gct caa aga tta ctc aaa gca aag     2163
Asp Glu Gly Ser Glu Glu Asp Lys Ala Gln Arg Leu Leu Lys Ala Lys
620                 625                 630                 635

aaa ctt acc agt gat gag gaa ggt gaa cct tcc gga aag aga aaa gca     2211
Lys Leu Thr Ser Asp Glu Glu Gly Glu Pro Ser Gly Lys Arg Lys Ala
636                 641                 646                 651
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gaa gat gat gat aaa gca aat aaa aag cat aag aag tat gtg atc agc     2259
Glu Asp Asp Asp Lys Ala Asn Lys Lys His Lys Lys Tyr Val Ile Ser
652                 657                 662                 667

gat gaa gag gaa gaa gat gat gat tga agtat gaaatatgaa aacattttat     2311
Asp Glu Glu Glu Glu Asp Asp Asp  *
668                 673

atattttatt gtacagttat aaatatgtaa acatgagtta ttttgattga aatgaatcga   2371

tttgcttttg tgtaatttta attgtaataa aacaatttaa aagcaaaaa              2420
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cccggctcgc tagccgtccg gcgggacgcc ggcgctgatg ggaaatccag ttatcaaaat    120

tgactcaaga agagagaacc taacagaaca ataacaatgg aagaaattgg gaacattatc    180

acaaagctat catcctgcca aactccaggc tcagatgtca caggttaaaa aaagtccttc    240

atgaaaaaga aagatcttaa gcagc  atg atg gat tca gaa gct cat gaa aag     292
                            Met Met Asp Ser Glu Ala His Glu Lys
                              1               5

agg cca cca ata cta aca tct tca aaa caa gat ata tca cct cat att      340
Arg Pro Pro Ile Leu Thr Ser Ser Lys Gln Asp Ile Ser Pro His Ile
 10                  15                  20                  25

aca aat gtt ggt gag atg aag cat tac ttg tgt ggc tgc tgt gca gcc      388
Thr Asn Val Gly Glu Met Lys His Tyr Leu Cys Gly Cys Cys Ala Ala
 26                  31                  36                  41

ttc aac aat gtc gca atc aca ttt ccc att cag aag gtc ctc ttt cga      436
Phe Asn Asn Val Ala Ile Thr Phe Pro Ile Gln Lys Val Leu Phe Arg
 42                  47                  52                  57

caa cag ctg tat ggc atc aaa acc cgg gat gca ata ctt cag ttg aga      484
Gln Gln Leu Tyr Gly Ile Lys Thr Arg Asp Ala Ile Leu Gln Leu Arg
 58                  63                  68                  73

agg gat gga ttt cga aat ttg tat cgt gga atc ctt ccc cca ttg atg      532
Arg Asp Gly Phe Arg Asn Leu Tyr Arg Gly Ile Leu Pro Pro Leu Met
 74                  79                  84                  89
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cag aag aca act acg ctt gca ctt atg ttt ggt ctg tat gag gat tta      580
Gln Lys Thr Thr Thr Leu Ala Leu Met Phe Gly Leu Tyr Glu Asp Leu
 90                  95                 100                 105

tcc tgc ctt ctc cac aag cat gtc agt gct cca gag ttt gca acc agt      628
Ser Cys Leu Leu His Lys His Val Ser Ala Pro Glu Phe Ala Thr Ser
106                 111                 116                 121

ggc gtg gcg gca gtg ctt gca ggg aca aca gaa gca att ttc act cca      676
Gly Val Ala Ala Val Leu Ala Gly Thr Thr Glu Ala Ile Phe Thr Pro
122                 127                 132                 137

ctg gaa aga gtt cag aca ttg ctt caa gac cac aag cat cat gac aaa      724
Leu Glu Arg Val Gln Thr Leu Leu Gln Asp His Lys His His Asp Lys
138                 143                 148                 153

ttt acc aac act tac cag gct ttc aag gca ctg aaa tgt cat gga att      772
Phe Thr Asn Thr Tyr Gln Ala Phe Lys Ala Leu Lys Cys His Gly Ile
154                 159                 164                 169

gga gag tat tat cga ggc ttg gtg ccc att ctt ttc cgg aat gga ctc      820
Gly Glu Tyr Tyr Arg Gly Leu Val Pro Ile Leu Phe Arg Asn Gly Leu
170                 175                 180                 185

agc aat gtc ttg ttt ttc ggc ctt cga ggt ccc att aag gag cat ctg      868
Ser Asn Val Leu Phe Phe Gly Leu Arg Gly Pro Ile Lys Glu His Leu
186                 191                 196                 201

cct acc gca acg act cac agt gct cat ctg gtc aat gat ttt atc tgt      916
Pro Thr Ala Thr Thr His Ser Ala His Leu Val Asn Asp Phe Ile Cys
202                 207                 212                 217

gga ggt cta ttg ggt gcc atg ttg gga ttc ttg ttt ttt cca att aat      964
Gly Gly Leu Leu Gly Ala Met Leu Gly Phe Leu Phe Phe Pro Ile Asn
218                 223                 228                 233

gtt gta aaa act cgc ata cag tct cag att ggt ggg gaa ttt cag tct     1012
Val Val Lys Thr Arg Ile Gln Ser Gln Ile Gly Gly Glu Phe Gln Ser
234                 239                 244                 249

ttc ccc aag gtt ttc caa aaa atc tgg ctg gaa cgg gac aga aaa ctg     1060
Phe Pro Lys Val Phe Gln Lys Ile Trp Leu Glu Arg Asp Arg Lys Leu
250                 255                 260                 265

ata aat ctt ttc aga ggt gcc cat ctg aat tac cat cgg tcc ctc atc     1108
Ile Asn Leu Phe Arg Gly Ala His Leu Asn Tyr His Arg Ser Leu Ile
266                 271                 276                 281

tct tgg ggc ata atc aat gca act tat gag ttc ttg tta aag gtt ata     1156
Ser Trp Gly Ile Ile Asn Ala Thr Tyr Glu Phe Leu Leu Lys Val Ile
282                 287                 292                 297

tga aaaa accatcagtt aagtgccatt tatcaactga atagaccttc taagaagcac     1213
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298
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tgctgccgcc tccacccagc ctccgcc atg gac ctc ttc ggg gac ctg ccg 111
Met Asp Leu Phe Gly Asp Leu Pro
1 5

gag ccc gag cgc tcg ccg cgc ccg gct gcc ggg aaa gaa gct cag aaa 159
Glu Pro Glu Arg Ser Pro Arg Pro Ala Ala Gly Lys Glu Ala Gln Lys
9 14 19 24

gga ccc ctg ctc ttt gat gac ctc cct ccg gcc agc agt act gac tca 207
Gly Pro Leu Leu Phe Asp Asp Leu Pro Pro Ala Ser Ser Thr Asp Ser
25 30 35 40

gga tca ggg gga cct ttg ctt ttt gat gat ctc cca ccc gct agc agt 255
Gly Ser Gly Gly Pro Leu Leu Phe Asp Asp Leu Pro Pro Ala Ser Ser
41 46 51 56

ggc gat tca ggt tct ctt gcc aca tca ata tcc cag atg gta aag act 303
Gly Asp Ser Gly Ser Leu Ala Thr Ser Ile Ser Gln Met Val Lys Thr
57 62 67 72

gaa ggg aaa gga gca aag aga aaa acc tcc gag gaa gag aag aat ggc 351
Glu Gly Lys Gly Ala Lys Arg Lys Thr Ser Glu Glu Glu Lys Asn Gly
73 78 83 88

agt gaa gag ctt gtg gaa aag aaa gtt tgt aaa gcc tct tcg gtg atc 399
Ser Glu Glu Leu Val Glu Lys Lys Val Cys Lys Ala Ser Ser Val Ile
89 94 99 104

ttt ggt ctg aag ggc tat gtg gct gag cgg aag ggt gag agg gag gag 447
Phe Gly Leu Lys Gly Tyr Val Ala Glu Arg Lys Gly Glu Arg Glu Glu
105 110 115 120

atg cag gat gcc cac gtc atc ctg aac gac atc acc gag gag tgt agg 495
Met Gln Asp Ala His Val Ile Leu Asn Asp Ile Thr Glu Glu Cys Arg
121 126 131 136

ccc cca tcg tcc ctc att act cgg gtt tca tat ttt gct gtt ttt gat 543
Pro Pro Ser Ser Leu Ile Thr Arg Val Ser Tyr Phe Ala Val Phe Asp
137 142 147 152

gga cat gga gga att cga gcc tca aaa ttt gct gca cag aat ttg cat 591

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Gly His Gly Gly Ile Arg Ala Ser Lys Phe Ala Ala Gln Asn Leu His
153                 158                 163                 168

caa aac tta atc aga aaa ttt cct aaa gga gat gta atc agt gta gag      639
Gln Asn Leu Ile Arg Lys Phe Pro Lys Gly Asp Val Ile Ser Val Glu
169                 174                 179                 184

aaa acc gtg aag aga tgc ctt ttg gac act ttc aag cat act gat gaa      687
Lys Thr Val Lys Arg Cys Leu Leu Asp Thr Phe Lys His Thr Asp Glu
185                 190                 195                 200

gag ttc ctt aaa caa gct tcc agc cag aag cct gcc tgg aaa gat ggg      735
Glu Phe Leu Lys Gln Ala Ser Ser Gln Lys Pro Ala Trp Lys Asp Gly
201                 206                 211                 216

tcc act gcc acg tgt gtt ctg gct gta gac aac att ctt tat att gcc      783
Ser Thr Ala Thr Cys Val Leu Ala Val Asp Asn Ile Leu Tyr Ile Ala
217                 222                 227                 232

aac ctc gga gat agt cgg gca atc ttg tgt cgt tat aat gag gag agt      831
Asn Leu Gly Asp Ser Arg Ala Ile Leu Cys Arg Tyr Asn Glu Glu Ser
233                 238                 243                 248

caa aaa cat gca gcc tta agc ctc agc aaa gag cat aat cca act cag      879
Gln Lys His Ala Ala Leu Ser Leu Ser Lys Glu His Asn Pro Thr Gln
249                 254                 259                 264

tat gaa gag cgg atg agg ata cag aag gct gga gga aac gtc agg gat      927
Tyr Glu Glu Arg Met Arg Ile Gln Lys Ala Gly Gly Asn Val Arg Asp
265                 270                 275                 280

ggg cgt gtt ttg ggc gtg cta gag gtg tca cgc tcc att ggg gac ggg      975
Gly Arg Val Leu Gly Val Leu Glu Val Ser Arg Ser Ile Gly Asp Gly
281                 286                 291                 296

cag tac aag cgc tgc ggt gtc acc tct gtg ccc gac atc aga cgc tgc     1023
Gln Tyr Lys Arg Cys Gly Val Thr Ser Val Pro Asp Ile Arg Arg Cys
297                 302                 307                 312

cag ctg acc ccc aat gac agg ttc att ttg ttg gcc tgt gat ggg ctc     1071
Gln Leu Thr Pro Asn Asp Arg Phe Ile Leu Leu Ala Cys Asp Gly Leu
313                 318                 323                 328

ttc aag gtc ttt acc cca gaa gaa gcc gtg aac ttc atc ttg tcc tgt     1119
Phe Lys Val Phe Thr Pro Glu Glu Ala Val Asn Phe Ile Leu Ser Cys
329                 334                 339                 344

ctc gag gat gaa aag atc cag acc cgg gaa ggg aag tcc gca gcc gaa     1167
Leu Glu Asp Glu Lys Ile Gln Thr Arg Glu Gly Lys Ser Ala Ala Glu
345                 350                 355                 360

gcc cgc tac gaa gca gcc tgc aac agg ctg gcc aac aag gcg gtg cag     1215
Ala Arg Tyr Glu Ala Ala Cys Asn Arg Leu Ala Asn Lys Ala Val Gln
361                 366                 371                 376

cgg ggc tcg gcc gac aac gtc act gtg atg gtg gtg cgg ata ggg cac     1263
Arg Gly Ser Ala Asp Asn Val Thr Val Met Val Val Arg Ile Gly His
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377                 382                 387                 392

tga gggg tggcgcgcgg ccaggagcac gcatggtatt gacttaaaag gttcattttg     1320
 *
393

tgtgtgtgca cattgtgtgt tttgtgtact cctgtgggac tcccatggtt gtaaataaag   1380

gtttctcttt ttttttccta aaaaaaaaaa aaaaaaa                            1417
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<400> 130

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aggtgagccc tcgccaaggt gacctcgcag gacactggtg aaggagcagt gaggaacctg    120

cagagtcaca cagttgacca attgagctgt gagcctggag cagatccgtg ggctgcagac    180

ccccgcccca gtgcctctcc ccctgcagcc ctgcccctcg aactgtgac    atg gag     235
                                                         Met Glu
                                                           1

aga gtg acc ctg gcc ctt ctc cta ctg gca ggc ctg act gcc ttg gaa      283
Arg Val Thr Leu Ala Leu Leu Leu Leu Ala Gly Leu Thr Ala Leu Glu
  3                   8                  13                  18

gcc aat gac cca ttt gcc aat aaa gac gat ccc ttc tac tat gac tgg      331
Ala Asn Asp Pro Phe Ala Asn Lys Asp Asp Pro Phe Tyr Tyr Asp Trp
 19                  24                  29                  34

aaa aac ctg cag ctg agc gga ctg atc tgc gga ggg ctc ctg gcc att      379
Lys Asn Leu Gln Leu Ser Gly Leu Ile Cys Gly Gly Leu Leu Ala Ile
 35                  40                  45                  50

gct ggg atc gcg gca gtt ctg agt ggc aaa tgc aaa tgc aag agc agc      427
Ala Gly Ile Ala Ala Val Leu Ser Gly Lys Cys Lys Cys Lys Ser Ser
 51                  56                  61                  66

cag aag cag cac agt cct gta cct gag aag gcc atc cca ctc atc act      475
Gln Lys Gln His Ser Pro Val Pro Glu Lys Ala Ile Pro Leu Ile Thr
 67                  72                  77                  82

cca ggc tct gcc act act tgc tga gcacaggact ggcctccagg gatggcctga     529
Pro Gly Ser Ala Thr Thr Cys  *
 83                  88
```

```
agcctaacac tggcccccag cacctcctcc cctgggaggc cttatcctca aggaaggact    589

tctctccaag ggcaggctgt taggcccctt tctgatcagg aggcttcttt atgaattaaa    649

ctcgccccac cacccccaaa aaaaaaaa                                       677
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<210> 131
<211> 1296
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (112)..(1080)

<400> 131

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aattgacccc tgtgtaccgg tccggatttg acggctctac ccacgcgtcc gcggacgcgt     60

gggcggacgc gtggggtcac cgtccaggtt ggactgcagc acctttgagc g atg gcg      117
                                                          Met Ala
                                                            1

gcg tct ggg gaa ccc cag agg cag tgg caa gag gag gtg gcg gcg gtg      165
Ala Ser Gly Glu Pro Gln Arg Gln Trp Gln Glu Glu Val Ala Ala Val
  3                   8                  13                  18

gta gtg gtg ggc tcc tgc atg acc gac ctg gtc agt ctt act tct cgt      213
Val Val Val Gly Ser Cys Met Thr Asp Leu Val Ser Leu Thr Ser Arg
 19                  24                  29                  34

ttg cca aaa act gga gaa acc atc cat gga cat aag ttt ttt att ggc      261
Leu Pro Lys Thr Gly Glu Thr Ile His Gly His Lys Phe Phe Ile Gly
 35                  40                  45                  50

ttt gga ggg aaa ggt gcc aac cag tgt gtc caa gct gct cgg ctt gga      309
Phe Gly Gly Lys Gly Ala Asn Gln Cys Val Gln Ala Ala Arg Leu Gly
 51                  56                  61                  66

gca atg acg tcc atg gtg tgt aag gtt ggc aaa gat tct ttt ggc aat      357
Ala Met Thr Ser Met Val Cys Lys Val Gly Lys Asp Ser Phe Gly Asn
 67                  72                  77                  82

gat tat ata gaa aac tta aaa cag aat gat att tct aca gaa ttt aca      405
Asp Tyr Ile Glu Asn Leu Lys Gln Asn Asp Ile Ser Thr Glu Phe Thr
 83                  88                  93                  98

tat cag act aaa gat gct gct aca gga act gct tct ata att gtc aat      453
Tyr Gln Thr Lys Asp Ala Ala Thr Gly Thr Ala Ser Ile Ile Val Asn
 99                 104                 109                 114

aat gaa ggc cag aat atc att gtc ata gtg gct gga gca aat tta ctt      501
Asn Glu Gly Gln Asn Ile Ile Val Ile Val Ala Gly Ala Asn Leu Leu
115                 120                 125                 130
```

```
ttg aat acg gag gat ctg agg gca gca acc aat gtc att agc aga gcc      549
Leu Asn Thr Glu Asp Leu Arg Ala Ala Thr Asn Val Ile Ser Arg Ala
131                 136                 141                 146

aaa gtc atg gtc tgc cag ctc gaa ata act cca gca act tct ttg gaa      597
Lys Val Met Val Cys Gln Leu Glu Ile Thr Pro Ala Thr Ser Leu Glu
147                 152                 157                 162

gcc cta aca atg gcc cgc agg agt gga gtg aaa acc ttg ttc aat cca      645
Ala Leu Thr Met Ala Arg Arg Ser Gly Val Lys Thr Leu Phe Asn Pro
163                 168                 173                 178

gcc cct gcc att gct gac ctg gat ccc cag ttc tac acc ctc tca gat      693
Ala Pro Ala Ile Ala Asp Leu Asp Pro Gln Phe Tyr Thr Leu Ser Asp
179                 184                 189                 194

gtg ttc tgc tgc aat gaa agt gag gct gag att tta act ggc ctc acg      741
Val Phe Cys Cys Asn Glu Ser Glu Ala Glu Ile Leu Thr Gly Leu Thr
195                 200                 205                 210

gtg ggc agc gct gca gat gct ggg gag gct gca tta gtg ctc ttg aaa      789
Val Gly Ser Ala Ala Asp Ala Gly Glu Ala Ala Leu Val Leu Leu Lys
211                 216                 221                 226

agg ggc tgc cag gtg gta atc att acc tta ggg gct gaa gga tgt gtg      837
Arg Gly Cys Gln Val Val Ile Ile Thr Leu Gly Ala Glu Gly Cys Val
227                 232                 237                 242

gtg ctg tca cag aca gaa cct gag cca aag cac att ccc aca gag aaa      885
Val Leu Ser Gln Thr Glu Pro Glu Pro Lys His Ile Pro Thr Glu Lys
243                 248                 253                 258

gtc aag gct gtg gat acc acg ggt gct ggt gac agc ttt gtg gga gct      933
Val Lys Ala Val Asp Thr Thr Gly Ala Gly Asp Ser Phe Val Gly Ala
259                 264                 269                 274

ctg gcc ttc tac ctg gct tac tat cca aat ctg tcc ttg gaa gac atg      981
Leu Ala Phe Tyr Leu Ala Tyr Tyr Pro Asn Leu Ser Leu Glu Asp Met
275                 280                 285                 290

ctc aac aga tcc aat ttc att gca gca gtc agt gtc cag gct gca gga     1029
Leu Asn Arg Ser Asn Phe Ile Ala Ala Val Ser Val Gln Ala Ala Gly
291                 296                 301                 306

aca cag tca tct tac cct tac aaa aaa gac ctt ccg ctt act ctg ttt     1077
Thr Gln Ser Ser Tyr Pro Tyr Lys Lys Asp Leu Pro Leu Thr Leu Phe
307                 312                 317                 322

tga ttgc tattagtccc aaaataaata tacctgggaa taaaatgtac ttgggggtgg     1134
 *
323

ctgctcctgg ctaatgctta ttagaaaatg tcctcgtccc ctttctttgc aaatattagt   1194

tcttttacga agtcatcctc aagcttcaat ttatttataa cgatgattct tttgctttcc   1254

atgcatttgc acaaaacaac cagaattaaa gattccacaa cc                      1296
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US 2003/0082175 A1

<210> 132
<211> 1160
<212> DNA
<213> Homo sapiens

<220>
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<400> 132
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cgggggagga gcccaag   atg cct ctg ctg ctc ctt gga gag aca gag cct      50
                     Met Pro Leu Leu Leu Leu Gly Glu Thr Glu Pro
                       1               5

ctt aag ttg gag cgg gac tgc cgg agc cca gtg gac ccc tgg gct gct      98
Leu Lys Leu Glu Arg Asp Cys Arg Ser Pro Val Asp Pro Trp Ala Ala
 12                  17                  22                  27

gcc agc ccc gac ctg gca ctt gct tgc ctg tgt cac tgt cag gat ttg     146
Ala Ser Pro Asp Leu Ala Leu Ala Cys Leu Cys His Cys Gln Asp Leu
 28                  33                  38                  43

tct agc ggc gca ttc cct aac agg ggt gtg ttg ggg gga gtc ctc ttt     194
Ser Ser Gly Ala Phe Pro Asn Arg Gly Val Leu Gly Gly Val Leu Phe
 44                  49                  54                  59

cca act gtc gaa atg gtt atc aaa gtg ttt gtt gct aca tct tct ggg     242
Pro Thr Val Glu Met Val Ile Lys Val Phe Val Ala Thr Ser Ser Gly
 60                  65                  70                  75

tcc ata gcg att agg aag aaa cag caa gaa gta gtg ggt ttt ttg gaa     290
Ser Ile Ala Ile Arg Lys Lys Gln Gln Glu Val Val Gly Phe Leu Glu
 76                  81                  86                  91

gcg aat aaa atc gac ttt aag gaa tta gat att gct gga gat gaa gac     338
Ala Asn Lys Ile Asp Phe Lys Glu Leu Asp Ile Ala Gly Asp Glu Asp
 92                  97                 102                 107

aac agg agg tgg atg aga gag aat gtt cct gga gag aaa aaa cct caa     386
Asn Arg Arg Trp Met Arg Glu Asn Val Pro Gly Glu Lys Lys Pro Gln
108                 113                 118                 123

aat ggg att cct ttg cct ccc cag atc ttc aat gag gag cag tac tgt     434
Asn Gly Ile Pro Leu Pro Pro Gln Ile Phe Asn Glu Glu Gln Tyr Cys
124                 129                 134                 139

ggg gat ttt gac tct ttc ttc tct gca aaa gaa gag aat att att tat     482
Gly Asp Phe Asp Ser Phe Phe Ser Ala Lys Glu Glu Asn Ile Ile Tyr
140                 145                 150                 155

tcc ttc ctt ggt ttg gct cct cct cca gac tca aag gga tca gag aag     530
Ser Phe Leu Gly Leu Ala Pro Pro Pro Asp Ser Lys Gly Ser Glu Lys
156                 161                 166                 171
```

```
gct gaa gaa ggt gga gaa act gag gca caa aaa gag ggc agt gaa gat      578
Ala Glu Glu Gly Gly Glu Thr Glu Ala Gln Lys Glu Gly Ser Glu Asp
172                 177                 182                 187

gtg ggc aac ctc cct gaa gcc cag gag aag aat gaa gaa gaa gga gag      626
Val Gly Asn Leu Pro Glu Ala Gln Glu Lys Asn Glu Glu Glu Gly Glu
188                 193                 198                 203

aca gcc aca gaa gag acg gaa gaa ata gcc atg gag ggt gcg gaa ggg      674
Thr Ala Thr Glu Glu Thr Glu Glu Ile Ala Met Glu Gly Ala Glu Gly
204                 209                 214                 219

gaa gcc gag gag gag gaa gaa act gca gaa gga gaa gag cct gga gaa      722
Glu Ala Glu Glu Glu Glu Glu Thr Ala Glu Gly Glu Glu Pro Gly Glu
220                 225                 230                 235

gac gaa gat tcc tag gccttttcat gcttcatttc ttccacttct ccagaaaatg      777
Asp Glu Asp Ser  *
236

gaagctatga agcaacattt caaatgtctc tccacaaacc aaactcaaca gaatactttg    837

gcttgaagcc ggcacaccca gggttactga ggacttatgc tgcctgacct ggttagatgt    897

acatggaggt atctcccgaa tcaatacctt catgtgcctg acagtcttgg cttttgaaga    957

ttttttttttc ttttttgctc tgcgatagct agaccatctt attaataata ctctgaaaaa   1017

aatgatttca aggcatggaa gttctctgtg atacaacaat acgtattctt caaatgcgcc   1077

ttatgctact tatctcagaa acaggtttta aaatgaagtg ctttccagag aaccatcata   1137

taaataaaga ttaatagaaa aat                                           1160
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<210> 133
<211> 947
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (227)..(853)

<400> 133

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atcgaacgca tgcggtaccg gtccggaatt cccgggtcga cccacgcgtc cgggcatctc     60

tgcacaggtc tccgattggt gcacagcaca gcctggcctt ttagggactg ttgtcgcgcg    120

tttaaagtga tagggaaagg gtccagtggc tgcttttatc gaccaatcaa atattttcct    180

gacagatccc aaaatattcc tgggccaatg gagggaggag cccaag   atg cct ctg     235
                                                     Met Pro Leu
                                                       1
```

```
ctg ctc ctt gga gag aca gag cct ctt aag ttg gag cgg gac tgc cgg      283
Leu Leu Leu Gly Glu Thr Glu Pro Leu Lys Leu Glu Arg Asp Cys Arg
  4                   9                  14                  19

agc cca gtg gac ccc tgg gct gct gcc agc ccc gac ctg gca ctt gct      331
Ser Pro Val Asp Pro Trp Ala Ala Ala Ser Pro Asp Leu Ala Leu Ala
 20                  25                  30                  35

tgc ctg tgt cac tgt cag gat ttg tct agc ggc gca ttc cct aac agg      379
Cys Leu Cys His Cys Gln Asp Leu Ser Ser Gly Ala Phe Pro Asn Arg
 36                  41                  46                  51

ggt gtg ttg ggg gga gtc ctc ttt cca act gtc gaa atg gtt atc aaa      427
Gly Val Leu Gly Gly Val Leu Phe Pro Thr Val Glu Met Val Ile Lys
 52                  57                  62                  67

gtg ttt gtt gct aca tct tct ggg tcc ata gcg att agg aag aaa cag      475
Val Phe Val Ala Thr Ser Ser Gly Ser Ile Ala Ile Arg Lys Lys Gln
 68                  73                  78                  83

caa gaa gta gtg ggt ttt ttg gaa gcg aat aaa atc gac ttt aag gaa      523
Gln Glu Val Val Gly Phe Leu Glu Ala Asn Lys Ile Asp Phe Lys Glu
 84                  89                  94                  99

tta gat att gct gga gat gaa gac aac agg agg tgg atg aga gag aat      571
Leu Asp Ile Ala Gly Asp Glu Asp Asn Arg Arg Trp Met Arg Glu Asn
100                 105                 110                 115

gtt cct gga gag aaa aaa cct caa aat ggg att cct ttg cct ccc cag      619
Val Pro Gly Glu Lys Lys Pro Gln Asn Gly Ile Pro Leu Pro Pro Gln
116                 121                 126                 131

atc ttc aat gag gag cag tac tgt ggg gat ttt gac tct ttc ttc tct      667
Ile Phe Asn Glu Glu Gln Tyr Cys Gly Asp Phe Asp Ser Phe Phe Ser
132                 137                 142                 147

gca aaa gaa gag aat att att tat tcc ttc ctt ggt ttg gct cct cct      715
Ala Lys Glu Glu Asn Ile Ile Tyr Ser Phe Leu Gly Leu Ala Pro Pro
148                 153                 158                 163

cca gac tca aag gaa gaa gaa gga gag aca gcc aca gaa gag acg gaa      763
Pro Asp Ser Lys Glu Glu Glu Gly Glu Thr Ala Thr Glu Glu Thr Glu
164                 169                 174                 179

gaa ata gcc atg gag ggt gcg gaa ggg gaa gcc gag gag gag gaa gaa      811
Glu Ile Ala Met Glu Gly Ala Glu Gly Glu Ala Glu Glu Glu Glu Glu
180                 185                 190                 195

act gca gaa gga gaa gag cct gga gaa gac gaa gat tcc tag gcctttt      860
Thr Ala Glu Gly Glu Glu Pro Gly Glu Asp Glu Asp Ser  *
196                 201                 206

catgcttcat ttcttccact tctccagaaa atggagctat tagcacattc aattcttccc    920

aaccaactca cagatcttgc ttaagcg                                       947
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<210> 134
<211> 1337
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (344)..(1192)

<400> 134
ggaggtaccg ctccggaatt cccgggtcga cccacgcgtc cggactcctg ttccgttgga 60

ggggcctgag gcgagcctga gcgcgctgtt ggccggaggg aagccggagg agaccgggtc 120

gactgggcag agcggcagag ggtcgaggag cctgctctgc acgcccaggg agtagaagtg 180

ggcagggagc agggtcacgt gagggagcgc gccgcgactg agcttgggtc cgactggagc 240

tcaggctcgc gacccagact ggtgggccag gcctccaagc cggccttaca cccaatccaa 300

ggaggacaga ccggacacag agggacggag cgagcaagga gac atg gct tca tca 355
Met Ala Ser Ser
1

ttc ctg ccc gcg ggg gcc atc acc ggc gac agc ggt gga gag ctg agc 403
Phe Leu Pro Ala Gly Ala Ile Thr Gly Asp Ser Gly Gly Glu Leu Ser
5 10 15 20

tca ggg gac gac tcc ggg gag gtg gag ttc ccc cat agc cct gag atc 451
Ser Gly Asp Asp Ser Gly Glu Val Glu Phe Pro His Ser Pro Glu Ile
21 26 31 36

gag gag acc agt tgc ctg gcc gag ctg ttt gag aag gct gcc gcg cac 499
Glu Glu Thr Ser Cys Leu Ala Glu Leu Phe Glu Lys Ala Ala Ala His
37 42 47 52

ctg caa ggc ctg att cag gtg gcc agc agg gag cag ctc ttg tac ctg 547
Leu Gln Gly Leu Ile Gln Val Ala Ser Arg Glu Gln Leu Leu Tyr Leu
53 58 63 68

tat gcc agg tac aaa cag gtc aaa gtt gga aat tgt aat act cct aaa 595
Tyr Ala Arg Tyr Lys Gln Val Lys Val Gly Asn Cys Asn Thr Pro Lys
69 74 79 84

cca agc ttc ttt gat ttt gaa gga aag caa aaa tgg gaa gct tgg aaa 643
Pro Ser Phe Phe Asp Phe Glu Gly Lys Gln Lys Trp Glu Ala Trp Lys
85 90 95 100

gca ctt ggt gat tca agc ccc agc caa gca atg cag gaa tat atc gca 691
Ala Leu Gly Asp Ser Ser Pro Ser Gln Ala Met Gln Glu Tyr Ile Ala
101 106 111 116

gta gtt aaa aaa cta gat cca ggt tgg aat cct cag ata cca gag aag 739
Val Val Lys Lys Leu Asp Pro Gly Trp Asn Pro Gln Ile Pro Glu Lys

```
117                 122                 127                 132

aaa gga aaa gaa gca aat aca ggt ttt ggt ggg cca gtt att agt tct      787
Lys Gly Lys Glu Ala Asn Thr Gly Phe Gly Gly Pro Val Ile Ser Ser
133                 138                 143                 148

cta tat cat gaa gaa acc atc agg gaa gaa gac aaa aat ata ttt gat      835
Leu Tyr His Glu Glu Thr Ile Arg Glu Glu Asp Lys Asn Ile Phe Asp
149                 154                 159                 164

tac tgc agg gaa aac aac att gac cat ata acc aaa gcc atc aaa tcg      883
Tyr Cys Arg Glu Asn Asn Ile Asp His Ile Thr Lys Ala Ile Lys Ser
165                 170                 175                 180

aaa aat gtg gat gtg aat gtg aaa gat gaa gag ggt agg gct cta ctt      931
Lys Asn Val Asp Val Asn Val Lys Asp Glu Glu Gly Arg Ala Leu Leu
181                 186                 191                 196

cac tgg gcc tgt gat cga gga cat aag gaa cta gtc aca gtg ttg ctg      979
His Trp Ala Cys Asp Arg Gly His Lys Glu Leu Val Thr Val Leu Leu
197                 202                 207                 212

caa cat aga gct gac att aac tgt cag gac aat gaa ggc caa aca gct     1027
Gln His Arg Ala Asp Ile Asn Cys Gln Asp Asn Glu Gly Gln Thr Ala
213                 218                 223                 228

cta cat tat gcc tct gcc tgt gag ttt ctg gat att gta gag ctg ctg     1075
Leu His Tyr Ala Ser Ala Cys Glu Phe Leu Asp Ile Val Glu Leu Leu
229                 234                 239                 244

ctc cag tct ggt gct gac ccc act ctc cga gac cag gat ggc tgc ctg     1123
Leu Gln Ser Gly Ala Asp Pro Thr Leu Arg Asp Gln Asp Gly Cys Leu
245                 250                 255                 260

cca gag gag gtg aca ggc tgc aaa aca gtt tct ttg gtg ctg cag cgg     1171
Pro Glu Glu Val Thr Gly Cys Lys Thr Val Ser Leu Val Leu Gln Arg
261                 266                 271                 276

cac aca act ggc aag gct taa tc aaaagactgg aaaactgcag tctgtaatag     1224
His Thr Thr Gly Lys Ala  *
277                 282

cataaggctt ccattatgaa agaaaactac aaaaataata cttcttttcc acccgtcttt   1284

ggtatgtatt ggctaataaa atcagttctg tggaactggg attttgaaaa aaa          1337
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<210> 135
<211> 4161
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (89)..(1939)

<400> 135

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ctgcggtacc ggtccggaat tcccgggtcg acccacgcgt ccggacgcct cgaagaatcc      60

gctatcggct gtctgcacaa ccggaatc   atg tcg agt ttg gcg gtg aga gac      112
                                 Met Ser Ser Leu Ala Val Arg Asp
                                   1               5

ccg gca atg gat cga tca ctg cgt tcc gtg ttc gtg ggg aac att cca      160
Pro Ala Met Asp Arg Ser Leu Arg Ser Val Phe Val Gly Asn Ile Pro
  9                  14                  19                  24

tat gag gca act gag gag cag tta aag gac att ttc tcg gag gtt ggt      208
Tyr Glu Ala Thr Glu Glu Gln Leu Lys Asp Ile Phe Ser Glu Val Gly
 25                  30                  35                  40

tct gtt gtc agt ttc cgg ctg gta tac gat aga gag acg gga aaa ccc      256
Ser Val Val Ser Phe Arg Leu Val Tyr Asp Arg Glu Thr Gly Lys Pro
 41                  46                  51                  56

aag ggc tat ggc ttc tgc gaa tac caa gac cag gag acc gcg ctt agt      304
Lys Gly Tyr Gly Phe Cys Glu Tyr Gln Asp Gln Glu Thr Ala Leu Ser
 57                  62                  67                  72

gcc atg cgg aac ctc aat ggg cgg gag ttc agt ggg aga gcg ctt cgg      352
Ala Met Arg Asn Leu Asn Gly Arg Glu Phe Ser Gly Arg Ala Leu Arg
 73                  78                  83                  88

gtg gac aat gct gcc agt gaa aag aat aag gag gag tta aag agc ctt      400
Val Asp Asn Ala Ala Ser Glu Lys Asn Lys Glu Glu Leu Lys Ser Leu
 89                  94                  99                 104

ggg cct gca gcg ccc att att gac tca ccc tat ggg gat ccc atc gat      448
Gly Pro Ala Ala Pro Ile Ile Asp Ser Pro Tyr Gly Asp Pro Ile Asp
105                 110                 115                 120

cca gaa gat gcc cct gaa tcg att acc aga gca gta gcc agt ctc ccc      496
Pro Glu Asp Ala Pro Glu Ser Ile Thr Arg Ala Val Ala Ser Leu Pro
121                 126                 131                 136

ccg gag cag atg ttt gag ctg atg aag cag atg aag ctc tgt gtc caa      544
Pro Glu Gln Met Phe Glu Leu Met Lys Gln Met Lys Leu Cys Val Gln
137                 142                 147                 152

aac agc cac cag gaa gct cga aac atg tta ctt caa aat cca caa ctg      592
Asn Ser His Gln Glu Ala Arg Asn Met Leu Leu Gln Asn Pro Gln Leu
153                 158                 163                 168

gct tat gca ctg ttg cag gca caa gta gtg atg aga atc atg gat cca      640
Ala Tyr Ala Leu Leu Gln Ala Gln Val Val Met Arg Ile Met Asp Pro
169                 174                 179                 184

gag att gct ctg aaa att ctg cat cgg aag ata cat gtc aca cca ctg      688
Glu Ile Ala Leu Lys Ile Leu His Arg Lys Ile His Val Thr Pro Leu
185                 190                 195                 200

atc cca ggc aaa tct cag tct gtg tct gtc tct ggc cct ggc cct ggc      736
```

```
Ile Pro Gly Lys Ser Gln Ser Val Ser Val Ser Gly Pro Gly Pro Gly
201                 206                 211                 216

cct ggc cct ggg ctc tgc cca gga cct aat gtt ctg ctg aac cag cag      784
Pro Gly Pro Gly Leu Cys Pro Gly Pro Asn Val Leu Leu Asn Gln Gln
217                 222                 227                 232

aat cct cca gct cct cag cct cag cat ttg gct aga aga cct gtg aag      832
Asn Pro Pro Ala Pro Gln Pro Gln His Leu Ala Arg Arg Pro Val Lys
233                 238                 243                 248

gac att cct cct ctg atg cag act cct atc cag ggt gga att cca gct      880
Asp Ile Pro Pro Leu Met Gln Thr Pro Ile Gln Gly Gly Ile Pro Ala
249                 254                 259                 264

cca ggg cca ata cca gct gca gtt ccc gga gct ggt cct ggt tcc tta      928
Pro Gly Pro Ile Pro Ala Ala Val Pro Gly Ala Gly Pro Gly Ser Leu
265                 270                 275                 280

act cct gga gga gca atg cag ccc caa ctt gga atg cca ggg gtt ggc      976
Thr Pro Gly Gly Ala Met Gln Pro Gln Leu Gly Met Pro Gly Val Gly
281                 286                 291                 296

cca gtg cct tta gag cgg gga caa gtg cag atg tca gat cct aga gct     1024
Pro Val Pro Leu Glu Arg Gly Gln Val Gln Met Ser Asp Pro Arg Ala
297                 302                 307                 312

cct ata cct cgc gga ccc gtg act cct ggt ggt ctg cct cct cga gga     1072
Pro Ile Pro Arg Gly Pro Val Thr Pro Gly Gly Leu Pro Pro Arg Gly
313                 318                 323                 328

ctg tta gga gat gct cca aat gac cca cgt gga ggg act ttg ctt tca     1120
Leu Leu Gly Asp Ala Pro Asn Asp Pro Arg Gly Gly Thr Leu Leu Ser
329                 334                 339                 344

gtc act gga gaa gtg gag ccc aga ggt tat ctg ggt cca ccc cat cag     1168
Val Thr Gly Glu Val Glu Pro Arg Gly Tyr Leu Gly Pro Pro His Gln
345                 350                 355                 360

ggt ccc ccc atg cat cat gcc tct ggt cat gac act cgt ggc cct tcc     1216
Gly Pro Pro Met His His Ala Ser Gly His Asp Thr Arg Gly Pro Ser
361                 366                 371                 376

tca cat gag atg agg gga ggg cca tta gga gat ccc aga ctg cta att     1264
Ser His Glu Met Arg Gly Gly Pro Leu Gly Asp Pro Arg Leu Leu Ile
377                 382                 387                 392

gga gag ccc aga ggc ccc atg ata gat caa agg ggt cta cct atg gat     1312
Gly Glu Pro Arg Gly Pro Met Ile Asp Gln Arg Gly Leu Pro Met Asp
393                 398                 403                 408

ggt aga ggt ggt aga gat tct cga gcg atg gag act cgt gcc atg gaa     1360
Gly Arg Gly Gly Arg Asp Ser Arg Ala Met Glu Thr Arg Ala Met Glu
409                 414                 419                 424

act gag gtc tta gag aca cgt gta atg gag agg aga gga atg gag acc     1408
Thr Glu Val Leu Glu Thr Arg Val Met Glu Arg Arg Gly Met Glu Thr
```

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425                 430                 435                 440

tgt gcg atg gaa acc aga ggg atg gaa gca agg ggc atg gat gca aga     1456
Cys Ala Met Glu Thr Arg Gly Met Glu Ala Arg Gly Met Asp Ala Arg
441                 446                 451                 456

gga ttg gag atg agg ggc cct gtc ccc agt tca aga ggc cct atg act     1504
Gly Leu Glu Met Arg Gly Pro Val Pro Ser Ser Arg Gly Pro Met Thr
457                 462                 467                 472

ggt gga att cag ggt cct ggt ccc att aat ata ggg gca ggt ggc cct     1552
Gly Gly Ile Gln Gly Pro Gly Pro Ile Asn Ile Gly Ala Gly Gly Pro
473                 478                 483                 488

cct cag gga ccc aga cag gtc cca ggc att tca ggg gtg ggg aat cct     1600
Pro Gln Gly Pro Arg Gln Val Pro Gly Ile Ser Gly Val Gly Asn Pro
489                 494                 499                 504

gga gct ggt atg cag ggt aca ggc ata caa gga aca ggc atg cag gga     1648
Gly Ala Gly Met Gln Gly Thr Gly Ile Gln Gly Thr Gly Met Gln Gly
505                 510                 515                 520

gca ggc ata caa gga gga ggg atg cag ggg gca ggc ata caa gga gtc     1696
Ala Gly Ile Gln Gly Gly Gly Met Gln Gly Ala Gly Ile Gln Gly Val
521                 526                 531                 536

agt ata caa gga gga ggt ata caa gga gga ggt ata cag ggg gca agc     1744
Ser Ile Gln Gly Gly Gly Ile Gln Gly Gly Gly Ile Gln Gly Ala Ser
537                 542                 547                 552

aag caa ggt gga agc cag cct agc agt ttt agt cct ggg cag agc cag     1792
Lys Gln Gly Gly Ser Gln Pro Ser Ser Phe Ser Pro Gly Gln Ser Gln
553                 558                 563                 568

gtc act cca cag gat cag gag aag gca gct ttg atc atg cag gtt ctt     1840
Val Thr Pro Gln Asp Gln Glu Lys Ala Ala Leu Ile Met Gln Val Leu
569                 574                 579                 584

caa ctg act gca gat cag att gcc atg ctg ccc cct gag caa agg cag     1888
Gln Leu Thr Ala Asp Gln Ile Ala Met Leu Pro Pro Glu Gln Arg Gln
585                 590                 595                 600

agt atc ctg att tta aag gaa caa atc cag aaa tcc act gga gcg tct     1936
Ser Ile Leu Ile Leu Lys Glu Gln Ile Gln Lys Ser Thr Gly Ala Ser
601                 606                 611                 616

tga aagg ttttagaaaa tatttggctg tagtctcaaa ttttattctg tagcatggag     1993
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617

aatgggtgca aaaagctgac ttctgtatcc ccacacttgg attagggttt ccctcctcct   2053

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tagttgcttt atctcaaagc tttcactgaa gggctgtaac tgaaaattat taaatgttag   4093

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gga agg ctg acc cag gcc ctg aac tca ccc ctc acc tgg gag cat gtt      96
Gly Arg Leu Thr Gln Ala Leu Asn Ser Pro Leu Thr Trp Glu His Val
 14                  19                  24                  29

tgg att tgc gtc ccc ggc ggc act cct gac tgt ctg aca gac acc ttc     144
Trp Ile Cys Val Pro Gly Gly Thr Pro Asp Cys Leu Thr Asp Thr Phe
 30                  35                  40                  45

aga gtg aag agg cca cat ctc agg cgc tct gcc agc aac ggt cat gtc     192
Arg Val Lys Arg Pro His Leu Arg Arg Ser Ala Ser Asn Gly His Val
 46                  51                  56                  61

cct ggg act cct gtc tac aga gaa aaa gaa gat atg tat gac gag att     240
Pro Gly Thr Pro Val Tyr Arg Glu Lys Glu Asp Met Tyr Asp Glu Ile
 62                  67                  72                  77

att gag tta aag aag tca ttg cac gtg cag aag agc gac gtg gac ctg     288
Ile Glu Leu Lys Lys Ser Leu His Val Gln Lys Ser Asp Val Asp Leu
 78                  83                  88                  93

atg aga acg aag ctc cgg cgc ctg gag gag gaa aac agc agg aag gac     336
Met Arg Thr Lys Leu Arg Arg Leu Glu Glu Glu Asn Ser Arg Lys Asp
 94                  99                 104                 109

cgg cag ata gag cag ctc ctg gat ccc agc cgc ggc acg gat ttt gtt     384
Arg Gln Ile Glu Gln Leu Leu Asp Pro Ser Arg Gly Thr Asp Phe Val
110                 115                 120                 125

cgg act ctg gca gag aaa agg ccc gat gcc agt tgg gtc att aac ggg     432
Arg Thr Leu Ala Glu Lys Arg Pro Asp Ala Ser Trp Val Ile Asn Gly
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126                 131                 136                 141

ctg aag cag agg atc ctg aag ctg gaa cag cag tgc aag gag aag gac      480
Leu Lys Gln Arg Ile Leu Lys Leu Glu Gln Gln Cys Lys Glu Lys Asp
142                 147                 152                 157

ggc acc atc agc aaa ctc cag acc gat atg aag act acc aac ctg gaa      528
Gly Thr Ile Ser Lys Leu Gln Thr Asp Met Lys Thr Thr Asn Leu Glu
158                 163                 168                 173

gag atg cgg atc gcc atg gag aca tac tac gag gag gtg cat cgt ctc      576
Glu Met Arg Ile Ala Met Glu Thr Tyr Tyr Glu Glu Val His Arg Leu
174                 179                 184                 189

cag acc ctc ttg gca agt tct gaa acc acc gga aag aag ccc ctg ggg      624
Gln Thr Leu Leu Ala Ser Ser Glu Thr Thr Gly Lys Lys Pro Leu Gly
190                 195                 200                 205

gag aag aag acg ggc gcc aaa agg cag aag aag atg ggc agt gcc ctc      672
Glu Lys Lys Thr Gly Ala Lys Arg Gln Lys Lys Met Gly Ser Ala Leu
206                 211                 216                 221

ctg agc ttg tcc cgg agt gtc cag gag ctc acg gaa gag aac cag agc      720
Leu Ser Leu Ser Arg Ser Val Gln Glu Leu Thr Glu Glu Asn Gln Ser
222                 227                 232                 237

ctg aag gag gac ctg gac cgc gtg ctg agc acc tcc cca acc atc tcc      768
Leu Lys Glu Asp Leu Asp Arg Val Leu Ser Thr Ser Pro Thr Ile Ser
238                 243                 248                 253

aag aca cag ggt tat gtg gag tgg agc aag ccc cgg ctg ctg agg cgc      816
Lys Thr Gln Gly Tyr Val Glu Trp Ser Lys Pro Arg Leu Leu Arg Arg
254                 259                 264                 269

att gtg gag ctg gag aag aaa cta agt gtg atg gag agc tca aaa tca      864
Ile Val Glu Leu Glu Lys Lys Leu Ser Val Met Glu Ser Ser Lys Ser
270                 275                 280                 285

cac gcc gca gag cca gtc aga tca cac ccg cca gcc tgc ctt gca tcc      912
His Ala Ala Glu Pro Val Arg Ser His Pro Pro Ala Cys Leu Ala Ser
286                 291                 296                 301

agc tct gcg ctg cac aga cag cca cga ggg gac cgc aac aag gac cac      960
Ser Ser Ala Leu His Arg Gln Pro Arg Gly Asp Arg Asn Lys Asp His
302                 307                 312                 317

gag cgt ctc cga ggg gct gtg aga gac ctg aag gaa gag cgg acc gcg     1008
Glu Arg Leu Arg Gly Ala Val Arg Asp Leu Lys Glu Glu Arg Thr Ala
318                 323                 328                 333

ctg cag gag cag cta ctg cag aga gat ttg gag gtg aag cag ctc ctg     1056
Leu Gln Glu Gln Leu Leu Gln Arg Asp Leu Glu Val Lys Gln Leu Leu
334                 339                 344                 349

cag gcg aag gcc gac ctg gag aag gag ctg gag tgc gcg agg gag ggc     1104
Gln Ala Lys Ala Asp Leu Glu Lys Glu Leu Glu Cys Ala Arg Glu Gly
350                 355                 360                 365
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Glu Glu Glu Arg Arg Glu Arg Glu Glu Val Leu Arg Glu Glu Ile Gln
366                 371                 376                 381

aca ctt acc agc aag ctc caa gaa ttg caa gaa atg aag aaa gaa gag     1200
Thr Leu Thr Ser Lys Leu Gln Glu Leu Gln Glu Met Lys Lys Glu Glu
382                 387                 392                 397

aaa gag gat tgc ccg gaa gtt cct cat aag gcc caa gag ctc cca gct     1248
Lys Glu Asp Cys Pro Glu Val Pro His Lys Ala Gln Glu Leu Pro Ala
398                 403                 408                 413

ccc act ccc agc agc agg cac tgc gag caa gac tgg ccg ccg gat tcc     1296
Pro Thr Pro Ser Ser Arg His Cys Glu Gln Asp Trp Pro Pro Asp Ser
414                 419                 424                 429

agc gag gag ggg ctc ccg cgg ccc cgc tcc ccc tgc tct gat ggg aga     1344
Ser Glu Glu Gly Leu Pro Arg Pro Arg Ser Pro Cys Ser Asp Gly Arg
430                 435                 440                 445

aga gac gcc gcg gcc aga gtc ctg cag gcc cag tgg aag gtg tac aag     1392
Arg Asp Ala Ala Ala Arg Val Leu Gln Ala Gln Trp Lys Val Tyr Lys
446                 451                 456                 461

cac aag aaa aaa aag gct gtt ctg gat gag gcg gct gtg gtg ctt cag     1440
His Lys Lys Lys Lys Ala Val Leu Asp Glu Ala Ala Val Val Leu Gln
462                 467                 472                 477

gca gct ttc agg gga cat ctc acg cgg aca aag ctc tta gca agc aaa     1488
Ala Ala Phe Arg Gly His Leu Thr Arg Thr Lys Leu Leu Ala Ser Lys
478                 483                 488                 493

gca cat ggc tca gag cca ccc agc gtg cca ggc ctc cca gac cag agc     1536
Ala His Gly Ser Glu Pro Pro Ser Val Pro Gly Leu Pro Asp Gln Ser
494                 499                 504                 509

tct cct gtg ccc cgc gtt ccg agc ccc atc gcc cag gcc acg ggc agc     1584
Ser Pro Val Pro Arg Val Pro Ser Pro Ile Ala Gln Ala Thr Gly Ser
510                 515                 520                 525

cct gtg cag gag gag gcc atc gtc atc atc cag tcc gct ctg cgg gca     1632
Pro Val Gln Glu Glu Ala Ile Val Ile Ile Gln Ser Ala Leu Arg Ala
526                 531                 536                 541

cac ctg gcc cgg gcc agg cac agt gct acc ggt aaa aga acc acc acc     1680
His Leu Ala Arg Ala Arg His Ser Ala Thr Gly Lys Arg Thr Thr Thr
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gca gct tct acc agg agg aga tcg gct tca gcc aca cac ggg gac gcc     1728
Ala Ala Ser Thr Arg Arg Arg Ser Ala Ser Ala Thr His Gly Asp Ala
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tcc tcc cca ccc ttc ctc gca gct ctt cct gac ccc tct ccc tca ggg     1776
Ser Ser Pro Pro Phe Leu Ala Ala Leu Pro Asp Pro Ser Pro Ser Gly
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Pro Gln Ala Leu Ala Pro Leu Pro Gly Asp Asp Val Asn Ser Asp Asp
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tcc gac gat att gtc att gca ccg tct ctg ccc acg aag aac ttt cca     1872
Ser Asp Asp Ile Val Ile Ala Pro Ser Leu Pro Thr Lys Asn Phe Pro
606                 611                 616                 621

gtt tag gtccccgtca ctgtctccac gccgtgatgg cagcgctgcc gaggacatag      1928
Val  *
622

gaaccacgac tggaaagata atttatcgtg ttaggagaag aacgatgata cctacttaac   1988

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Case: 2:16-cv-00536-JRG-RSP Document 1-2 Filed 12/16/16 Page 488 of 1000 PageID #: 488

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Val Leu Val Phe Leu Cys Ser Leu Leu Ala Pro Met Val Leu Ala Ser
 47                  52                  57                  62

gca gct gaa aag gag aag gaa atg gac cct ttt cat tat gat tac cag     361
Ala Ala Glu Lys Glu Lys Glu Met Asp Pro Phe His Tyr Asp Tyr Gln
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acc ctg agg att ggg gga ctg gtg ttc gct gtg gtc ctc ttc tcg gtt     409
Thr Leu Arg Ile Gly Gly Leu Val Phe Ala Val Val Leu Phe Ser Val
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Gly Ile Leu Leu Ile Leu Ser Arg Arg Cys Lys Cys Ser Phe Asn Gln
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Lys Pro Arg Ala Pro Gly Asp Glu Glu Ala Gln Val Glu Asn Leu Ile
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Oligo Ref: 75650.0

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actctgtaag attctctgct acttattcaa gttgacacg   atg ccc ttc aca ctc     234
                                               Met Pro Phe Thr Leu
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cac ctg agg tcc cgc ctt ccc tct gcc ata agg agt ttg att cta caa      282
His Leu Arg Ser Arg Leu Pro Ser Ala Ile Arg Ser Leu Ile Leu Gln
  6                  11                  16                  21

aag aaa cca aac atc aga aat aca tcc agc atg gct gga gag ctc cga      330
Lys Lys Pro Asn Ile Arg Asn Thr Ser Ser Met Ala Gly Glu Leu Arg
 22                  27                  32                  37

cca gcc agc ctg gtg gtc ctg ccc agg tcc ctt gct cca gct ttt gaa      378
Pro Ala Ser Leu Val Val Leu Pro Arg Ser Leu Ala Pro Ala Phe Glu
 38                  43                  48                  53

aga ttc tgc cag gtc aac act ggt cct cta ccc ctg ctg ggc cag agt      426
Arg Phe Cys Gln Val Asn Thr Gly Pro Leu Pro Leu Leu Gly Gln Ser
 54                  59                  64                  69

gag cca gaa aag tgg atg ctg ccc cct caa ggt gct atc tca gag acc      474
Glu Pro Glu Lys Trp Met Leu Pro Pro Gln Gly Ala Ile Ser Glu Thr
 70                  75                  80                  85

agg atg ggc cat ccc cag ttc tgg aaa tac gag ttc ggt gcc tgc acc      522
Arg Met Gly His Pro Gln Phe Trp Lys Tyr Glu Phe Gly Ala Cys Thr
 86                  91                  96                 101

ggc agc ctg gct tcg ctg gag cag tac tcg gag cag ctg aag gac atg      570
Gly Ser Leu Ala Ser Leu Glu Gln Tyr Ser Glu Gln Leu Lys Asp Met
102                 107                 112                 117

gtg gcc ttc ttc ctg ggc tgc agc ttc tcc ctg gag gag gcc ttg gag      618
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Val Ala Phe Phe Leu Gly Cys Ser Phe Ser Leu Glu Glu Ala Leu Glu
118                 123                 128                 133

aaa gcg ggg ctc ccc aga aga gac cca gca ggt cac agc cag gcg ggt      666
Lys Ala Gly Leu Pro Arg Arg Asp Pro Ala Gly His Ser Gln Ala Gly
134                 139                 144                 149

gca tac aag aca aca gtg cct tgt gtt acc cat gct ggc ttc tgc tgc      714
Ala Tyr Lys Thr Thr Val Pro Cys Val Thr His Ala Gly Phe Cys Cys
150                 155                 160                 165

cct ctg gtg gtc acg atg agg ccc att ccc aag gac aag ctg gaa ggg      762
Pro Leu Val Val Thr Met Arg Pro Ile Pro Lys Asp Lys Leu Glu Gly
166                 171                 176                 181

ctg gtg cgg gcc tgc tgc tcc ctc gga ggt gag cag ggg caa cct gtt      810
Leu Val Arg Ala Cys Cys Ser Leu Gly Gly Glu Gln Gly Gln Pro Val
182                 187                 192                 197

cac atg ggc gac cca gaa ctg ttg gga atc aaa gag ctt tcc aaa cct      858
His Met Gly Asp Pro Glu Leu Leu Gly Ile Lys Glu Leu Ser Lys Pro
198                 203                 208                 213

gcc tac ggg gat gcc atg gtg tgt ccc cca ggg gag gtt cca gtg ttc      906
Ala Tyr Gly Asp Ala Met Val Cys Pro Pro Gly Glu Val Pro Val Phe
214                 219                 224                 229

tgg cct tct ccg ctg acc agt ctc gga gct gtc agc agc tgt gag acc      954
Trp Pro Ser Pro Leu Thr Ser Leu Gly Ala Val Ser Ser Cys Glu Thr
230                 235                 240                 245

cca ctg gct ttt gcc agc atc cca ggc tgc aca gtt atg act gac ctg     1002
Pro Leu Ala Phe Ala Ser Ile Pro Gly Cys Thr Val Met Thr Asp Leu
246                 251                 256                 261

aag gat gca aag gct cca cct ggt tgt ctc acc cca gag aga att cca     1050
Lys Asp Ala Lys Ala Pro Pro Gly Cys Leu Thr Pro Glu Arg Ile Pro
262                 267                 272                 277

gag gtc cat cac att tcc caa gat cct ctg cac tac agc atc gcg tca     1098
Glu Val His His Ile Ser Gln Asp Pro Leu His Tyr Ser Ile Ala Ser
278                 283                 288                 293

gtc tct gct tct cag aag atc aga gaa cta gag tct atg atc ggc ata     1146
Val Ser Ala Ser Gln Lys Ile Arg Glu Leu Glu Ser Met Ile Gly Ile
294                 299                 304                 309

gac cca ggg aac cgg ggg att ggg cac ctg ctc tgt aaa gat gag ctg     1194
Asp Pro Gly Asn Arg Gly Ile Gly His Leu Leu Cys Lys Asp Glu Leu
310                 315                 320                 325

ctg aag gcc tct ctc tcg ctg tcc cat gcc cgc tca gtg ctc atc acc     1242
Leu Lys Ala Ser Leu Ser Leu Ser His Ala Arg Ser Val Leu Ile Thr
326                 331                 336                 341

act ggg ttc ccc aca cat ttc aat cat gag cct cca gaa gag aca gat     1290
Thr Gly Phe Pro Thr His Phe Asn His Glu Pro Pro Glu Glu Thr Asp
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342                 347                 352                 357

ggc cca cca gga gct gtt gct ctg gtt gcc ttc ctg cag gcc ttg gag     1338
Gly Pro Pro Gly Ala Val Ala Leu Val Ala Phe Leu Gln Ala Leu Glu
358                 363                 368                 373

aag gag gtc gcc ata atc gtt gac cag aga gcc tgg aac ttg cac cag     1386
Lys Glu Val Ala Ile Ile Val Asp Gln Arg Ala Trp Asn Leu His Gln
374                 379                 384                 389

aag att gtt gaa gat gct gtt gag caa ggt gtt ctg aag acg cag atc     1434
Lys Ile Val Glu Asp Ala Val Glu Gln Gly Val Leu Lys Thr Gln Ile
390                 395                 400                 405

ccg ata tta act tac caa ggt gga tca gtg gaa gct gct cag gca ttc     1482
Pro Ile Leu Thr Tyr Gln Gly Gly Ser Val Glu Ala Ala Gln Ala Phe
406                 411                 416                 421

ctg tgc aaa aat ggg gac ccg cag aca cct aga ttt gac cac ctg gtg     1530
Leu Cys Lys Asn Gly Asp Pro Gln Thr Pro Arg Phe Asp His Leu Val
422                 427                 432                 437

gcc ata gag cgt gcc gga aga gct gct gat ggc aat tac tac aat gca     1578
Ala Ile Glu Arg Ala Gly Arg Ala Ala Asp Gly Asn Tyr Tyr Asn Ala
438                 443                 448                 453

agg aag atg aac atc aag cac ttg gtt gac ccc att gac gat ctt ttt     1626
Arg Lys Met Asn Ile Lys His Leu Val Asp Pro Ile Asp Asp Leu Phe
454                 459                 464                 469

ctt gct gcg aag aag att cct gga atc tca tca act gga gtc ggt gat     1674
Leu Ala Ala Lys Lys Ile Pro Gly Ile Ser Ser Thr Gly Val Gly Asp
470                 475                 480                 485

gga ggc aac gag ctt ggg atg ggt aaa gtc aag gag gct gtg agg agg     1722
Gly Gly Asn Glu Leu Gly Met Gly Lys Val Lys Glu Ala Val Arg Arg
486                 491                 496                 501

cac ata cgg cac ggg gat gtc atc gcc tgc gac gtg gag gct gac ttt     1770
His Ile Arg His Gly Asp Val Ile Ala Cys Asp Val Glu Ala Asp Phe
502                 507                 512                 517

gcc gtc att gct ggt gtt tct aac tgg gga ggc tat gcc ctg gcc tgc     1818
Ala Val Ile Ala Gly Val Ser Asn Trp Gly Gly Tyr Ala Leu Ala Cys
518                 523                 528                 533

gca ctc tac atc ctg tac tca tgt gct gtc cac agt cag tac ctg agg     1866
Ala Leu Tyr Ile Leu Tyr Ser Cys Ala Val His Ser Gln Tyr Leu Arg
534                 539                 544                 549

aaa gca gtc gga ccc tcc agg gca cct gga gat cag gcc tgg act cag     1914
Lys Ala Val Gly Pro Ser Arg Ala Pro Gly Asp Gln Ala Trp Thr Gln
550                 555                 560                 565

gcc ctc ccg tcg gtc att aag gaa gaa aaa atg ctg ggc atc ttg gtg     1962
Ala Leu Pro Ser Val Ile Lys Glu Glu Lys Met Leu Gly Ile Leu Val
566                 571                 576                 581
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cag cac aaa gtc cgg agt ggc gtc tcg ggc atc gtg ggc atg gag gtg     2010
Gln His Lys Val Arg Ser Gly Val Ser Gly Ile Val Gly Met Glu Val
582                 587                 592                 597

gat ggg ctg ccc ttc cac aac acc cac gcc gag atg atc cag aag ctg     2058
Asp Gly Leu Pro Phe His Asn Thr His Ala Glu Met Ile Gln Lys Leu
598                 603                 608                 613

gtg gac gtc acc acg gca cag gtg taa ccgtc catgttccgt gtgagcagag     2110
Val Asp Val Thr Thr Ala Gln Val  *
614                 619

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cccactttct gggaggggtt agtgcaggtg ctgtggacaa aggacaacat ttctctgggg   2290

ctttttaact tttattccta agactctaaa ggcgttgatt tcaaccctcc ttcactctgg   2350

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caagatacca aaatgcatga aatttataaa ggaaatatta ctccccaatt gaataaaaac    180

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gattatgaag ggatgaaaag tggaaaagga cggccaataa gttttgtaga ctcattccct    300

ctttccattt ggatttgtca accaacaaga tatgcagagt cacaaaaaga gccgcagact    360

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aagcggaaga agctcttgaa ggagtattat agtacagagt ctgagccttt gacaaatggt    480

ggtcagaagc cttcttcatc agatacattt ttcagatttt ccccttcctc gtcagaggca    540

gatattcatc tcctagttc atg ttc ata aac atg tca gta tgc aga tta atc      592
                     Met Phe Ile Asn Met Ser Val Cys Arg Leu Ile
                       1               5

act acc aag tat ctg ctt cta ctt ttc ctg cat gag tca ctt atc ctg      640
Thr Thr Lys Tyr Leu Leu Leu Leu Phe Leu His Glu Ser Leu Ile Leu
 12                  17                  22                  27

ctt tca gag aac tta agg aaa gat gta gaa gct gta act ggc agt cct      688
Leu Ser Glu Asn Leu Arg Lys Asp Val Glu Ala Val Thr Gly Ser Pro
 28                  33                  38                  43

gct agt cag aca tcc att tgt att gga att tta ctt aga agt gca gaa      736
Ala Ser Gln Thr Ser Ile Cys Ile Gly Ile Leu Leu Arg Ser Ala Glu
 44                  49                  54                  59

ctg gct ctt ttg ctc cat cca gtg gat caa gca aat act ctt aag tct      784
Leu Ala Leu Leu Leu His Pro Val Asp Gln Ala Asn Thr Leu Lys Ser
 60                  65                  70                  75

cct gtt tct gaa agt gtg agc cca gtg gta cct gat tat ttg cct aca      832
Pro Val Ser Glu Ser Val Ser Pro Val Val Pro Asp Tyr Leu Pro Thr
 76                  81                  86                  91

gaa aat ggg gat ttt ttg tct tca aaa aga aaa caa att agt agg gat      880
Glu Asn Gly Asp Phe Leu Ser Ser Lys Arg Lys Gln Ile Ser Arg Asp
 92                  97                 102                 107

ata aat aga att aga agt gta act gtt aat cat atg tca gac aac aga      928
Ile Asn Arg Ile Arg Ser Val Thr Val Asn His Met Ser Asp Asn Arg
108                 113                 118                 123

tct atg agt gtt gac ctt agc cat atc cct tta aag gat cct ttg ctt      976
Ser Met Ser Val Asp Leu Ser His Ile Pro Leu Lys Asp Pro Leu Leu
124                 129                 134                 139

ttt aaa tca gct agt gat aca aat ctg caa aaa ggc att tct ttt atg     1024
Phe Lys Ser Ala Ser Asp Thr Asn Leu Gln Lys Gly Ile Ser Phe Met
140                 145                 150                 155

gac tat tta tca gat aaa cat tta ggg aaa ata agt gaa gat gaa agt     1072
Asp Tyr Leu Ser Asp Lys His Leu Gly Lys Ile Ser Glu Asp Glu Ser
156                 161                 166                 171

agt gga ctt gtt tac aaa agt ggc tca gga gaa att gga tca gaa aca     1120
Ser Gly Leu Val Tyr Lys Ser Gly Ser Gly Glu Ile Gly Ser Glu Thr
172                 177                 182                 187

agt gac aaa aag gat tca ttt tat aca gat tca agt agt gtc tta aac     1168
Ser Asp Lys Lys Asp Ser Phe Tyr Thr Asp Ser Ser Ser Val Leu Asn
188                 193                 198                 203
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tac aga gaa gat tcg aat ata ctt tca ttt gat agt gat ggt aat caa     1216
Tyr Arg Glu Asp Ser Asn Ile Leu Ser Phe Asp Ser Asp Gly Asn Gln
204                 209                 214                 219

aac ata ctt tca agt act tta act agt aaa gga aat gaa acc ata gag     1264
Asn Ile Leu Ser Ser Thr Leu Thr Ser Lys Gly Asn Glu Thr Ile Glu
220                 225                 230                 235

tcc atc ttt aaa gct gaa gat ttg ctt cca gaa gca gct tca ctc tct     1312
Ser Ile Phe Lys Ala Glu Asp Leu Leu Pro Glu Ala Ala Ser Leu Ser
236                 241                 246                 251

gaa aac ctg gat atc agt aaa gaa gag acc ccc cca gtt aga aca ctt     1360
Glu Asn Leu Asp Ile Ser Lys Glu Glu Thr Pro Pro Val Arg Thr Leu
252                 257                 262                 267

aaa tca cag tca tct tta agt gga aag cct aag gaa cgt tgc cca ccc     1408
Lys Ser Gln Ser Ser Leu Ser Gly Lys Pro Lys Glu Arg Cys Pro Pro
268                 273                 278                 283

aac ctg gct cct ctc tgt gtt tct tat aag aat atg aaa aga agc tct     1456
Asn Leu Ala Pro Leu Cys Val Ser Tyr Lys Asn Met Lys Arg Ser Ser
284                 289                 294                 299

tca caa atg tca ttg gat acc att tca ctt gac agc atg ata ttg gaa     1504
Ser Gln Met Ser Leu Asp Thr Ile Ser Leu Asp Ser Met Ile Leu Glu
300                 305                 310                 315

gaa cag tta tta gaa agt gat gga agt gat agc cat atg ttt ttg gaa     1552
Glu Gln Leu Leu Glu Ser Asp Gly Ser Asp Ser His Met Phe Leu Glu
316                 321                 326                 331

aaa gga aat aaa aag aac tca act aca aat tac agg ggc aca gca gaa     1600
Lys Gly Asn Lys Lys Asn Ser Thr Thr Asn Tyr Arg Gly Thr Ala Glu
332                 337                 342                 347

agt gtg aat gct ggt gca aac cta cag aat tat ggt gaa act tct cca     1648
Ser Val Asn Ala Gly Ala Asn Leu Gln Asn Tyr Gly Glu Thr Ser Pro
348                 353                 358                 363

gat gcc atc agt aca aat tca gag ggt gct cag gaa aat cat gat gac     1696
Asp Ala Ile Ser Thr Asn Ser Glu Gly Ala Gln Glu Asn His Asp Asp
364                 369                 374                 379

ctg atg tcc gtt gtg gta ttt aaa att act ggt gtt aat ggg gaa att     1744
Leu Met Ser Val Val Val Phe Lys Ile Thr Gly Val Asn Gly Glu Ile
380                 385                 390                 395

gac atc cga ggg gaa gat aca gaa atc tgt ctt caa gtg aac cag gtg     1792
Asp Ile Arg Gly Glu Asp Thr Glu Ile Cys Leu Gln Val Asn Gln Val
396                 401                 406                 411

aca cca gac caa tta ggc aat atc agc ctt cgg cat tac ctt tgt aat     1840
Thr Pro Asp Gln Leu Gly Asn Ile Ser Leu Arg His Tyr Leu Cys Asn
412                 417                 422                 427

cgt cca gtt ggt tcc gat cag aaa gct gta att cat tcc aaa tcc tct     1888
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Arg Pro Val Gly Ser Asp Gln Lys Ala Val Ile His Ser Lys Ser Ser
428                 433                 438                 443

cct gag att tct ctg aga ttt gaa agt ggg cct ggt gct gta ata cac     1936
Pro Glu Ile Ser Leu Arg Phe Glu Ser Gly Pro Gly Ala Val Ile His
444                 449                 454                 459

tct tta ctt gca gaa aaa aat gga ttt ctg cag tgc cac ata gaa aac     1984
Ser Leu Leu Ala Glu Lys Asn Gly Phe Leu Gln Cys His Ile Glu Asn
460                 465                 470                 475

ttc agc act gag ttt ctt aca tct tct ctt atg aat att caa cat ttt     2032
Phe Ser Thr Glu Phe Leu Thr Ser Ser Leu Met Asn Ile Gln His Phe
476                 481                 486                 491

ttg gaa gat gaa act gtt gca aca gta atg cca atg aag ata caa gtt     2080
Leu Glu Asp Glu Thr Val Ala Thr Val Met Pro Met Lys Ile Gln Val
492                 497                 502                 507

tct aac acg aaa ata aat tta aaa gat gat agt ccc cgg agt agt aca     2128
Ser Asn Thr Lys Ile Asn Leu Lys Asp Asp Ser Pro Arg Ser Ser Thr
508                 513                 518                 523

gta tcc ctt gaa cca gct cct gta act gta cat att gat cat ctt gtg     2176
Val Ser Leu Glu Pro Ala Pro Val Thr Val His Ile Asp His Leu Val
524                 529                 534                 539

gta gag aga agt gac gat ggc tct ttt cat atc aga gat tct cac atg     2224
Val Glu Arg Ser Asp Asp Gly Ser Phe His Ile Arg Asp Ser His Met
540                 545                 550                 555

ctt aac act gga aat gat ttg aaa gaa aat gtc aaa agc gat tca gtg     2272
Leu Asn Thr Gly Asn Asp Leu Lys Glu Asn Val Lys Ser Asp Ser Val
556                 561                 566                 571

ctg ctg acc agt gga aag tat gat ctg aag aaa caa cgc agt gtc acg     2320
Leu Leu Thr Ser Gly Lys Tyr Asp Leu Lys Lys Gln Arg Ser Val Thr
572                 577                 582                 587

caa gcc act cag aca agc cca ggg gtt cct tgg cct tct cag tca gct     2368
Gln Ala Thr Gln Thr Ser Pro Gly Val Pro Trp Pro Ser Gln Ser Ala
588                 593                 598                 603

aac ttt cct gag ttc tcc ttt gac ttc act agg gaa cag ctc atg gaa     2416
Asn Phe Pro Glu Phe Ser Phe Asp Phe Thr Arg Glu Gln Leu Met Glu
604                 609                 614                 619

gag aat gaa tct ctt aaa cag gaa ctg gct aaa gct aaa atg gct ctt     2464
Glu Asn Glu Ser Leu Lys Gln Glu Leu Ala Lys Ala Lys Met Ala Leu
620                 625                 630                 635

gca gag gct cac ttg gaa aaa gat gct ctt ctt cat cat ata aag aag     2512
Ala Glu Ala His Leu Glu Lys Asp Ala Leu Leu His His Ile Lys Lys
636                 641                 646                 651

atg aca gtt gaa tag caggagtggc agtcaaaact gaaattatag ctctggagta     2567
Met Thr Val Glu  *
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652

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Ile Pro Ser Gln Val Ser Asp Tyr Asp Tyr Phe Ser Val Ser Gly Asp
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Trp Pro Pro Glu Arg Trp Gln Lys Leu Glu Ser Val Leu Pro Pro Glu
151                 156                 161                 166

cgc tta cca gta cag aga gaa gag gaa tga c tgcatgaatc tacctgagtt      944
Arg Leu Pro Val Gln Arg Glu Glu Glu  *
167                 172

gctggcattg ggaggccagt tactggaaag gaatggaaaa aagaagcctc caaaagggaa   1004

aaacttctga caatatgatg ctgtgcgaga aatatttaca gcacattaag acgatctgta   1064

ttattaaata aataattttc aaatgttaaa cagtattaaa tggcacctga ttttgtgtta   1124

aattttagtt ccctgttgtt taatgccccc aaaatatgca gacctttggg aatataaaaa   1184

tattgcaccc acatgtctta atggggctga atttcagatt atttgttaca tatacttatt   1244

atattgattg ttgggttttg attttggtgc ttgctgctga aataaattga aaattaatat   1304

tcaataaaaa tgatgtattt gtcacttgct gttaaggtag aacaagaagg aacacatatt   1364

atacacataa tgatgggaat tacattgtga tttgtactat ctacaaagga gtaactgcca   1424

gttaggaaga acagtaaaca gtgatgttaa aataaaacaa tgatttgcta aaatcataaa   1484

aaaa                                                                1488
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<400> 143

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tccgggggga cagtgtctcc aggtagtgag gcccaacctc tttaaaacaa acaaacaaac    120

aaacaaaaaa ccaaaatgca aacgtgagta gagaatgaaa tacacagttt aaatgccctc    180

actatctttg ggttactaat atactaagcc tttctggact aagtaaaaga tgcaggttcc    240

tgcggctagg gatagaagcc agactggcgt cttcagaatc tcccaccaag gctgtacctc    300

tggaggagtt ctaggtttgg atttggtcat ctcaagaaga gacttcag atg gat ttt     357
                                                    Met Asp Phe
                                                      1

aaa att gaa cac act tgg gat ggt ttt cca gtg aag cat gag ccc gta      405
Lys Ile Glu His Thr Trp Asp Gly Phe Pro Val Lys His Glu Pro Val
```

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 4                   9                  14                  19

ttt atc agg ctg aat cca ggt gac aga gga gtg atg atg gac att agt      453
Phe Ile Arg Leu Asn Pro Gly Asp Arg Gly Val Met Met Asp Ile Ser
 20                  25                  30                  35

gct cca ttt ttc agg gat cct cca gcc cca ctt gga gaa cca gga aaa      501
Ala Pro Phe Phe Arg Asp Pro Pro Ala Pro Leu Gly Glu Pro Gly Lys
 36                  41                  46                  51

cct ttc aat gaa ctg tgg gat tat gaa gtt gtg gaa gca ttt ttc ttg      549
Pro Phe Asn Glu Leu Trp Asp Tyr Glu Val Val Glu Ala Phe Phe Leu
 52                  57                  62                  67

aat gat ata act gag caa tat tta gaa gtt gaa ctt tgt ccc cac gga      597
Asn Asp Ile Thr Glu Gln Tyr Leu Glu Val Glu Leu Cys Pro His Gly
 68                  73                  78                  83

cag cat tta gtg ctt tta ctt tct gga aga aga aat gtg tgg aaa caa      645
Gln His Leu Val Leu Leu Leu Ser Gly Arg Arg Asn Val Trp Lys Gln
 84                  89                  94                  99

gaa ctt cct tta tcg ttc aga gtg tcc aga gga gag aca aaa tgg gaa      693
Glu Leu Pro Leu Ser Phe Arg Val Ser Arg Gly Glu Thr Lys Trp Glu
100                 105                 110                 115

ggc aaa gct tat ctc cct tgg agt tat ttt cca cca aat gtg aca aaa      741
Gly Lys Ala Tyr Leu Pro Trp Ser Tyr Phe Pro Pro Asn Val Thr Lys
116                 121                 126                 131

ttc aat tca ttt gca att cat gga tca aaa gat aaa cga agt tat gaa      789
Phe Asn Ser Phe Ala Ile His Gly Ser Lys Asp Lys Arg Ser Tyr Glu
132                 137                 142                 147

gct ctt tat cct gta cct cag cat gaa ctg cag caa gga caa aaa cct      837
Ala Leu Tyr Pro Val Pro Gln His Glu Leu Gln Gln Gly Gln Lys Pro
148                 153                 158                 163

gat ttc cat tgc cta gaa tac ttc aag tct ttc aat ttt aac aca ctg      885
Asp Phe His Cys Leu Glu Tyr Phe Lys Ser Phe Asn Phe Asn Thr Leu
164                 169                 174                 179

ctt gga gaa gag tgg aaa caa ccg gaa tca gac ctg tgg cta ata gag      933
Leu Gly Glu Glu Trp Lys Gln Pro Glu Ser Asp Leu Trp Leu Ile Glu
180                 185                 190                 195

aaa tgt gat ata tag gagtaataga taaccatacc gatcattttt tcctctatac      988
Lys Cys Asp Ile  *
196

cttttaagat aaacaaaaaa taaatatcaa ttttttaaga tgtcatgcat acatttcaac   1048

aacaaatatc ttcatagaag tcactgaaaa tatagtatct gtggcaaatt gtatatgatt   1108

aacaagaaaa tatatgattc tttgtagatg atttcatctg taaagtcaca atgtttctca   1168

gagtcactta gtccaggatg ttgcattccc agcacacagt acagttattc ttgaaaacta   1228
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caagtgaaaa agggggaaca attgaggttg tccaaggcca cctagaggac tgtcttgcac 1288

taccttgtga ttcaaccatt tcattcctag atatataccc cagaaaaatg actgctcata 1348

gcagctttat tcataatagc acaaaattgt aaacagtgaa atttccatcc ataggaaaat 1408

ggatagacaa actacaatat agtcagtgga atactgttca tttaaaaaag gactgctgat 1468

acatgcaaca acctgtatga atctcaaaaa cattaagttg agcaaaacaa accaaacata 1528

acatactatc taattacttt tatattaaag ccacttccag gcaaaactaa tatttgatga 1588

tagataccag aacagtggct gcttagagtg agggcaggga attcaaattg aatggaaaag 1648

gggcctgagg aaattttccg gggtgattga aatgttttgt attttgatct ggatgatggt 1708

tatgtagctg catatatttg tcaacattcc tcatgctgta tgtttagatt tgtgatttta 1768

ctatatgtaa attaattcct taataaaata ctattataaa ataagctgta aattaaatgg 1828

aattaacttc aagtttacat tgagtttata tgtttccatt gaacaatcac tagtgatggt 1888

taaatgtggc ttatcgactt actcatttct tatatatgtt ctctatctaa aaagagagct 1948

ggtgtaagat aaatgctaac ttttacaaaa ggtattatta agtatcctga ctacacatca 2008

tggtggcagt gttaggcatc ttagataaat tgagaaatta ttcttaaaac tgacaatagc 2068

aactaattaa tttgatatag aaacgatctg cctgttttag atacgaatgg catattttaa 2128

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atcaaaataa aaacaagata tattttagag caaa 2222

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<220>
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ccgggcggag gcccgctcgt gtggaagtcg tcgacgccgc cgctcgtccg tcctcccgtc 120

cgttctcgct cccggccgcc atc atg ctg gcg ctc atc tcc cgc ctg ctg 170
Met Leu Ala Leu Ile Ser Arg Leu Leu
1 5

gac tgg ttc cgt tcg ctc ttc tgg aag gaa gag atg gag ctg acg ctc 218

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Asp Trp Phe Arg Ser Leu Phe Trp Lys Glu Glu Met Glu Leu Thr Leu
 10                  15                  20                  25

gtg ggg ctg cag tac tcg ggc aag acc acc ttc gtc aat gtc atc gcg      266
Val Gly Leu Gln Tyr Ser Gly Lys Thr Thr Phe Val Asn Val Ile Ala
 26                  31                  36                  41

tca ggt caa ttc agt gaa gat atg ata ccc aca gtg ggc ttc aac atg      314
Ser Gly Gln Phe Ser Glu Asp Met Ile Pro Thr Val Gly Phe Asn Met
 42                  47                  52                  57

agg aag gta act aaa ggt aac gtc aca ata aag atc tgg gac ata gga      362
Arg Lys Val Thr Lys Gly Asn Val Thr Ile Lys Ile Trp Asp Ile Gly
 58                  63                  68                  73

gga caa ccc cga ttt cga agc atg tgg gag cgg tat tgc aga gga gtc      410
Gly Gln Pro Arg Phe Arg Ser Met Trp Glu Arg Tyr Cys Arg Gly Val
 74                  79                  84                  89

aat gct att gtt tac atg ata gat gct gca gat cgt gaa aag ata gaa      458
Asn Ala Ile Val Tyr Met Ile Asp Ala Ala Asp Arg Glu Lys Ile Glu
 90                  95                 100                 105

gct tcc cga aat gag cta cat aat ctt cta gat aaa cca cag tta caa      506
Ala Ser Arg Asn Glu Leu His Asn Leu Leu Asp Lys Pro Gln Leu Gln
106                 111                 116                 121

gga att cca gtg cta gtg ctt gga aac aag aga gat ctt cct aat gcc      554
Gly Ile Pro Val Leu Val Leu Gly Asn Lys Arg Asp Leu Pro Asn Ala
122                 127                 132                 137

ttg gat gag aaa cag cta att gaa aaa atg aat ctg tct gct att cag      602
Leu Asp Glu Lys Gln Leu Ile Glu Lys Met Asn Leu Ser Ala Ile Gln
138                 143                 148                 153

gat aga gaa att tgc tgc tat tca att tct tgc aaa gaa aag gat aat      650
Asp Arg Glu Ile Cys Cys Tyr Ser Ile Ser Cys Lys Glu Lys Asp Asn
154                 159                 164                 169

ata gat atc aca ctt cag tgg ctt att cag cat tca aaa tct aga aga      698
Ile Asp Ile Thr Leu Gln Trp Leu Ile Gln His Ser Lys Ser Arg Arg
170                 175                 180                 185

agc tga agcatctcct gaagtcttcc agtccttctt ggctataatc ctagaattat      754
Ser  *
186

tgtccgttcc tctgaagtaa ttcccagaat acggtccttc ctaaacccca gaaattgcct    814

ttttcagagt ttatttctca tgtgcactgc tgaagatgaa tatccctaat ccttcataaa    874

gaatcagcta gagttgtcat gataaagtca gcctagtcaa gaaaataaaa tattaaaaaa    934

caataatata atgataataa ttgaagaata aagtcaactt gccaaaaaaa aagtgtttta    994

cagagaaata gcacctttgg taaaaagtat ttttaaaatt tggttaggtc gctaaggggc   1054
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tcaaagtata caagtatctg catcatttgg gtgtaccctc ccagaaactc catccaagtc 1114

tgagggacac tgggttaact agcagtatgg ctatgtatct agaggcagtt attgggacca 1174

agagatgcgt ggatgctgga ggtctgtcat gctgacggca atggaaagag gctggaagca 1234

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gagggttgaa agatgggttg aggcacttga gaaactcttg gaagctgagt ttccaatcag 1954

cattttcatc agacagttca atgagagcat caacacagag tcccctaagc aacttgttgt 2014

tctcctggtc tggatacgtt gtaatattga tggcagtttc attctgttcc acaaacttca 2074

ggaattcact ggagtccagg cgagaatcac cattatcaaa gttcttaaaa tacttgtcta 2134

ggatttcact gtagttgctg cctttagaga accagccatc tggaatgatc tcagcttcca 2194

gccactggat gatgcgacgt cggagctcat cacggttgga ctgatagcaa acaactgggc 2254

tggcagatgg acttacggat ttcttctctt tgcagtgtcc atcgtaatca acctggattt 2314

tggatccagt gaggcaggca tctcgatgca gttcacagtg gttgaggtag gtcttgccat 2374

tactgccaca cacaggcctc ttgtgaggtt tgcattgctc aatgcagaga caggtgggtt 2434

ccccttttctc tgtgactgca cattcccggc cggctccaca aaacacattg gcacagatct 2494

tggatttgct ccttagctct tcctcggcgc ggacccaggc gaccgccacc agcgcgagcg 2554

cgagcgcgag ccagcgtttc cacatcgtgg tctggtccag gtctcctggg ggcgcggggc 2614

aggacggcgg cagcgagctg taagcggagg tgggagctcc g 2655

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cgagaggact gccttgctca cctgtcccct cggcgcggcc ccggggagct cccgagaggc    120

ccccgggatc gctggccctc cgaactccac agca    atg agc aag ttg ggc aag     172
                                         Met Ser Lys Leu Gly Lys
                                           1

ttc ttt aaa ggg ggc ggc tct tct aag agc cga gcc gct ccc agt ccc      220
Phe Phe Lys Gly Gly Gly Ser Ser Lys Ser Arg Ala Ala Pro Ser Pro
  7                  12                  17                  22

cag gag gcc ctg gtc cga ctt cgg gag act gag gag atg ctg ggc aag      268
Gln Glu Ala Leu Val Arg Leu Arg Glu Thr Glu Glu Met Leu Gly Lys
 23                  28                  33                  38

aaa caa gag tac ctg gaa aat cga atc cag aga gaa atc gcc ctg gcc      316
Lys Gln Glu Tyr Leu Glu Asn Arg Ile Gln Arg Glu Ile Ala Leu Ala
 39                  44                  49                  54

aag aag cac ggc acg cag aat aag cga gct gca tta cag gca cta aag      364
Lys Lys His Gly Thr Gln Asn Lys Arg Ala Ala Leu Gln Ala Leu Lys
 55                  60                  65                  70

aga aag aag agg ttc gag aaa cag ctc act cag att gat ggc aca ctt      412
Arg Lys Lys Arg Phe Glu Lys Gln Leu Thr Gln Ile Asp Gly Thr Leu
 71                  76                  81                  86

tct acc att gag ttc cag aga gaa gcc ctg gag aac tca cac acc aac      460
Ser Thr Ile Glu Phe Gln Arg Glu Ala Leu Glu Asn Ser His Thr Asn
 87                  92                  97                 102

act gag gtg ttg agg aac atg ggc ttt gca gca aaa gcg atg aaa tct      508
Thr Glu Val Leu Arg Asn Met Gly Phe Ala Ala Lys Ala Met Lys Ser
103                 108                 113                 118

gtt cat gaa aac atg gat ctg aac aaa ata gat gat ttg atg caa gag      556
Val His Glu Asn Met Asp Leu Asn Lys Ile Asp Asp Leu Met Gln Glu
119                 124                 129                 134

atc aca gag caa cag gat atc gcc caa gaa atc tca gaa gca ttt tct      604
Ile Thr Glu Gln Gln Asp Ile Ala Gln Glu Ile Ser Glu Ala Phe Ser
135                 140                 145                 150

caa cgg gtt ggc ttt ggt gat gac ttt gat gag gat gag ttg atg gca      652
Gln Arg Val Gly Phe Gly Asp Asp Phe Asp Glu Asp Glu Leu Met Ala
151                 156                 161                 166
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gaa ctt gaa gaa ttg gaa cag gag gaa tta aat aag aag atg aca aat      700
Glu Leu Glu Glu Leu Glu Gln Glu Glu Leu Asn Lys Lys Met Thr Asn
167                 172                 177                 182

atc cgc ctt cca aat gtg cct tcc tct tct ctc cca gca cag cca aat      748
Ile Arg Leu Pro Asn Val Pro Ser Ser Ser Leu Pro Ala Gln Pro Asn
183                 188                 193                 198

aga aaa cca ggc atg tcg tcc act gca cgt cga tcc cga gca gca tct      796
Arg Lys Pro Gly Met Ser Ser Thr Ala Arg Arg Ser Arg Ala Ala Ser
199                 204                 209                 214

tcc cag agg gca gaa gaa gag gat gat gat atc aaa caa ttg gca gct      844
Ser Gln Arg Ala Glu Glu Glu Asp Asp Asp Ile Lys Gln Leu Ala Ala
215                 220                 225                 230

tgg gct acc taa act aaaacacatt tttgatacct aaattaatga gctatagata      899
Trp Ala Thr  *
231

aaatataaaa aatgttttta ccaagttcag aagttaacaa agactctgct ttataattat    959

attgaatgaa taattgtgtt ttaagcctcc taagtaaaag taaaaaagga gtcatgtgca   1019

tacatagaat cagtgatgga ggccaggcac ggtatctcat gcctataatc ccagcacttt   1079

gggaggctga ggcagttgag accaggagtt cgagtccagc ctgaccaaca tgaagaaacc   1139

ctgtctgtac taaaaataca aaaattagcc ggacatggtg gcaggcacct gtgatcccag   1199

ctacttggga ggctgagtca ggagaattgc ttgagcccag gagatggagg ttgcagtgag   1259

ccaagatcat gccactgcac tccagactgg gcaacagagg gagactccgt ctcaaaaact   1319

aaaaaaaaaa atacatttag tatagcgggg ggtgggggggg agaaataatg ttatttccta   1379

tgcgaatgac gtgtatccct gtacccatgg taaatgtaaa tatactgtgt ctcttttggg   1439

agg                                                                 1442
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<210> 146
<211> 527
<212> DNA
<213> Homo sapiens

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<222> (165)..(527)

<400> 146

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acatagcgaa accccgcctc agaaaaagag agggagagag gaaagcagtg gagttattgg    120
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tcaaagagag tgacagtgag gattcacatt tgggttattt caag atg agc ttc cta      176
                                                    Met Ser Phe Leu
                                                      1

ctg ccc aag ctg act agc aaa aag gaa gta gac cag gcg ata aaa agt      224
Leu Pro Lys Leu Thr Ser Lys Lys Glu Val Asp Gln Ala Ile Lys Ser
  5                  10                  15                  20

act gct gag aag gtg ttg gtt ctc agg ttt ggg aga gat gaa gat cct      272
Thr Ala Glu Lys Val Leu Val Leu Arg Phe Gly Arg Asp Glu Asp Pro
 21                  26                  31                  36

gtc tgt ctg cag cta gat gat att ctt tct aag acc tct tct gac tta      320
Val Cys Leu Gln Leu Asp Asp Ile Leu Ser Lys Thr Ser Ser Asp Leu
 37                  42                  47                  52

agt aaa atg gct gct ata tac ctg gta gat gtg gac caa act gca gtt      368
Ser Lys Met Ala Ala Ile Tyr Leu Val Asp Val Asp Gln Thr Ala Val
 53                  58                  63                  68

tat aca cag tat ttt gac atc agt tat att cca tct act gtc ttt ttc      416
Tyr Thr Gln Tyr Phe Asp Ile Ser Tyr Ile Pro Ser Thr Val Phe Phe
 69                  74                  79                  84

ttc aat ggg cag cat atg aaa gtg gat tat ggg caa tat tgg agt gtt      464
Phe Asn Gly Gln His Met Lys Val Asp Tyr Gly Gln Tyr Trp Ser Val
 85                  90                  95                 100

gta aga gga cat atg ggg ttc aag aag tcc ttc ctg aag gag acc ttc      512
Val Arg Gly His Met Gly Phe Lys Lys Ser Phe Leu Lys Glu Thr Phe
101                 106                 111                 116

gat tat aag tta taa                                                  527
Asp Tyr Lys Leu  *
117
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<210> 147
<211> 6955
<212> DNA
<213> Homo sapiens

<220>
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<222> (330)..(3839)

<400> 147

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ttcccgtcac gccccgccgc ctggggctgg gcagtgaccg taaagctgtt cgctcggtgc     120

gacgcaagtc tcagctcagc gcgcttatcc tgggtccacc ggcgctaccg ccccccgacg     180
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tgagagagcg aagttcttgg gccgcgctcc ctccctacct gggtgccctc cccctccggg    240

agcctgggtc cccggggcgg tcgcggcggc tgcatcctca ggccaggccg cgggggggagg    300

gggcggcacg ggcctccgaa agcggggcc  atg gag ccc aga gag tcg ggg aag      353
                                 Met Glu Pro Arg Glu Ser Gly Lys
                                   1               5

gct cct gtg acg ttt gat gac atc act gtg tac tta ctc cag gag gaa      401
Ala Pro Val Thr Phe Asp Asp Ile Thr Val Tyr Leu Leu Gln Glu Glu
  9                  14                  19                  24

tgg gtg ctg ctg agc cag caa cag aag gag ctc tgt ggt tcc aac aag      449
Trp Val Leu Leu Ser Gln Gln Gln Lys Glu Leu Cys Gly Ser Asn Lys
 25                  30                  35                  40

ctg gtg gca cca ctg gga cca act gtt gcc aat cct gag ctg ttc cgc      497
Leu Val Ala Pro Leu Gly Pro Thr Val Ala Asn Pro Glu Leu Phe Arg
 41                  46                  51                  56

aag ttc gga cga ggg cca gag cca tgg ctt ggc agc gtc cag ggc cag      545
Lys Phe Gly Arg Gly Pro Glu Pro Trp Leu Gly Ser Val Gln Gly Gln
 57                  62                  67                  72

agg agc ctt ctg gag cat cac cca gga aaa aaa cag atg ggc tac atg      593
Arg Ser Leu Leu Glu His His Pro Gly Lys Lys Gln Met Gly Tyr Met
 73                  78                  83                  88

gga gaa atg gag gtg caa ggt ccc acc agg gag agt gga cag tcc ctc      641
Gly Glu Met Glu Val Gln Gly Pro Thr Arg Glu Ser Gly Gln Ser Leu
 89                  94                  99                 104

ccg cct cag aag aaa gcc tac ctt tcc cac ctc agt aca ggc agt gga      689
Pro Pro Gln Lys Lys Ala Tyr Leu Ser His Leu Ser Thr Gly Ser Gly
105                 110                 115                 120

cac atc gag gga gac tgg gcc gga aga aac agg aaa ctt ctg aag ccc      737
His Ile Glu Gly Asp Trp Ala Gly Arg Asn Arg Lys Leu Leu Lys Pro
121                 126                 131                 136

cgg tcc atc cag aag tcg tgg ttt gtg cag ttt ccg tgg ctg atc atg      785
Arg Ser Ile Gln Lys Ser Trp Phe Val Gln Phe Pro Trp Leu Ile Met
137                 142                 147                 152

aat gag gag cag acg gct ctg ttc tgc tct gct tgc cga gaa tac ccc      833
Asn Glu Glu Gln Thr Ala Leu Phe Cys Ser Ala Cys Arg Glu Tyr Pro
153                 158                 163                 168

tcc atc agg gac aaa cgg tca aga cta ata gaa ggt tat aca gga cca      881
Ser Ile Arg Asp Lys Arg Ser Arg Leu Ile Glu Gly Tyr Thr Gly Pro
169                 174                 179                 184

ttc aag gtg gag act ctc aaa tac cac gcg aag agc aag gcc cac atg      929
Phe Lys Val Glu Thr Leu Lys Tyr His Ala Lys Ser Lys Ala His Met
185                 190                 195                 200

ttc tgt gtc aat gcc ttg gca gcg agg gac ccc atc tgg gca gcc cgg      977
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Phe Cys Val Asn Ala Leu Ala Ala Arg Asp Pro Ile Trp Ala Ala Arg
201                 206                 211                 216

ttc cgg agc atc aga gac cca cct gga gat gtt ctg gcc agc ccg gag     1025
Phe Arg Ser Ile Arg Asp Pro Pro Gly Asp Val Leu Ala Ser Pro Glu
217                 222                 227                 232

ccg ctc ttc act gca gat tgc ccc ata ttc tac ccc cca ggg cct ctg     1073
Pro Leu Phe Thr Ala Asp Cys Pro Ile Phe Tyr Pro Pro Gly Pro Leu
233                 238                 243                 248

gga gga ttt gat agc atg gct gag ctc ctg cca agt tca aga gct gaa     1121
Gly Gly Phe Asp Ser Met Ala Glu Leu Leu Pro Ser Ser Arg Ala Glu
249                 254                 259                 264

cta gag gac cct ggg ggg gat gga gca att cct gca atg tat cta gac     1169
Leu Glu Asp Pro Gly Gly Asp Gly Ala Ile Pro Ala Met Tyr Leu Asp
265                 270                 275                 280

tgc att tca gat ttg agg caa aaa gaa atc act gat ggc atc cac agc     1217
Cys Ile Ser Asp Leu Arg Gln Lys Glu Ile Thr Asp Gly Ile His Ser
281                 286                 291                 296

tcc tca gac att aat att tta tat aat gat gca gta gaa tcc tgc att     1265
Ser Ser Asp Ile Asn Ile Leu Tyr Asn Asp Ala Val Glu Ser Cys Ile
297                 302                 307                 312

cag gac cct tct gca gag ggg ctg tcg gag gag gtt cct gtg gtg ttt     1313
Gln Asp Pro Ser Ala Glu Gly Leu Ser Glu Glu Val Pro Val Val Phe
313                 318                 323                 328

gag gag ctg ccg gtg gtg ttc gag gat gtg gca gtg tat ttc acc cgg     1361
Glu Glu Leu Pro Val Val Phe Glu Asp Val Ala Val Tyr Phe Thr Arg
329                 334                 339                 344

gag gag tgg ggc atg cta gac aag cgg cag aag gag ctg tac aga gac     1409
Glu Glu Trp Gly Met Leu Asp Lys Arg Gln Lys Glu Leu Tyr Arg Asp
345                 350                 355                 360

gtg atg cgg atg aac tac gag ctg ttg gca tcc ttg gga cct gct gct     1457
Val Met Arg Met Asn Tyr Glu Leu Leu Ala Ser Leu Gly Pro Ala Ala
361                 366                 371                 376

gcc aag cca gac ttg atc tcc aaa ctg gag cgg agg gct gca ccc tgg     1505
Ala Lys Pro Asp Leu Ile Ser Lys Leu Glu Arg Arg Ala Ala Pro Trp
377                 382                 387                 392

atc aag gac cca aat ggg cca aag tgg ggg aaa ggt cgt cct cca ggg     1553
Ile Lys Asp Pro Asn Gly Pro Lys Trp Gly Lys Gly Arg Pro Pro Gly
393                 398                 403                 408

aac aag aag atg gtg gca gtg aga gag gca gac aca cag gcc tcg gct     1601
Asn Lys Lys Met Val Ala Val Arg Glu Ala Asp Thr Gln Ala Ser Ala
409                 414                 419                 424

gca gac tcc gcg ttg ctt cca ggc tct ccc gtg gag gcc cgt gcc tcc     1649
Ala Asp Ser Ala Leu Leu Pro Gly Ser Pro Val Glu Ala Arg Ala Ser
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425                 430                 435                 440

tgc tgc agt tcc agc att tgt gag gaa gga gat gga cct agg aga atc     1697
Cys Cys Ser Ser Ser Ile Cys Glu Glu Gly Asp Gly Pro Arg Arg Ile
441                 446                 451                 456

aag agg aca tac agg ccc cgt tcc att cag agg tca tgg ttt ggg cag     1745
Lys Arg Thr Tyr Arg Pro Arg Ser Ile Gln Arg Ser Trp Phe Gly Gln
457                 462                 467                 472

ttc cca tgg tta gta att gac ccc aaa gag acc aaa ctc ttc tgc tca     1793
Phe Pro Trp Leu Val Ile Asp Pro Lys Glu Thr Lys Leu Phe Cys Ser
473                 478                 483                 488

gcc tgc ata gaa aga cct aat ctc cat gat aaa tca tct cgg tta gtc     1841
Ala Cys Ile Glu Arg Pro Asn Leu His Asp Lys Ser Ser Arg Leu Val
489                 494                 499                 504

aga ggt tac acg ggg cct ttt aaa gtg gag act tta aaa tac cat gaa     1889
Arg Gly Tyr Thr Gly Pro Phe Lys Val Glu Thr Leu Lys Tyr His Glu
505                 510                 515                 520

gtc agc aaa gcg cac agg ctc tgt gtc aac acg gtt gaa atc aag gaa     1937
Val Ser Lys Ala His Arg Leu Cys Val Asn Thr Val Glu Ile Lys Glu
521                 526                 531                 536

gac acc cct cac act gcc ctc gtt cca gag atc tcc agc gac ctc atg     1985
Asp Thr Pro His Thr Ala Leu Val Pro Glu Ile Ser Ser Asp Leu Met
537                 542                 547                 552

gcc aac atg gag cac ttt ttc aat gcc gcc tac tcc att gca tac cac     2033
Ala Asn Met Glu His Phe Phe Asn Ala Ala Tyr Ser Ile Ala Tyr His
553                 558                 563                 568

tca agg ccc ctg aat gac ttt gag aag atc ctg cag ctc ctc caa agc     2081
Ser Arg Pro Leu Asn Asp Phe Glu Lys Ile Leu Gln Leu Leu Gln Ser
569                 574                 579                 584

acg ggg acc gtg ata tta ggc aag tac cgc aat cgc acg gcg tgc act     2129
Thr Gly Thr Val Ile Leu Gly Lys Tyr Arg Asn Arg Thr Ala Cys Thr
585                 590                 595                 600

cag ttc atc aag tac atc tca gag acc ctg aag agg gag atc ctg gag     2177
Gln Phe Ile Lys Tyr Ile Ser Glu Thr Leu Lys Arg Glu Ile Leu Glu
601                 606                 611                 616

gac gtg cgg aac tcg ccc tgt gtg agc gtg ctg ctg gac agc tcc acc     2225
Asp Val Arg Asn Ser Pro Cys Val Ser Val Leu Leu Asp Ser Ser Thr
617                 622                 627                 632

gac gcc tcc gag cag gcc tgc gtg ggg att tac atc cgc tac ttc aag     2273
Asp Ala Ser Glu Gln Ala Cys Val Gly Ile Tyr Ile Arg Tyr Phe Lys
633                 638                 643                 648

cag atg gag gtg aaa gag tcc tac atc act ctg gcc cct ctc tac agt     2321
Gln Met Glu Val Lys Glu Ser Tyr Ile Thr Leu Ala Pro Leu Tyr Ser
649                 654                 659                 664
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gag aca gca gat ggg tac ttc gag acc atc gtt tct gcc ctg gat gag     2369
Glu Thr Ala Asp Gly Tyr Phe Glu Thr Ile Val Ser Ala Leu Asp Glu
665                 670                 675                 680

ctg gac atc ccc ttc cgg aag cct ggc tgg gtg gtg ggg ctg ggg acg     2417
Leu Asp Ile Pro Phe Arg Lys Pro Gly Trp Val Val Gly Leu Gly Thr
681                 686                 691                 696

gat ggc tca gcc atg ttg agc tgc aga gga ggc ctt gtg gaa aag ttc     2465
Asp Gly Ser Ala Met Leu Ser Cys Arg Gly Gly Leu Val Glu Lys Phe
697                 702                 707                 712

cag gag gtc atc ccg cag ctg ctc cct gtc cac tgc gtg gcc cac cgg     2513
Gln Glu Val Ile Pro Gln Leu Leu Pro Val His Cys Val Ala His Arg
713                 718                 723                 728

ctg cac ctg gct gtg gtg gac gcc tgc ggg agc atc gat ctg gtg aag     2561
Leu His Leu Ala Val Val Asp Ala Cys Gly Ser Ile Asp Leu Val Lys
729                 734                 739                 744

aag tgt gac cgg cac atc cgc acc gtc ttc aag ttt tat cag tcc tca     2609
Lys Cys Asp Arg His Ile Arg Thr Val Phe Lys Phe Tyr Gln Ser Ser
745                 750                 755                 760

aac aag agg ctg aac gag ctg cag gaa ggt gcg gcg cct ctg gag cag     2657
Asn Lys Arg Leu Asn Glu Leu Gln Glu Gly Ala Ala Pro Leu Glu Gln
761                 766                 771                 776

gag atc atc cgc ctg aag gat ctg aat gcg gtc cgc tgg gtg gcc agc     2705
Glu Ile Ile Arg Leu Lys Asp Leu Asn Ala Val Arg Trp Val Ala Ser
777                 782                 787                 792

agg agg cgc acg ctg cac gcg ctg ctc gtg agc tgg ccc gcc ctg gcc     2753
Arg Arg Arg Thr Leu His Ala Leu Leu Val Ser Trp Pro Ala Leu Ala
793                 798                 803                 808

agg cac ctc cag agg gtg gca gag gct ggg ggc cag att ggg cac cgg     2801
Arg His Leu Gln Arg Val Ala Glu Ala Gly Gly Gln Ile Gly His Arg
809                 814                 819                 824

gcc aaa ggg atg ctg aag ctc atg cgc ggc ttc cac ttt gtc aag ttc     2849
Ala Lys Gly Met Leu Lys Leu Met Arg Gly Phe His Phe Val Lys Phe
825                 830                 835                 840

tgc cac ttc ctg ttg gac ttc ctg agc atc tac agg cct ctg tcc gag     2897
Cys His Phe Leu Leu Asp Phe Leu Ser Ile Tyr Arg Pro Leu Ser Glu
841                 846                 851                 856

gtg tgc cag aag gag atc gtg ctg att aca gag gtg aac gcc acg ctg     2945
Val Cys Gln Lys Glu Ile Val Leu Ile Thr Glu Val Asn Ala Thr Leu
857                 862                 867                 872

ggc cgc gcc tac gtg gca ctg gag agc ctc cgt cac cag gca ggg ccc     2993
Gly Arg Ala Tyr Val Ala Leu Glu Ser Leu Arg His Gln Ala Gly Pro
873                 878                 883                 888
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aaa gag gaa gaa ttc aac gcc agc ttc aag gat ggg cgg ctc cac ggc     3041
Lys Glu Glu Glu Phe Asn Ala Ser Phe Lys Asp Gly Arg Leu His Gly
889                 894                 899                 904

atc tgc ttg gac aaa ctg gag gta gcg gaa cag cgg ttc cag gcg gat     3089
Ile Cys Leu Asp Lys Leu Glu Val Ala Glu Gln Arg Phe Gln Ala Asp
905                 910                 915                 920

agg gag agg aca gtc ctg acg ggg att gag tac ctc cag cag agg ttt     3137
Arg Glu Arg Thr Val Leu Thr Gly Ile Glu Tyr Leu Gln Gln Arg Phe
921                 926                 931                 936

gac gca gac cga ccc cca cag ctg aag aac atg gag gtg ttt gac acc     3185
Asp Ala Asp Arg Pro Pro Gln Leu Lys Asn Met Glu Val Phe Asp Thr
937                 942                 947                 952

atg gcc tgg cca agt ggg att gaa ctt gcc agt ttt ggg aat gat gac     3233
Met Ala Trp Pro Ser Gly Ile Glu Leu Ala Ser Phe Gly Asn Asp Asp
953                 958                 963                 968

att ctc aac ctg gcc agg tat ttc gag tgc tcc ctc cca aca gga tac     3281
Ile Leu Asn Leu Ala Arg Tyr Phe Glu Cys Ser Leu Pro Thr Gly Tyr
969                 974                 979                 984

agt gag gaa gct ctg ctg gag gag tgg ctg ggc ctg aaa acc att gcc     3329
Ser Glu Glu Ala Leu Leu Glu Glu Trp Leu Gly Leu Lys Thr Ile Ala
985                 990                 995                1000

cag cac ctc ccg ttc tcc atg ctt tgc aaa aac gcc ctg gcc cag cac     3377
Gln His Leu Pro Phe Ser Met Leu Cys Lys Asn Ala Leu Ala Gln His
1001                1006                1011                1016

tgc cgc ttc ccc ctg cta agc aag ctc atg gcc gtg gtg gtc tgt gtg     3425
Cys Arg Phe Pro Leu Leu Ser Lys Leu Met Ala Val Val Val Cys Val
1017                1022                1027                1032

ccc atc tcc acc tct tgc tgt gag cgg ggg ttc aag gcc atg aac cga     3473
Pro Ile Ser Thr Ser Cys Cys Glu Arg Gly Phe Lys Ala Met Asn Arg
1033                1038                1043                1048

atc agg acc gat gag agg acc aag ctc tcc aac gag gtg ctc aac atg     3521
Ile Arg Thr Asp Glu Arg Thr Lys Leu Ser Asn Glu Val Leu Asn Met
1049                1054                1059                1064

ctc atg atg aca gct gtg aac ggt gtg gcc gtc acg gag tac gac ccc     3569
Leu Met Met Thr Ala Val Asn Gly Val Ala Val Thr Glu Tyr Asp Pro
1065                1070                1075                1080

cag ccc gcc atc cag cac tgg tac ctg acc tcc tca ggc cgg cgt ttc     3617
Gln Pro Ala Ile Gln His Trp Tyr Leu Thr Ser Ser Gly Arg Arg Phe
1081                1086                1091                1096

agc cat gtc tac acc tgt gcc cag gtg cca gcc cgc tcc cct gca agc     3665
Ser His Val Tyr Thr Cys Ala Gln Val Pro Ala Arg Ser Pro Ala Ser
1097                1102                1107                1112

gcc agg ctc agg aag gag gag atg gga gcc ctc tat gtg gag gag ccc     3713
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 Ala Arg Leu Arg Lys Glu Glu Met Gly Ala Leu Tyr Val Glu Glu Pro
1113                1118                1123                1128

 agg acc cag aag cca ccc atc ctg ccc tcc agg gaa gca gcg gag gtt     3761
 Arg Thr Gln Lys Pro Pro Ile Leu Pro Ser Arg Glu Ala Ala Glu Val
1129                1134                1139                1144

 ctg aag gac tgc atc atg gag cct ccc gag aga ctc ctg tat ccc cac     3809
 Leu Lys Asp Cys Ile Met Glu Pro Pro Glu Arg Leu Leu Tyr Pro His
1145                1150                1155                1160

 acc agc cag gag gcc ccc ggg atg tcc tga g ggacagggag tccttgggac     3860
 Thr Ser Gln Glu Ala Pro Gly Met Ser  *
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agtctgtctg cagccaaa  atg tcc aac aga aac aac aac aag ctt ccc agc      171
                    Met Ser Asn Arg Asn Asn Asn Lys Leu Pro Ser
                      1               5

aac ctg ccg cag tta cag aat cta atc aag cga gac ccg ccg gcc tac      219
Asn Leu Pro Gln Leu Gln Asn Leu Ile Lys Arg Asp Pro Pro Ala Tyr
 12                  17                  22                  27

atc gag gag ttt cta cag cag tat aat cac tac aaa tcc aat gtg gag      267
Ile Glu Glu Phe Leu Gln Gln Tyr Asn His Tyr Lys Ser Asn Val Glu
 28                  33                  38                  43

att ttc aaa ttg caa cca aat aaa ccc agc aaa gaa cta gca gag ctg      315
Ile Phe Lys Leu Gln Pro Asn Lys Pro Ser Lys Glu Leu Ala Glu Leu
 44                  49                  54                  59

gtg atg ttt atg gca cag att agt cac tgc tac cca gag tac cta agt      363
Val Met Phe Met Ala Gln Ile Ser His Cys Tyr Pro Glu Tyr Leu Ser
 60                  65                  70                  75

aat ttt cct caa gag gtg aaa gat ctt ctc tcc tgc aat cat acc gta      411
Asn Phe Pro Gln Glu Val Lys Asp Leu Leu Ser Cys Asn His Thr Val
 76                  81                  86                  91

ttg gat cca gat ctg cga atg aca ttt tgc aaa gct ttg atc ttg ctg      459
Leu Asp Pro Asp Leu Arg Met Thr Phe Cys Lys Ala Leu Ile Leu Leu
 92                  97                 102                 107

aga aat aag aat ctc atc aat cca tca agc ctg cta gaa ctc ttc ttt      507
Arg Asn Lys Asn Leu Ile Asn Pro Ser Ser Leu Leu Glu Leu Phe Phe
108                 113                 118                 123

gaa ctt ttt cgt tgc cat gat aaa ctt ctg cga aag act tta tac aca      555
Glu Leu Phe Arg Cys His Asp Lys Leu Leu Arg Lys Thr Leu Tyr Thr
124                 129                 134                 139
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cat att gtg act gat atc aag aat ata aat gca aaa cac aag aac aat      603
His Ile Val Thr Asp Ile Lys Asn Ile Asn Ala Lys His Lys Asn Asn
140                 145                 150                 155

aaa gtg aat gta gta ttg caa aat ttc atg tac acc atg tta aga gat      651
Lys Val Asn Val Val Leu Gln Asn Phe Met Tyr Thr Met Leu Arg Asp
156                 161                 166                 171

agc aat gca acc gca gcc aag atg tct tta gat gta atg att gaa ctc      699
Ser Asn Ala Thr Ala Ala Lys Met Ser Leu Asp Val Met Ile Glu Leu
172                 177                 182                 187

tac aga agg aac atc tgg aat gat gca aaa act gtc aat gtt atc aca      747
Tyr Arg Arg Asn Ile Trp Asn Asp Ala Lys Thr Val Asn Val Ile Thr
188                 193                 198                 203

act gca tgt ttc tct aag gtc acc aag ata tta gtt gcc gct ttg aca      795
Thr Ala Cys Phe Ser Lys Val Thr Lys Ile Leu Val Ala Ala Leu Thr
204                 209                 214                 219

ttc ttt ctt ggg aaa gat gaa gat gaa aaa cag gac agt gac tcc gaa      843
Phe Phe Leu Gly Lys Asp Glu Asp Glu Lys Gln Asp Ser Asp Ser Glu
220                 225                 230                 235

tct gag gat gat gga cca aca gca aga gac ctg cta gta caa tat gct      891
Ser Glu Asp Asp Gly Pro Thr Ala Arg Asp Leu Leu Val Gln Tyr Ala
236                 241                 246                 251

aca ggg aag aaa agt tcc aaa aac aag aaa aag ttg gaa aag gca atg      939
Thr Gly Lys Lys Ser Ser Lys Asn Lys Lys Lys Leu Glu Lys Ala Met
252                 257                 262                 267

aaa gtg ctc aag aaa cac agg aag aat aaa aaa cca gag gtg ttt aac      987
Lys Val Leu Lys Lys His Arg Lys Asn Lys Lys Pro Glu Val Phe Asn
268                 273                 278                 283

ttt tca gcc att cac ttg att cat gat ccc caa gat ttt gcg gaa aaa     1035
Phe Ser Ala Ile His Leu Ile His Asp Pro Gln Asp Phe Ala Glu Lys
284                 289                 294                 299

cta cta aag cag ctt gag tgc tgt aag gag agg ttt gaa gtg aag atg     1083
Leu Leu Lys Gln Leu Glu Cys Cys Lys Glu Arg Phe Glu Val Lys Met
300                 305                 310                 315

atg ctc atg aac ctt atc tcc aga ttg gtg gga att cat gag ctt ttc     1131
Met Leu Met Asn Leu Ile Ser Arg Leu Val Gly Ile His Glu Leu Phe
316                 321                 326                 331

ctc ttc aat ttc tat ccc ttt ttg caa agg ttt ctg cag ccc cac caa     1179
Leu Phe Asn Phe Tyr Pro Phe Leu Gln Arg Phe Leu Gln Pro His Gln
332                 337                 342                 347

aga gaa gta acc aag atc ctt ctg ttt gct gca caa gca tct cat cac     1227
Arg Glu Val Thr Lys Ile Leu Leu Phe Ala Ala Gln Ala Ser His His
348                 353                 358                 363
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cta gta ccc cca gag att att caa tca ttg ctt atg act gtg gca aac     1275
Leu Val Pro Pro Glu Ile Ile Gln Ser Leu Leu Met Thr Val Ala Asn
364                 369                 374                 379

aat ttt gtt acc gac aag aac tct gga gaa gtc atg aca gta gga atc     1323
Asn Phe Val Thr Asp Lys Asn Ser Gly Glu Val Met Thr Val Gly Ile
380                 385                 390                 395

aat gct ata aag gag ata aca gct cga tgt cct ctg gcc atg act gaa     1371
Asn Ala Ile Lys Glu Ile Thr Ala Arg Cys Pro Leu Ala Met Thr Glu
396                 401                 406                 411

gaa ctt ctc caa gac ctg gct cag tat aaa aca cac aag gat aag aat     1419
Glu Leu Leu Gln Asp Leu Ala Gln Tyr Lys Thr His Lys Asp Lys Asn
412                 417                 422                 427

gta atg atg tct gct aga act ttg att cac ctc ttc cga aca ctg aat     1467
Val Met Met Ser Ala Arg Thr Leu Ile His Leu Phe Arg Thr Leu Asn
428                 433                 438                 443

cct cag atg ctg cag aag aaa ttc cgg ggt aag cct aca gag gcc tcc     1515
Pro Gln Met Leu Gln Lys Lys Phe Arg Gly Lys Pro Thr Glu Ala Ser
444                 449                 454                 459

ata gaa gca aga gta caa gaa tat gga gaa tta gat gct aaa gat tac     1563
Ile Glu Ala Arg Val Gln Glu Tyr Gly Glu Leu Asp Ala Lys Asp Tyr
460                 465                 470                 475

att cca gga gca gaa gtt ctg gaa gtt gag aaa gaa gag aat gct gaa     1611
Ile Pro Gly Ala Glu Val Leu Glu Val Glu Lys Glu Glu Asn Ala Glu
476                 481                 486                 491

aat gat gaa gat gga tgg gaa agt acc agt ctc agt gag gag gag gat     1659
Asn Asp Glu Asp Gly Trp Glu Ser Thr Ser Leu Ser Glu Glu Glu Asp
492                 497                 502                 507

gct gat ggt gaa tgg att gat gtg caa cac tct tcc gat gaa gaa cag     1707
Ala Asp Gly Glu Trp Ile Asp Val Gln His Ser Ser Asp Glu Glu Gln
508                 513                 518                 523

caa gaa atc tcc aag aag ctg aac agc atg ccc atg gag gag cgg aag     1755
Gln Glu Ile Ser Lys Lys Leu Asn Ser Met Pro Met Glu Glu Arg Lys
524                 529                 534                 539

gcc aaa gct gca gcc atc agc act agc cga gtt tta act cag gaa gac     1803
Ala Lys Ala Ala Ala Ile Ser Thr Ser Arg Val Leu Thr Gln Glu Asp
540                 545                 550                 555

ttc cag aaa atc cgc atg gcc caa atg aga aaa gaa ctt gat gct gcc     1851
Phe Gln Lys Ile Arg Met Ala Gln Met Arg Lys Glu Leu Asp Ala Ala
556                 561                 566                 571

ccc ggg aaa tcc cag aag agg aaa tac att gaa ata gac agt gat gaa     1899
Pro Gly Lys Ser Gln Lys Arg Lys Tyr Ile Glu Ile Asp Ser Asp Glu
572                 577                 582                 587

gag ccc agg ggt gaa tta ctt tct ctt cgg gac att gaa cgc ctt cat     1947
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Glu Pro Arg Gly Glu Leu Leu Ser Leu Arg Asp Ile Glu Arg Leu His
588                 593                 598                 603

aaa aag cca aag tct gac aaa gag aca aga cta gca act gca atg gct     1995
Lys Lys Pro Lys Ser Asp Lys Glu Thr Arg Leu Ala Thr Ala Met Ala
604                 609                 614                 619

gga aag aca gac cga aaa gaa ttt gtg agg aag aaa acc aaa aca aat     2043
Gly Lys Thr Asp Arg Lys Glu Phe Val Arg Lys Lys Thr Lys Thr Asn
620                 625                 630                 635

cca ttt tcc agt tcg aca aat aaa gag aag aaa aaa cag aag aac ttt     2091
Pro Phe Ser Ser Ser Thr Asn Lys Glu Lys Lys Lys Gln Lys Asn Phe
636                 641                 646                 651

atg atg atg cgg tat agc cag aat gtc cgg tca aaa aat aag cgt tcc     2139
Met Met Met Arg Tyr Ser Gln Asn Val Arg Ser Lys Asn Lys Arg Ser
652                 657                 662                 667

ttc cga gaa aaa cag ttg gca cta cga gat gca ctt ttg aaa aag aga     2187
Phe Arg Glu Lys Gln Leu Ala Leu Arg Asp Ala Leu Leu Lys Lys Arg
668                 673                 678                 683

aaa aga atg aag taa cttcctggca agttttccat tcctagaaga atgctaagtt     2242
Lys Arg Met Lys  *
684

tgtgtccttg ctctgaaaat tggtaaatca agcatgtttg tttacattaa aaagtccaga   2302

cacactgtat tgtgaaaact gctgaacatg tggcagcaat tttgtgtttt tattttggag   2362

acggctaatg gtaggaatgt taatgtaaat agtggtggta atgtaaaatc atttcattta   2422

tcattcatgc aaaaaaaagt atgtattgag tgcctattca ttgtcactgt agatgcaaaa   2482

cgaatgagct gtaacccctt cactcaaggc attgacagct tagctgtgag ggtggacaca   2542

catatgtgta tttacagtgc agtgtaaata gttctgtagt agaggttaac tccatatttc   2602

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ccgggcacta ctccagtgtg gtcccctctg gagggcggag gggatgagga gctgcgccct    240

aatccttatg tccgc atg cct tac aga tgg tgg gca gtg gtg gtg ctg gct      291
                Met Pro Tyr Arg Trp Trp Ala Val Val Val Leu Ala
                  1               5                  10

gcg ttc ccc tcc cta ggg gca ggt ggg gag act ccc gaa gcc cct ccg      339
Ala Phe Pro Ser Leu Gly Ala Gly Gly Glu Thr Pro Glu Ala Pro Pro
 13                  18                  23                  28

gag tca tgg acc cag cta tgg ttc ttc cga ttt gtg gtg aat gct gct      387
Glu Ser Trp Thr Gln Leu Trp Phe Phe Arg Phe Val Val Asn Ala Ala
 29                  34                  39                  44

ggc tat gcc agc ttt atg gta cct ggc tac ctc ctg gtg cag tac ttc      435
Gly Tyr Ala Ser Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Phe
 45                  50                  55                  60

agg cgg aag aac tac ctg gag acc ggt agg ggc ctc tgc ttt ccc ctg      483
Arg Arg Lys Asn Tyr Leu Glu Thr Gly Arg Gly Leu Cys Phe Pro Leu
 61                  66                  71                  76

gtg aaa gct tgt gtg ttt ggc aat gag ccc aag gcc tct gat gag gtt      531
Val Lys Ala Cys Val Phe Gly Asn Glu Pro Lys Ala Ser Asp Glu Val
 77                  82                  87                  92

ccc ctg gcg ccc cga aca gag gcg gca gag acc acc ccg atg tgg cag      579
Pro Leu Ala Pro Arg Thr Glu Ala Ala Glu Thr Thr Pro Met Trp Gln
 93                  98                 103                 108

gcc ctg aag ctg ctc ttc tgt gcc aca ggg ctc cag gtg tct tat ctg      627
Ala Leu Lys Leu Leu Phe Cys Ala Thr Gly Leu Gln Val Ser Tyr Leu
109                 114                 119                 124

act tgg ggt gtg ctg cag gaa aga gtg atg acc cgc agc tat ggg gcc      675
Thr Trp Gly Val Leu Gln Glu Arg Val Met Thr Arg Ser Tyr Gly Ala
125                 130                 135                 140

aca gcc aca tca ccg ggt gag cgc ttt acg gac tcg cag ttc ctg gtg      723
Thr Ala Thr Ser Pro Gly Glu Arg Phe Thr Asp Ser Gln Phe Leu Val
141                 146                 151                 156

cta atg aac cga gtg ctg gca ctg att gtg gct ggc ctc tcc tgt gtt      771
Leu Met Asn Arg Val Leu Ala Leu Ile Val Ala Gly Leu Ser Cys Val
157                 162                 167                 172

ctc tgc aag cag ccc cgg cat ggg gca ccc atg tac cgg tac tcc ttt      819
Leu Cys Lys Gln Pro Arg His Gly Ala Pro Met Tyr Arg Tyr Ser Phe
173                 178                 183                 188

gcc agc ctg tcc aat gtg ctt agc agc tgg tgc caa tac gaa gct ctt      867
Ala Ser Leu Ser Asn Val Leu Ser Ser Trp Cys Gln Tyr Glu Ala Leu
```

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189                 194                 199                 204

aag ttc gtc agc ttc ccc acc cag gtg ctg gcc aag gcc tct aag gtg      915
Lys Phe Val Ser Phe Pro Thr Gln Val Leu Ala Lys Ala Ser Lys Val
205                 210                 215                 220

atc cct gtc atg ctg atg gga aag ctt gtg tct cgg cgc agc tac gaa      963
Ile Pro Val Met Leu Met Gly Lys Leu Val Ser Arg Arg Ser Tyr Glu
221                 226                 231                 236

cac tgg gag tac ctg aca gcc acc ctc atc tcc att ggg gtc agc atg     1011
His Trp Glu Tyr Leu Thr Ala Thr Leu Ile Ser Ile Gly Val Ser Met
237                 242                 247                 252

ttt ctg cta tcc agc gga cca gag ccc cgc agc tcc cca gcc acc aca     1059
Phe Leu Leu Ser Ser Gly Pro Glu Pro Arg Ser Ser Pro Ala Thr Thr
253                 258                 263                 268

ctc tca ggc ctc atc tta ctg gca ggt tat att gct ttt gac agc ttc     1107
Leu Ser Gly Leu Ile Leu Leu Ala Gly Tyr Ile Ala Phe Asp Ser Phe
269                 274                 279                 284

acc tca aac tgg cag gat gcc ctg ttt gcc tat aag atg tca tcg gtg     1155
Thr Ser Asn Trp Gln Asp Ala Leu Phe Ala Tyr Lys Met Ser Ser Val
285                 290                 295                 300

cag atg atg ttt ggg gtc aat ttc ttc tcc tgc ctc ttc aca gtg ggc     1203
Gln Met Met Phe Gly Val Asn Phe Phe Ser Cys Leu Phe Thr Val Gly
301                 306                 311                 316

tca ctg cta gaa cag ggg gcc cta ctg gag gga acc cgc ttc atg ggg     1251
Ser Leu Leu Glu Gln Gly Ala Leu Leu Glu Gly Thr Arg Phe Met Gly
317                 322                 327                 332

cga cac agt gag ttt gct gcc cat gcc ctg cta ctc tcc atc tgc tcc     1299
Arg His Ser Glu Phe Ala Ala His Ala Leu Leu Leu Ser Ile Cys Ser
333                 338                 343                 348

gca tgt ggc cag ctc ttc atc ttt tac acc att ggg cag ttt ggg gct     1347
Ala Cys Gly Gln Leu Phe Ile Phe Tyr Thr Ile Gly Gln Phe Gly Ala
349                 354                 359                 364

gcc gtc ttc acc atc atc atg acc ctc cgc cag gcc ttt gcc atc ctt     1395
Ala Val Phe Thr Ile Ile Met Thr Leu Arg Gln Ala Phe Ala Ile Leu
365                 370                 375                 380

ctt tcc tgc ctt ctc tat ggc cac act gtc act gtg gtg gga ggg ctg     1443
Leu Ser Cys Leu Leu Tyr Gly His Thr Val Thr Val Val Gly Gly Leu
381                 386                 391                 396

ggg gtg gct gtg gtc ttt gct gcc ctc ctg ctc aga gtc tac gcg cgg     1491
Gly Val Ala Val Val Phe Ala Ala Leu Leu Leu Arg Val Tyr Ala Arg
397                 402                 407                 412

ggc cgt cta aag caa cgg gga aag aag gct gtg cct gtt gag tct cct     1539
Gly Arg Leu Lys Gln Arg Gly Lys Lys Ala Val Pro Val Glu Ser Pro
413                 418                 423                 428
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gtg cag aag gtt tga gggtggaaag ggcctgaggg gtgaagtgaa ataggaccct     1594
Val Gln Lys Val  *
429

cccaccatcc ccttctgctg taacctctga gggagctggc tgaaagggca aaatgcaggt   1654

gttttctcag tatcacagac cagctctgca gcaggggatt ggggagccca ggaggcagcc   1714

ttccctttg ccttaagtca cccatcttcc agtaagcagt ttattctgag ccccgggggt    1774

agacagtcct cagtgagggg ttttggggag tttggggtca agagagcata ggtaggttcc   1834

acagttactc ttcccacaag ttcccttaag tcttgcccta gctgtgctct gccaccttcc   1894

agactcactc ccctctgcaa atacctgcat ttcttaccct ggtgagaaaa gcacaagcgg   1954

tgtaggctcc aatgctgctt tcccaggagg gtgaagatgg tgctgtgctg aggaaagggg   2014

atgcagagcc ctgcccagca ccaccacctc ctatgctcct ggatccctag gctctgttcc   2074

atgagcctgt tgcaggtttt ggtactttag aaatgtaact ttttgctctt ataattttat   2134

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cagcccgcta caggatacgt gatggacgcc cagagacacc gccctccagc tggtggggga    180

ggagccccag ccaccaagaa gtagcagtag ctgatgtgca gtttggcccc   atg aga     236
                                                         Met Arg
                                                           1

ttt cat caa gat caa ctt cag gta ctt tta gtg ttt acc aaa gaa gat      284
Phe His Gln Asp Gln Leu Gln Val Leu Leu Val Phe Thr Lys Glu Asp
  3                   8                  13                  18

aac caa tgt aat gga ttc tgc agg gca tgt gaa aaa gca ggg ttt aag      332
Asn Gln Cys Asn Gly Phe Cys Arg Ala Cys Glu Lys Ala Gly Phe Lys
 19                  24                  29                  34

tgt aca gtt acc aag gag gct cag gct gtc ctt gcc tgt ttc ctg gac      380
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Cys Thr Val Thr Lys Glu Ala Gln Ala Val Leu Ala Cys Phe Leu Asp
 35                  40                  45                  50

aaa cat cat gac att atc atc ata gac cac aga aat cct cga cag ctg      428
Lys His His Asp Ile Ile Ile Ile Asp His Arg Asn Pro Arg Gln Leu
 51                  56                  61                  66

gat gca gag gca ctg tgc agg tct atc aga tca tca aaa ctc tca gaa      476
Asp Ala Glu Ala Leu Cys Arg Ser Ile Arg Ser Ser Lys Leu Ser Glu
 67                  72                  77                  82

aac aca gtt att gtt ggt gta gta cgc agg gtg gat aga gaa gag ttg      524
Asn Thr Val Ile Val Gly Val Val Arg Arg Val Asp Arg Glu Glu Leu
 83                  88                  93                  98

tcc gta atg cct ttc att tct gct gga ttt aca agg agg tat gta gaa      572
Ser Val Met Pro Phe Ile Ser Ala Gly Phe Thr Arg Arg Tyr Val Glu
 99                 104                 109                 114

aac ccc aac atc atg gcc tgc tac aat gaa ctg ctc cag ctg gag ttt      620
Asn Pro Asn Ile Met Ala Cys Tyr Asn Glu Leu Leu Gln Leu Glu Phe
115                 120                 125                 130

gga gag gtg cga tca caa ctg aaa ctc agg gct tgt aac tca gta ttc      668
Gly Glu Val Arg Ser Gln Leu Lys Leu Arg Ala Cys Asn Ser Val Phe
131                 136                 141                 146

act gca tta gaa aac agt gaa gat gca att gaa att aca agc gaa gac      716
Thr Ala Leu Glu Asn Ser Glu Asp Ala Ile Glu Ile Thr Ser Glu Asp
147                 152                 157                 162

cgt ttt ata cag tat gca aat cct gca ttt gaa aca aca atg ggc tat      764
Arg Phe Ile Gln Tyr Ala Asn Pro Ala Phe Glu Thr Thr Met Gly Tyr
163                 168                 173                 178

cag tca ggt gaa tta ata ggg aag gag tta gga gaa gtg cct ata aat      812
Gln Ser Gly Glu Leu Ile Gly Lys Glu Leu Gly Glu Val Pro Ile Asn
179                 184                 189                 194

gaa aaa aag gct gac ttg ctc gat act ata aat tca tgc atc agg ata      860
Glu Lys Lys Ala Asp Leu Leu Asp Thr Ile Asn Ser Cys Ile Arg Ile
195                 200                 205                 210

ggc aag gag tgg caa gga att tac tat gcc aaa aag aaa aac gga gat      908
Gly Lys Glu Trp Gln Gly Ile Tyr Tyr Ala Lys Lys Lys Asn Gly Asp
211                 216                 221                 226

aat ata caa caa aat gtg aag ata ata cct gtc att gga cag gga gga      956
Asn Ile Gln Gln Asn Val Lys Ile Ile Pro Val Ile Gly Gln Gly Gly
227                 232                 237                 242

aaa att aga cac tat gtg tcc att atc aga gtg tgc aat ggc aac aat     1004
Lys Ile Arg His Tyr Val Ser Ile Ile Arg Val Cys Asn Gly Asn Asn
243                 248                 253                 258

aag gct gag aaa ata tcc gaa tgt gtt cag tct gac act cat aca gat     1052
Lys Ala Glu Lys Ile Ser Glu Cys Val Gln Ser Asp Thr His Thr Asp
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259                 264                 269                 274

aat cag aca ggc aaa cat aaa gac agg aga aaa ggc tca cta gac gtc     1100
Asn Gln Thr Gly Lys His Lys Asp Arg Arg Lys Gly Ser Leu Asp Val
275                 280                 285                 290

aaa gct gtt gcc tcc cgt gca act gaa gtt tcc agc cag aga cga cac     1148
Lys Ala Val Ala Ser Arg Ala Thr Glu Val Ser Ser Gln Arg Arg His
291                 296                 301                 306

tct tcc atg gcc cgg ata cat tcc atg aca att gag gcg ccc atc acc     1196
Ser Ser Met Ala Arg Ile His Ser Met Thr Ile Glu Ala Pro Ile Thr
307                 312                 317                 322

aag gta atc aat att atc aat gct gcc cag gaa agt agt ccc atg cct     1244
Lys Val Ile Asn Ile Ile Asn Ala Ala Gln Glu Ser Ser Pro Met Pro
323                 328                 333                 338

gtg aca gaa gcc cta gac cgt gtg ctg gaa att cta aga acc act gag     1292
Val Thr Glu Ala Leu Asp Arg Val Leu Glu Ile Leu Arg Thr Thr Glu
339                 344                 349                 354

tta tat tca cca cag ttt ggt gct aaa gat gat gat ccc cat gcc aat     1340
Leu Tyr Ser Pro Gln Phe Gly Ala Lys Asp Asp Asp Pro His Ala Asn
355                 360                 365                 370

gac ctt gtt ggg ggc tta atg tct gat ggt ttg cga aga cta tca ggg     1388
Asp Leu Val Gly Gly Leu Met Ser Asp Gly Leu Arg Arg Leu Ser Gly
371                 376                 381                 386

aat gaa tat gtt ctt tca aca aaa aac act caa atg gtt tca agc aat     1436
Asn Glu Tyr Val Leu Ser Thr Lys Asn Thr Gln Met Val Ser Ser Asn
387                 392                 397                 402

ata atc act ccc atc tcc ctt gat gat gtc cca cca cgg ata gct cgg     1484
Ile Ile Thr Pro Ile Ser Leu Asp Asp Val Pro Pro Arg Ile Ala Arg
403                 408                 413                 418

gcc atg gaa aat gag gaa tac tgg gac ttt gat att ttt gaa ctg gag     1532
Ala Met Glu Asn Glu Glu Tyr Trp Asp Phe Asp Ile Phe Glu Leu Glu
419                 424                 429                 434

gct gcc acc cac aat agg cct ttg att tat ctt ggt ctc aaa atg ttt     1580
Ala Ala Thr His Asn Arg Pro Leu Ile Tyr Leu Gly Leu Lys Met Phe
435                 440                 445                 450

gct cgc ttt gga atc tgt gaa ttc tta cac tgc tcc gag tca acg cta     1628
Ala Arg Phe Gly Ile Cys Glu Phe Leu His Cys Ser Glu Ser Thr Leu
451                 456                 461                 466

aga tca tgg tta caa att atc gaa gcc aat tat cat tcc tcc aat ccc     1676
Arg Ser Trp Leu Gln Ile Ile Glu Ala Asn Tyr His Ser Ser Asn Pro
467                 472                 477                 482

tac cac aat tct aca cat tct gct gat gtg ctt cat gcc act gcc tat     1724
Tyr His Asn Ser Thr His Ser Ala Asp Val Leu His Ala Thr Ala Tyr
483                 488                 493                 498
```

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ttt ctc tcc aag gag agg ata aag gaa act tta gat cca att gat gag     1772
Phe Leu Ser Lys Glu Arg Ile Lys Glu Thr Leu Asp Pro Ile Asp Glu
499                 504                 509                 514

gtc gct gca ctc atc gca gcc acc att cat gat gtg gat cac cct ggg     1820
Val Ala Ala Leu Ile Ala Ala Thr Ile His Asp Val Asp His Pro Gly
515                 520                 525                 530

aga acc aac tcc ttc ctg tgt aat gct gga agt gag ctg gcc att ttg     1868
Arg Thr Asn Ser Phe Leu Cys Asn Ala Gly Ser Glu Leu Ala Ile Leu
531                 536                 541                 546

tac aat gac act gct gtg ctg gag agc cac cat gcg gcc ttg gcc ttc     1916
Tyr Asn Asp Thr Ala Val Leu Glu Ser His His Ala Ala Leu Ala Phe
547                 552                 557                 562

cag ctg acc act gga gat gat aaa tgc aat ata ttt aaa aac atg gag     1964
Gln Leu Thr Thr Gly Asp Asp Lys Cys Asn Ile Phe Lys Asn Met Glu
563                 568                 573                 578

agg aat gat tat cgg aca ctg cgc cag ggg att atc gac atg gtc tta     2012
Arg Asn Asp Tyr Arg Thr Leu Arg Gln Gly Ile Ile Asp Met Val Leu
579                 584                 589                 594

gcc aca gaa atg aca aag cac ttt gag cat gtc aac aaa ttt gtc aac     2060
Ala Thr Glu Met Thr Lys His Phe Glu His Val Asn Lys Phe Val Asn
595                 600                 605                 610

agc atc aac aaa ccc ttg gca aca cta gaa gaa aat ggg gaa act gat     2108
Ser Ile Asn Lys Pro Leu Ala Thr Leu Glu Glu Asn Gly Glu Thr Asp
611                 616                 621                 626

aaa aac cag gaa gtg ata aac act atg ctt agg act cca gag aac cgg     2156
Lys Asn Gln Glu Val Ile Asn Thr Met Leu Arg Thr Pro Glu Asn Arg
627                 632                 637                 642

acc cta atc aaa cga atg ctg att aaa tgt gct gat gtg tcc aat ccc     2204
Thr Leu Ile Lys Arg Met Leu Ile Lys Cys Ala Asp Val Ser Asn Pro
643                 648                 653                 658

tgc cga ccc ctg cag tac tgc atc gag tgg gct gca cgc att tcg gaa     2252
Cys Arg Pro Leu Gln Tyr Cys Ile Glu Trp Ala Ala Arg Ile Ser Glu
659                 664                 669                 674

gaa tat ttt tct cag act gat gaa gag aag cag cag ggc tta cct gtg     2300
Glu Tyr Phe Ser Gln Thr Asp Glu Glu Lys Gln Gln Gly Leu Pro Val
675                 680                 685                 690

gtg atg cca gtg ttt gac aga aat acc tgc agc atc ccc aaa tcc caa     2348
Val Met Pro Val Phe Asp Arg Asn Thr Cys Ser Ile Pro Lys Ser Gln
691                 696                 701                 706

atc tct ttc att gat tac ttc atc aca gac atg ttt gat gct tgg gat     2396
Ile Ser Phe Ile Asp Tyr Phe Ile Thr Asp Met Phe Asp Ala Trp Asp
707                 712                 717                 722
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gcc ttt gta gac ctg cct gat tta atg cag cat ctt gac aac aac ttt     2444
Ala Phe Val Asp Leu Pro Asp Leu Met Gln His Leu Asp Asn Asn Phe
723                 728                 733                 738

aaa tac tgg aaa gga ctg gac gaa atg aag ctg cgg aac ctc cga cca     2492
Lys Tyr Trp Lys Gly Leu Asp Glu Met Lys Leu Arg Asn Leu Arg Pro
739                 744                 749                 754

cct cct gaa tag tgg gagacaccac ccagagccct gaagctttgt tccttcggtc     2547
Pro Pro Glu  *
755

atttggaatt cctgagggca gccagagctc cttggtcctt tcagtactag gcagaacagc   2607

ccccgatctg catagcctgt gaaagcccac ggggacatca gtaaccttct gcagccacca   2667

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cactatagaa atattcatgt atgttaaact tttctgattg aggctaactg gaaaaagctg   3267

gggtcgtatt ctaagtgcta aagaaggctg cttctactgt atagaaccca gggctctgaa   3327

acagctctag ccgcctaatg cacttcacag gtaactcccc aaggtaaaac tagactctct   3387

tgttggttcg caaagaaaag ttaggactta acacttttt ctaaaatttt ataattcaat   3447

ttccaaaagt ctactctatt ttatactgtt tctacaaaat attccttata aaaacaaaga   3507

acaaaaattg aatatttaat gaattgacat tttataacca acctgttttt atctacggtg   3567

ggaatctttg atgccagaaa tttataaaga ggttctgtat cttcacacct tgaataagca   3627

taataccata aaaaatgaca cttgacatgt caatgtattt gtcatttcat tttaaactcg   3687

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ttgccctttt ccataggcta tgccaataaa accttatgtt ccccttcttt tttttcagtg 180

aaggggggaaa attccgaaat taaaaagtgg tcatgggtta aggcccaaat gtgttttacc 240

ttttagttta tgaaaaaatt caattttggt acaaattggt gatatgaaaa ctccccttttt 300

ttgcaacccg ctgagtaagt tttaaaattt tagtgaaaaa aaaaaaaaac aaactaaagt 360

ctaaaactag aagtaatgta cattttccaa tctcatggtc tcatccccca agataataaa 420

atcgctccat gagtttttttt gtttgtttaa ttttgtattt taataaaagc aaatgcaatg 480

taacaaaagc gtgttgaagc atatcatggt ttaacttact gctcccacca caaaatattt 540

tgtcttttac ttatcgtttc agaaatcagt accattaaag ccttaaacag aaaactaatt 600

ccaatctgaa aaaggtacaa aaaggcacat aaaatcccag tgcttctgta ctgtaaaatt 660

caagtgtaac tgagctcagt gttttcacgg cgctccgcga gc atg ttt gcg gtg 714
Met Phe Ala Val
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ggc tgc agc gtg ggt ccc ttc ctg cac tac tgg tac ttg tcg ctg gac 762
Gly Cys Ser Val Gly Pro Phe Leu His Tyr Trp Tyr Leu Ser Leu Asp
5 10 15 20

cgc cta ttc cct gcg tct ggc ctc cga ggc ttc cca aat gtc ctc aag 810
Arg Leu Phe Pro Ala Ser Gly Leu Arg Gly Phe Pro Asn Val Leu Lys
21 26 31 36

aag gtc ctc gtg gat cag ctg gta gcc tct cca ttg ctg ggc gtc tgg 858
Lys Val Leu Val Asp Gln Leu Val Ala Ser Pro Leu Leu Gly Val Trp
37 42 47 52

tac ttc ttg ggc ctt ggc tgc ctg gag ggt cag aca gtg ggt gag agc 906
Tyr Phe Leu Gly Leu Gly Cys Leu Glu Gly Gln Thr Val Gly Glu Ser
53 58 63 68

tgc cag gag ctg cgg gag aag ttc tgg gaa ttc tac aag gca gac tgg 954
Cys Gln Glu Leu Arg Glu Lys Phe Trp Glu Phe Tyr Lys Ala Asp Trp
69 74 79 84

tgc gtg tgg cct gct gcg cag ttc gtg aac ttc ctc ttc gtg ccc cct 1002

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Cys Val Trp Pro Ala Ala Gln Phe Val Asn Phe Leu Phe Val Pro Pro
 85                  90                  95                 100

caa ttt cga gtc acc tac atc aac ggc ctg acg ctg ggc tgg gac acg     1050
Gln Phe Arg Val Thr Tyr Ile Asn Gly Leu Thr Leu Gly Trp Asp Thr
101                 106                 111                 116

tac ctg tcc tac ttg aag tac cgg agc cca gtt cct ctg aca ccc cca     1098
Tyr Leu Ser Tyr Leu Lys Tyr Arg Ser Pro Val Pro Leu Thr Pro Pro
117                 122                 127                 132

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Gly Cys Val Ala Leu Asp Thr Arg Ala Asp  *
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tgtcccatcc tcagcacagg gcccactctg ccaaccagtc tcaagcacca gcccctcaac   1449

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aagtttcaca tagggccagg cagcctctgt gtttctttcc ctggtcctga actgtggaaa   1629

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ctgtaatctc agcccttccc gaggctgagg tggaaggatt gctcaaggcc aggtgttcga   1749

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Lys Phe His Glu Gln Lys Leu Leu Lys Gln Val Asp Phe Leu Asn Trp
  6                  11                  16                  21

gag gtc acc gac cac aac ctg cac gag ctg cgc gtg ctg cgg cgt tac      209
Glu Val Thr Asp His Asn Leu His Glu Leu Arg Val Leu Arg Arg Tyr
 22                  27                  32                  37

cgg ctg cag cgg cgg gag gac tac acg cgc tac aac cag ctg agc cgt      257
Arg Leu Gln Arg Arg Glu Asp Tyr Thr Arg Tyr Asn Gln Leu Ser Arg
 38                  43                  48                  53

gcc gtg cgt gag ctg gcg cgg cgc ctg cgc gac ctg ccc gaa cgc gac      305
Ala Val Arg Glu Leu Ala Arg Arg Leu Arg Asp Leu Pro Glu Arg Asp
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cag ttc cgc gtg cgc gct tcg gcc gcg ctg ctg gac aag ctg tat gct      353
Gln Phe Arg Val Arg Ala Ser Ala Ala Leu Leu Asp Lys Leu Tyr Ala
 70                  75                  80                  85

ctc ggc ttg gtg ccc acg cgc ggt tcg ctg gag ctc tgc gac ttc gtc      401
Leu Gly Leu Val Pro Thr Arg Gly Ser Leu Glu Leu Cys Asp Phe Val
 86                  91                  96                 101

acg gcc tcg tcc ttc tgc cgc cgc cgc ctc ccc acc gtg ctc ctc aag      449
Thr Ala Ser Ser Phe Cys Arg Arg Arg Leu Pro Thr Val Leu Leu Lys
102                 107                 112                 117

ctg cgc atg gcg cag cac ctt cag gct gcc gtg gcc ttt gtg gag caa      497
Leu Arg Met Ala Gln His Leu Gln Ala Ala Val Ala Phe Val Glu Gln
118                 123                 128                 133

ggg cac gta cgc gtg ggc cct gac gtg gtt acc gac ccc gcc ttc ctt      545
Gly His Val Arg Val Gly Pro Asp Val Val Thr Asp Pro Ala Phe Leu
134                 139                 144                 149

gtc acg cgc agc atg gag gac ttt gtc act tgg gtg gac tcg tcc aag      593
Val Thr Arg Ser Met Glu Asp Phe Val Thr Trp Val Asp Ser Ser Lys
150                 155                 160                 165

atc aag cgg cac gtg cta gag tac aat gag gag cgc gat gac ttc gat      641
Ile Lys Arg His Val Leu Glu Tyr Asn Glu Glu Arg Asp Asp Phe Asp
166                 171                 176                 181

ctg gaa gcc tag cgg atctcccact ttgcatggct gtcttttaca gatgggaaaa      696
Leu Glu Ala  *
182

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ccttgttttc caggaaatgt tcttagaact tggactactg attattaatt gactgtgcct    876

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09650536.1 Patent Application

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 10                  15                  20                  25

cca aaa aag gag atc cac aca gtt cca gac atg ggc aaa tgg aag cgt      327
Pro Lys Lys Glu Ile His Thr Val Pro Asp Met Gly Lys Trp Lys Arg
 26                  31                  36                  41

tct cag gca tac gct gac tac atc gga ttc atc ctt acc ctc aac gaa      375
Ser Gln Ala Tyr Ala Asp Tyr Ile Gly Phe Ile Leu Thr Leu Asn Glu
 42                  47                  52                  57

ggt gtg aag ggg aag aag ctg acc ttc gag tac aga gtc tcc gag gcc      423
Gly Val Lys Gly Lys Lys Leu Thr Phe Glu Tyr Arg Val Ser Glu Ala
 58                  63                  68                  73

att gag aaa cta gtc gct ctt ctc aac acg ctg gac agg tgg att gat      471
Ile Glu Lys Leu Val Ala Leu Leu Asn Thr Leu Asp Arg Trp Ile Asp
 74                  79                  84                  89

gag act cct cca gtg gac cag ccc tct cgg ttt ggg aat aag gca tac      519
Glu Thr Pro Pro Val Asp Gln Pro Ser Arg Phe Gly Asn Lys Ala Tyr
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Thr Val Val Pro Thr His Leu Ala Ala Ala Val Pro Glu Val Ala Val
122                 127                 132                 137

tac cta aag gag tca gtg ggg aac tcc acg cgc att gac tac ggc aca      663
Tyr Leu Lys Glu Ser Val Gly Asn Ser Thr Arg Ile Asp Tyr Gly Thr
138                 143                 148                 153

ggg cat gag gca gcc ttc gct gct ttc ctc tgc tgt ctc tgc aag att      711
Gly His Glu Ala Ala Phe Ala Ala Phe Leu Cys Cys Leu Cys Lys Ile
154                 159                 164                 169

ggg gtg ctc cgg gtg gat gac caa ata gct att gtc ttc aag gtg ttc      759
Gly Val Leu Arg Val Asp Asp Gln Ile Ala Ile Val Phe Lys Val Phe
170                 175                 180                 185

aat cgg tac ctt gag gtt atg cgg aaa ctc cag aaa aca tac agg atg      807
Asn Arg Tyr Leu Glu Val Met Arg Lys Leu Gln Lys Thr Tyr Arg Met
186                 191                 196                 201

gag cca gcc ggc agc cag gga gtg tgg ggt ctg gat gac ttc cag ttt      855
Glu Pro Ala Gly Ser Gln Gly Val Trp Gly Leu Asp Asp Phe Gln Phe
202                 207                 212                 217

ctg ccc ttc atc tgg ggc agt tcg cag ctg ata gac cac cca tac ctg      903
Leu Pro Phe Ile Trp Gly Ser Ser Gln Leu Ile Asp His Pro Tyr Leu
218                 223                 228                 233

gag ccc aga cac ttt gtg gat gag aag gcc gtg aat gag aac cac aag      951
Glu Pro Arg His Phe Val Asp Glu Lys Ala Val Asn Glu Asn His Lys
234                 239                 244                 249

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Asp Tyr Met Phe Leu Glu Cys Ile Leu Phe Ile Thr Glu Met Lys Thr
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266                 271                 276                 281

cct tcc tgg tcc aaa gtg aac cag ggt ctc atc cgc atg tat aag gcc     1095
Pro Ser Trp Ser Lys Val Asn Gln Gly Leu Ile Arg Met Tyr Lys Ala
282                 287                 292                 297

gag tgc ctg gag aag ttc cct gtg atc cag cac ttc aag ttc ggg agc     1143
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298                 303                 308                 313

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Phe Leu Pro Pro Glu Asn Leu Ile Thr Ser Ile Ser Ala Val Pro Ile
23 28 33 38

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Ser Gln Lys Glu Glu Val Ala Asp Phe Gln Leu Ser Val Asp Ser Leu
39 44 49 54

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183                 188                 193                 198

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aat aaa gaa gca gca gat gat aaa agt gta gca aaa gca gca cag gag     1025
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247                 252                 257                 262

cgt ctg gga gta tat ttt gat gaa tat tca gga gaa tca ttt tat cgt     1169
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263                 268                 273                 278

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279                 284                 289                 294

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Leu Lys Thr Ile Lys Gly Thr Ala Val Val Asp Leu Ser Gly Asn Gly
295                 300                 305                 310

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Tyr Ala Thr Arg Asp Leu Ala Ala Ala Ile Asp Arg Met Asp Lys Tyr
327                 332                 337                 342

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Asn Phe Asp Thr Met Ile Tyr Val Thr Asp Lys Gly Gln Lys Lys His
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423                 428                 433                 438

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503                 508                 513                 518

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Gln Asp Phe Gln Pro Arg His Ile Val Ser Tyr Leu Leu Thr Leu Ser
519                 524                 529                 534

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535                 540                 545                 550

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Pro Glu Val Ala Gly Ala Arg Leu His Leu Phe Lys Ala Val Arg Ser
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Lys Tyr Pro Leu Pro Leu Ile Glu Lys Glu Lys Ile Ser His Asn Thr
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Val Asp Leu Ile Ile Lys Ile Tyr Phe Lys Asn Val His Pro Gln Tyr
81 86 91 96

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97 102 107 112

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Val Arg Lys Glu Leu Glu Glu Ile Ala Arg Thr His Pro Asp Gln Phe
193                 198                 203                 208

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Val Leu Gly Asp Gly Ala Ser Gly Lys Thr Ser Leu Thr Thr Cys Phe
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Ala Gln Glu Thr Phe Gly Lys Gln Tyr Lys Gln Thr Ile Gly Leu Asp
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Lys Tyr Ile Tyr Gly Ala Gln Gly Val Leu Leu Val Tyr Asp Ile Thr
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Docket No. 7156.060

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ctg aca ggc ctc gtt gcc ttc cta gag ttc ctt gtt cgg aac aat gta      883
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Phe Phe Gln Ile Gly Phe Val Leu Tyr Pro Pro Ser Gly Gly Pro Ala
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tgt tgg cat tat gca gta acc att gtc atc gtt gga atg aat tat gct     1075
Cys Trp His Tyr Ala Val Thr Ile Val Ile Val Gly Met Asn Tyr Ala
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Phe Ile Thr Trp Leu Val Lys Ser Arg Leu Lys Arg Leu Cys Ser Ser
242                 247                 252                 257

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Glu Met  *
274

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Ile Thr Gly Leu Arg Val Ser Val Gly Leu Leu Leu Val Lys Ser Val
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92 97 102 107

agc aag gac cgc tat ttc tat ttt ggg aag ctt gat ggc cag atc tcc 446
Ser Lys Asp Arg Tyr Phe Tyr Phe Gly Lys Leu Asp Gly Gln Ile Ser
108 113 118 123

tct gcc tac ccc agc caa gag ggg cag gtg ctg gtg ggc atc tat ggc 494
Ser Ala Tyr Pro Ser Gln Glu Gly Gln Val Leu Val Gly Ile Tyr Gly
124 129 134 139

cag tat caa ctc ctt ggc atc aag agc att ggc ttt gaa tgg aat tat 542
Gln Tyr Gln Leu Leu Gly Ile Lys Ser Ile Gly Phe Glu Trp Asn Tyr
140 145 150 155

cca cta gag gag ccg acc act gag cca cca gtt aat ctc aca tac tca 590
Pro Leu Glu Glu Pro Thr Thr Glu Pro Pro Val Asn Leu Thr Tyr Ser
156 161 166 171

```
gca aac tca ccc gtg ggt cgc tag ggtggggtat ggggccatcc gagctgaggc     644
Ala Asn Ser Pro Val Gly Arg  *
172                 177

catctgggtg gtggtggctg atggtactgg agtaactgag tcgggacgct gaatctgaat    704

ccaccaataa ataaaggttc tgcagaatca gtgaaaaaac aaaacaaaca caacaaaaaa    764

gtagt                                                               769
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<210> 160
<211> 1142
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (333)..(569)

<220>
<221> misc_feature
<222> (1)...(1142)
<223> n = a,t,c or g

<400> 160

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gcttgaccac attgaaagaa ccggaccgga attcccgggt cgacccacgc gtccgcccgg     60

tggactgtag aggcggcagc gagctagagc ccgagtcgca gctccgggcc gcagagcgct    120

gggcgagcgc gagcgccagg gcaccggcag ggcaggcagc tgcgcgcggc tggagtcatg    180

ctatactgaa aagacacttc atcaagataa ctctgggaga agcagaaaac cctgtgccag    240

ggacaggaaa gataggagaa agaaagttta tcagaatttt ttaaacctgt ctcagaaata    300

acaacatatt ttaatcagag atttatgttg ct  atg agg aca gat tca tca aaa      353
                                     Met Arg Thr Asp Ser Ser Lys
                                       1               5

atg act gac gtg gag tct ggg gtc gcc aat ttt gca tct tca gca agg      401
Met Thr Asp Val Glu Ser Gly Val Ala Asn Phe Ala Ser Ser Ala Arg
  8                  13                  18                  23

gca ggc cgc cgg aat gcc tta cca gac atc cag agt tca gct gcc aca      449
Ala Gly Arg Arg Asn Ala Leu Pro Asp Ile Gln Ser Ser Ala Ala Thr
 24                  29                  34                  39

gac gga acc tca gat ttg ccc ctc aaa ctg gag gct ctc tcc gtg aag      497
Asp Gly Thr Ser Asp Leu Pro Leu Lys Leu Glu Ala Leu Ser Val Lys
 40                  45                  50                  55

gaa gat gca aaa gag aaa gat gaa aaa aca aca caa gac caa ttg gaa      545
Glu Asp Ala Lys Glu Lys Asp Glu Lys Thr Thr Gln Asp Gln Leu Glu
 56                  61                  66                  71
```

```
aag cct caa aat gaa gaa aaa tga aggctcataa tctatcaaga gtgctgaatt     599
Lys Pro Gln Asn Glu Glu Lys  *
 72                  77

tctgcatgtt gaaagactta gtggttctgt tttcttgaga catttaatct ggtggtaact    659

gtggtaacat tgcagcccta agcagcatgt gtatattaga taattgtgtt gtgatgctac    719

tcactttgat tgcaatgatg atgtccaagg taagctatta aaagggcagg ttacttccaa    779

atcgcactgg aagggaaaag gttaaggatt aatacatgat cacagaaatg cataccactg    839

ttctgtaaaa ccccaaccaa aattcactgt tctcttttgg atttatttag cctgatgtat    899

ttttaattca atttttatgg tgatgggcaa atcattcttg gtaaatgtaa atcaaacatg    959

attgatttaa aacttcatgg gaatttgtag gaaaattatg ggacattttt gggtgaggaa   1019

aggaacaata gtncaaaact ncacatgggn tagagtgtgt ttgtttttttg gcccaaaatt  1079

gccccagact tttttcccca aacctcaaaa acgtcttggg gnaaattgta aaggttttgn   1139

tta                                                                 1142
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<210> 161
<211> 2260
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (56)..(1387)

<400> 161

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atttggccct cgaggccaag aattcggcac gagggtgcgc gcctgggacc tgaac atg      58
                                                            Met
                                                              1

gac ttc ccg tgc ctc tgg cta ggg ctg ttg ctg cct ttg gta gct gcg      106
Asp Phe Pro Cys Leu Trp Leu Gly Leu Leu Leu Pro Leu Val Ala Ala
  2                   7                  12                  17

ctg gat ttc aac tac cac cgc cag gaa ggg atg gaa gcg ttt ttg aag      154
Leu Asp Phe Asn Tyr His Arg Gln Glu Gly Met Glu Ala Phe Leu Lys
 18                  23                  28                  33

act gtt gcc caa aac tac agt tct gtc act cac tta cac agt att ggg      202
Thr Val Ala Gln Asn Tyr Ser Ser Val Thr His Leu His Ser Ile Gly
 34                  39                  44                  49

aaa tct gtg aaa ggt aga aac ctg tgg gtt ctt gtt gtg ggg cgg ttt      250
Lys Ser Val Lys Gly Arg Asn Leu Trp Val Leu Val Val Gly Arg Phe
 50                  55                  60                  65
```

```
cca aag gaa cac aga att ggg att cca gag ttc aaa tac gtg gca aat      298
Pro Lys Glu His Arg Ile Gly Ile Pro Glu Phe Lys Tyr Val Ala Asn
 66                  71                  76                  81

atg cat gga gat gag act gtt ggg cgg gag ctg ctg ctc cat ctg att      346
Met His Gly Asp Glu Thr Val Gly Arg Glu Leu Leu Leu His Leu Ile
 82                  87                  92                  97

gac tat ctc gta acc agt gat ggc aaa gac cct gaa atc aca aat ctg      394
Asp Tyr Leu Val Thr Ser Asp Gly Lys Asp Pro Glu Ile Thr Asn Leu
 98                 103                 108                 113

atc aat agt acc cgg ata cac atc atg cct tcc atg aac cca gat gga      442
Ile Asn Ser Thr Arg Ile His Ile Met Pro Ser Met Asn Pro Asp Gly
114                 119                 124                 129

ttt gaa gcc gtc aaa aag cct gac tgt tat tac agc atc gga agg gaa      490
Phe Glu Ala Val Lys Lys Pro Asp Cys Tyr Tyr Ser Ile Gly Arg Glu
130                 135                 140                 145

aat tat aac cag tat gac ttg aat cga aat ttc ccc gat gct ttt gaa      538
Asn Tyr Asn Gln Tyr Asp Leu Asn Arg Asn Phe Pro Asp Ala Phe Glu
146                 151                 156                 161

tat aat aat gtc tca agg cag cct gaa act gtg gca gtc atg aag tgg      586
Tyr Asn Asn Val Ser Arg Gln Pro Glu Thr Val Ala Val Met Lys Trp
162                 167                 172                 177

ctg aaa aca gag acg ttt gtc ctc tct gca aac ctc cat ggt ggt gcc      634
Leu Lys Thr Glu Thr Phe Val Leu Ser Ala Asn Leu His Gly Gly Ala
178                 183                 188                 193

ctc gtg gcc agt tac cca ttt gat aat ggt gtt caa gca act ggg gca      682
Leu Val Ala Ser Tyr Pro Phe Asp Asn Gly Val Gln Ala Thr Gly Ala
194                 199                 204                 209

tta tac tcc cga agc tta acg cct gat gat gat gtt ttt caa tat ctt      730
Leu Tyr Ser Arg Ser Leu Thr Pro Asp Asp Asp Val Phe Gln Tyr Leu
210                 215                 220                 225

gca cat acc tat gct tca aga aat ccc aac atg aag aaa gga gac gag      778
Ala His Thr Tyr Ala Ser Arg Asn Pro Asn Met Lys Lys Gly Asp Glu
226                 231                 236                 241

tgt aaa aac aaa atg aac ttt cct aat ggt gtt aca aat gga tac tct      826
Cys Lys Asn Lys Met Asn Phe Pro Asn Gly Val Thr Asn Gly Tyr Ser
242                 247                 252                 257

tgg tat cca ctc caa ggt gga atg caa gat tac aac tac atc tgg gcc      874
Trp Tyr Pro Leu Gln Gly Gly Met Gln Asp Tyr Asn Tyr Ile Trp Ala
258                 263                 268                 273

cag tgt ttt gaa att acg ttg gag ctg tca tgc tgt aaa tat cct cgt      922
Gln Cys Phe Glu Ile Thr Leu Glu Leu Ser Cys Cys Lys Tyr Pro Arg
274                 279                 284                 289
```

```
gag gag aag ctt cca tcc ttt tgg aat aat aac aaa gcc tca tta att      970
Glu Glu Lys Leu Pro Ser Phe Trp Asn Asn Asn Lys Ala Ser Leu Ile
290                 295                 300                 305

gaa tat ata aag cag gtg cac cta ggt gta aag ggt caa gtt ttt gat     1018
Glu Tyr Ile Lys Gln Val His Leu Gly Val Lys Gly Gln Val Phe Asp
306                 311                 316                 321

cag aat gga aat cca tta ccc aat gta att gtg gaa gtc caa gac aga     1066
Gln Asn Gly Asn Pro Leu Pro Asn Val Ile Val Glu Val Gln Asp Arg
322                 327                 332                 337

aaa cat atc tgc ccc tat aga acc aac aaa tat gga gag tat tat ctc     1114
Lys His Ile Cys Pro Tyr Arg Thr Asn Lys Tyr Gly Glu Tyr Tyr Leu
338                 343                 348                 353

ctt ctc ttg cct ggg tct tat ata ata aat gtt aca gtc cct gga cat     1162
Leu Leu Leu Pro Gly Ser Tyr Ile Ile Asn Val Thr Val Pro Gly His
354                 359                 364                 369

gat cca cac atc aca aag gtg att att ccg gag aaa tcc cag aac ttc     1210
Asp Pro His Ile Thr Lys Val Ile Ile Pro Glu Lys Ser Gln Asn Phe
370                 375                 380                 385

agt gct ctt aaa aag gat att cta ctt cca ttc caa ggg caa ttg gat     1258
Ser Ala Leu Lys Lys Asp Ile Leu Leu Pro Phe Gln Gly Gln Leu Asp
386                 391                 396                 401

tct atc cca gta tca aat cct tca tgc cca atg att cct cta tac aga     1306
Ser Ile Pro Val Ser Asn Pro Ser Cys Pro Met Ile Pro Leu Tyr Arg
402                 407                 412                 417

aat ttg cca gac cac tca gct gca aca aag cct agt ttg ttc tta ttt     1354
Asn Leu Pro Asp His Ser Ala Ala Thr Lys Pro Ser Leu Phe Leu Phe
418                 423                 428                 433

tta gtg agt ctt ttg cac ata ttc ttc aaa taa agtaaaat gtgaaactca     1405
Leu Val Ser Leu Leu His Ile Phe Phe Lys  *
434                 439                 444

acccacatca ccacctggaa tcagggattg ctcactccag gttactgcaa ccctaactca   1465

ctctagtggg accttgactg gagaaactcc acgatcttcc tgaagaagag aaatggatgt   1525

ttccaaattc cacaataagc aatatgtggt gataatgaaa agaatgattc agtcttgacg   1585

gtgaatggaa gacacttacc taacaagtac tgctcattta cactcaaatt aatcttgaag   1645

tagtcttaaa atgtgtaaga agttaaaact tgagaagcaa aaaaatgcct gcaaaaagaa   1705

gatcattttg tatacagaga accggatgaa tataagcaat gaagatgaac atttattgat   1765

cttctacata caagacttca ccataaggcc aggagcagtg gctcacacct tgtaatccca   1825

gcactttggg aggccaaggt gggcggatca ccttgaggtc aggagttcaa aaccagcctg   1885

accaacatgg tgaaaccctg tctctactaa atattagcgg ggtgtggtgg cgggcacctg   1945
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```
taatcgcagc ctttcaggag gctgagacag gagaatcgct tgaaccctag aggcggagtt   2005

tgcagtgagc cgagatagtg ccattgtact ccagcttggg caacagagta agactctgtc   2065

tcaaaaaaaa aaaaccaaaa ccaaccaccc aaaaaaaccc cctcccctgg ggggctcctg   2125

gggaaaaaat ttaaggggcc atatttattt atttttaaaa aaaggggggaa atggtcctta   2185

ggccgggaat tggttttgca accgttctag gaaaggggggg agaaaatttg gacccacttc   2245

ttatgggccc aggaa                                                    2260
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<210> 162
<211> 633
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (162)..(476)

<400> 162

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gtgtggtgga attcccggag aaggtgaaat tctgtgtgct ccctccggcg agagactttg     60

tcagctcccg cacagtaaca tcctgaataa agtcaaaact caaccaacag gtggaagtcc    120

aagaatccga gtggaggctc accgaggcga aggggccaac c     atg gga aag gag      173
                                                  Met Gly Lys Glu
                                                    1

agt gga tgg gac tca ggc agg gct gct gta gca gct gtg gtc gga gga       221
Ser Gly Trp Asp Ser Gly Arg Ala Ala Val Ala Ala Val Val Gly Gly
  5                  10                  15                  20

gtt gtg gct gtg ggg act gtg ctc gtg gcg ctc agt gcc atg ggc ttc       269
Val Val Ala Val Gly Thr Val Leu Val Ala Leu Ser Ala Met Gly Phe
 21                  26                  31                  36

acc tca gta gga atc gcc gca tcc tcc ata gca gcc aag atg atg tct       317
Thr Ser Val Gly Ile Ala Ala Ser Ser Ile Ala Ala Lys Met Met Ser
 37                  42                  47                  52

aca gca gcc att gcc aac ggg ggc gga gtt gct gct ggc agt ctg gtg       365
Thr Ala Ala Ile Ala Asn Gly Gly Gly Val Ala Ala Gly Ser Leu Val
 53                  58                  63                  68

gct att ctg cag tca gtg ggg gca gct gga ctc tct gtg aca tct aaa       413
Ala Ile Leu Gln Ser Val Gly Ala Ala Gly Leu Ser Val Thr Ser Lys
 69                  74                  79                  84

gtt atc ggg ggc ttt gct ggg aca gct ctt ggg gcc tgg ctg ggt tca       461
Val Ile Gly Gly Phe Ala Gly Thr Ala Leu Gly Ala Trp Leu Gly Ser
 85                  90                  95                 100
```

```
ccc cct tcc agc tga acaccacact gaggcaggga gttggctctc ttggtggaga      516
Pro Pro Ser Ser  *
101

tgactttcct gggcctctgg atgacaatct tccaaaggac aagtctccta ctcccaaaac     576

tatttaagga agcatgaaaa ataaagatgc tggttatctt ctcctaaaaa aaaaaaa       633
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<210> 163
<211> 1152
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (210)..(977)

<400> 163

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atttggccct cgaggccaag aattcggcac gaggaagttt atcaggaaag gagcttaaaa      60

gagaaccaaa ttcagcctgt gttggaactc tcagtcccag aggggtgtgg tttgtagctc     120

tccggcctgc tgttggactt aggctgtgac ccacagaagg acgccagaaa gtactcaaga     180

cattcacggt gccccggtca gcactcgcc  atg acg aag act tct aca tgc ata      233
                                 Met Thr Lys Thr Ser Thr Cys Ile
                                   1               5

tac cac ttc ctt gtt ctg agc tgg tat act ttc ctc aat tat tac atc      281
Tyr His Phe Leu Val Leu Ser Trp Tyr Thr Phe Leu Asn Tyr Tyr Ile
  9                  14                  19                  24

tca cag gaa gga aaa gac gag gtg aaa ccc aaa atc ttg gca aat ggt      329
Ser Gln Glu Gly Lys Asp Glu Val Lys Pro Lys Ile Leu Ala Asn Gly
 25                  30                  35                  40

gca agg tgg aaa tat atg acg ctg ctt aat ctg ctc ttg cag acc att      377
Ala Arg Trp Lys Tyr Met Thr Leu Leu Asn Leu Leu Leu Gln Thr Ile
 41                  46                  51                  56

ttc tac ggg gtc acc tgc ctg gat gat gtg ctg aaa aga acc aaa ggg      425
Phe Tyr Gly Val Thr Cys Leu Asp Asp Val Leu Lys Arg Thr Lys Gly
 57                  62                  67                  72

gga aaa gac att aag ttc cta act gcc ttc aga gac ctg ctt ttc acc      473
Gly Lys Asp Ile Lys Phe Leu Thr Ala Phe Arg Asp Leu Leu Phe Thr
 73                  78                  83                  88

act ctg gct ttt cct gta tcc acg ttt gta ttt ttg gca ttc tgg atc      521
Thr Leu Ala Phe Pro Val Ser Thr Phe Val Phe Leu Ala Phe Trp Ile
 89                  94                  99                 104

ctc ttt ctc tac aat cga gat ctc att tac ccc aag gtc cta gat act      569
```

```
Leu Phe Leu Tyr Asn Arg Asp Leu Ile Tyr Pro Lys Val Leu Asp Thr
105                 110                 115                 120

gtc atc ccc gtg tgg ctg aat cat gca atg cac act ttc ata ttc ccc      617
Val Ile Pro Val Trp Leu Asn His Ala Met His Thr Phe Ile Phe Pro
121                 126                 131                 136

atc aca ttg gct gaa gtc gtc ctc agg cct cac tcc tat cca tca aag      665
Ile Thr Leu Ala Glu Val Val Leu Arg Pro His Ser Tyr Pro Ser Lys
137                 142                 147                 152

aag aca gga ctc acc ttg ctg gct gct gcc agc att gct tac atc agc      713
Lys Thr Gly Leu Thr Leu Leu Ala Ala Ala Ser Ile Ala Tyr Ile Ser
153                 158                 163                 168

cgc atc cta tgg ctc tac ttt gag acg ggt acc tgg gtg tat cct gtg      761
Arg Ile Leu Trp Leu Tyr Phe Glu Thr Gly Thr Trp Val Tyr Pro Val
169                 174                 179                 184

ttt gcc aaa ctc agc ctc ttg ggt cta gca gct ttc ttc tct ctc agc      809
Phe Ala Lys Leu Ser Leu Leu Gly Leu Ala Ala Phe Phe Ser Leu Ser
185                 190                 195                 200

tac gtc ttc atc gcc agc atc tac cta ctt gga gag aag ctc aac cac      857
Tyr Val Phe Ile Ala Ser Ile Tyr Leu Leu Gly Glu Lys Leu Asn His
201                 206                 211                 216

tgg aaa tgg gtt tct gtt cag atc ttg caa aga tgg agg cta gaa tct      905
Trp Lys Trp Val Ser Val Gln Ile Leu Gln Arg Trp Arg Leu Glu Ser
217                 222                 227                 232

gtt gga atc tgc ttc cag tgg ccc gat tgg aag tca cca gcc aag cac      953
Val Gly Ile Cys Phe Gln Trp Pro Asp Trp Lys Ser Pro Ala Lys His
233                 238                 243                 248

caa ctg gtc aag aat atc agg tga aatatcaggg ctataaaaat atttctagcc    1007
Gln Leu Val Lys Asn Ile Arg  *
249                 254

cttgctacta tctgacagca gttaaaggaa taaaacaagt cggggtgaat ctaacttcct   1067

atctgccaac taggatactt tctactggga aaaatgcttc tcaatcaaga aaatatttat   1127

aataaacata attttccaat tacaa                                        1152
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<210> 164
<211> 1250
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (255)..(608)

<400> 164

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ctttgattgg gcgtgatgta tataactatc tattcgatga tgaagatacc ccaccaaacc      60

caaaaaaaga gatctctcga ggatccgaat tcgcggccgc gtcgacccgg aagtccagga     120

gtcgacgtgt gcagaagtcc ttatagtcca gggcctgttt ccctgtagca gctccttatt     180

gctggagaag gagaaaagtg cccaagatcc tttcaggatt aatttattca aaaaggaaat     240

aaaaaatact caat  atg caa aag tct tgt gaa gaa aat gag gga aaa cca       290
                 Met Gln Lys Ser Cys Glu Glu Asn Glu Gly Lys Pro
                   1               5                  10

cag aac atg cca aag gcc gag gaa gat cgc cct ttg gag gat gta cca       338
Gln Asn Met Pro Lys Ala Glu Glu Asp Arg Pro Leu Glu Asp Val Pro
 13                  18                  23                  28

cag gag gca gaa gga aat cct caa cct tcc gaa gaa ggc gta agc cag       386
Gln Glu Ala Glu Gly Asn Pro Gln Pro Ser Glu Glu Gly Val Ser Gln
 29                  34                  39                  44

gaa gca gaa gga aac ccc aga gga ggg ccg aat cag cct ggc cag gga       434
Glu Ala Glu Gly Asn Pro Arg Gly Gly Pro Asn Gln Pro Gly Gln Gly
 45                  50                  55                  60

ttt aaa gag gac aca ccc gtt agg cat ttg gac cct gaa gaa atg ata       482
Phe Lys Glu Asp Thr Pro Val Arg His Leu Asp Pro Glu Glu Met Ile
 61                  66                  71                  76

aga gga gta gat gag ctt gaa agg ctt agg gaa gag ata aga aga gta       530
Arg Gly Val Asp Glu Leu Glu Arg Leu Arg Glu Glu Ile Arg Arg Val
 77                  82                  87                  92

aga aac aag ttt gtg atg atg cat tgg aag caa aga cat tca cgc agc       578
Arg Asn Lys Phe Val Met Met His Trp Lys Gln Arg His Ser Arg Ser
 93                  98                 103                 108

cgt cct tat cct gtg tgc ttt agg cct tga a ttcatttttg cctaatatta       629
Arg Pro Tyr Pro Val Cys Phe Arg Pro  *
109                 114

aaatctggcc ccagctttct ttctgttagc attttctgat gtatctttga cctccatttt     689

acttttaatc atctgatgaa attttgtttt aggtaatttc cttggtacca gcatctcatt     749

ggattttgga ttttgaccca ttttccaggt ctatttttca attggaaact ttcacacatt     809

tgcatgggaa tatgttcatt ccatgttgta aagtaaaaca taacaggtta tggcaaagca     869

gcatatttaa tatcagctca catatgtagg ataaaattcc aaactttgtg tgtgtgcgtg     929

tgtgtataca tacatccata taacatatat cacaaactta accaagctta tttctgtgtg     989

gtgtgaaatt ttatttgttt tcttcttttt gttcttttttg cttatatgta ctttttaatg    1049

aacacgtgtc tcacacacaa aaagaattaa ggatttttt tacaagtaag agtcaaataa    1109
```

tttgcaacca gcttatgagg gcaatggggg cacctaaact cttgatgaaa gaactttaaa 1169

aagaaatgta aacctcaaat tacctctgga tctcttagcc agaggaataa actggcaatt 1229

attacagata aaaaaaaaaa a 1250

<210> 165
<211> 1435
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (244)..(798)

<400> 165
ccattgctta ctacaccgaa ggtcaatgcc tcttgacacc ctaatcaagg aaataaaata 60

aagctgactg agatccgctc ggaaaatctt tctggatcta aactcccagt gcgctttgcg 120

ccccaagtgg ccatcgcgcc tgcgccccgc gcggccggtt actcgcttac cggaggcttc 180

agtccccggc ggcgcggcga cagctagggt tcacggccac tggggcagag gagccgcgag 240

aag atg tgg gtt ttt ggt tac ggg tcc ctg atc tgg aag gtg gat ttc 288
Met Trp Val Phe Gly Tyr Gly Ser Leu Ile Trp Lys Val Asp Phe
1 5 10

ccc tat cag gac aag ctg gtc gga tac atc acc aac tac agc agg cgc 336
Pro Tyr Gln Asp Lys Leu Val Gly Tyr Ile Thr Asn Tyr Ser Arg Arg
16 21 26 31

ttc tgg cag ggc agc acg gac cac cgc ggg gtc ccc ggc aag cct gga 384
Phe Trp Gln Gly Ser Thr Asp His Arg Gly Val Pro Gly Lys Pro Gly
32 37 42 47

aga gtt gtg act ctt gtt gaa gat cct gcg gga tgt gta tgg ggt gtt 432
Arg Val Val Thr Leu Val Glu Asp Pro Ala Gly Cys Val Trp Gly Val
48 53 58 63

gct tac aga ttg cca gta gga aag gaa gaa gaa gta aaa gca tac ctt 480
Ala Tyr Arg Leu Pro Val Gly Lys Glu Glu Glu Val Lys Ala Tyr Leu
64 69 74 79

gac ttc aga gaa aaa gga ggc tac aga acc aca aca gtc att ttt tat 528
Asp Phe Arg Glu Lys Gly Gly Tyr Arg Thr Thr Thr Val Ile Phe Tyr
80 85 90 95

cca aaa gat ccc aca aca aaa cca ttc agt gta ttg cta tat att gga 576
Pro Lys Asp Pro Thr Thr Lys Pro Phe Ser Val Leu Leu Tyr Ile Gly
96 101 106 111

aca tgt gat aat cct gat tat ctt ggt cct gca cct ctg gaa gac att 624
Thr Cys Asp Asn Pro Asp Tyr Leu Gly Pro Ala Pro Leu Glu Asp Ile

```
112                 117                 122                 127

gct gaa caa att ttt aat gca gct ggt cca agt gga aga aat aca gaa      672
Ala Glu Gln Ile Phe Asn Ala Ala Gly Pro Ser Gly Arg Asn Thr Glu
128                 133                 138                 143

tat ctt ttt gaa ctt gca aat tct att agg aac ctt gtg cca gaa gaa      720
Tyr Leu Phe Glu Leu Ala Asn Ser Ile Arg Asn Leu Val Pro Glu Glu
144                 149                 154                 159

gca gat gag cat ctt ttc gct ttg gaa aaa tta gta aag gaa cgt tta      768
Ala Asp Glu His Leu Phe Ala Leu Glu Lys Leu Val Lys Glu Arg Leu
160                 165                 170                 175

gaa ggg aaa cag aac ctc aat tgc ata taa t ttagtcttca gagaattaac      819
Glu Gly Lys Gln Asn Leu Asn Cys Ile  *
176                 181

ttcagtgcac aatgacaata tgatttggaa atacgtttac ttaaagatct tatttttaat    879

gtagtgagga tattatttaa acttttattt taactggaaa tgtcctgaag cgcatattta    939

aaatattggg atacagtgaa agaaaaattc aaattttaat aacataaaga tttcctaact    999

ttatgttatt gaacacttac tcactagaag tgagttcttt agaaaaatac agtgaaggac   1059

tcagttcagt cttgttttta tcagagtgat aatcatcctg tttcacatcc caatactatt   1119

ttgaaattct aaacaattaa accaaaattc caataaatat aaggttatgc cttcaatata   1179

ttcctataca attctgtaac catggtttaa aatacacaag cttaaaataa catgcttaga   1239

aatacacaat aatatgaaca gtatttcagc cttaattgtg aatttccttg ttattcaagt   1299

attaaatgaa atcttttgag tttttagcca aaaattggca tttttaaaat acgaaaattt   1359

ccttggaatt ataatgtact gtacctcttc ttttttaaat aaaggcattt tactatatgg   1419

aaaataaaaa aaaaaa                                                  1435
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<210> 166
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<220>
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<400> 166

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                         Met Gly Ser Ser Met Ser Ala Ala Thr Ala
                           1               5
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cgg agg ccg gtg ttt gac gac aag gag gac gtg aac ttc gac cac ttc       98
Arg Arg Pro Val Phe Asp Asp Lys Glu Asp Val Asn Phe Asp His Phe
 11                  16                  21                  26

cag atc ctt cgg gcc att ggg aag ggc agc ttt ggc aag gtg tgc att      146
Gln Ile Leu Arg Ala Ile Gly Lys Gly Ser Phe Gly Lys Val Cys Ile
 27                  32                  37                  42

gtg cag aag cgg gac acg gag aag atg tac gcc atg aag tac atg aac      194
Val Gln Lys Arg Asp Thr Glu Lys Met Tyr Ala Met Lys Tyr Met Asn
 43                  48                  53                  58

aag cag cag tgc atc gag cgc gac gag gtc cgc aac gtc ttc cgg gag      242
Lys Gln Gln Cys Ile Glu Arg Asp Glu Val Arg Asn Val Phe Arg Glu
 59                  64                  69                  74

ctg gag atc ctg cag gag atc gag cac gtc ttc ctg gtg aac ctc tgg      290
Leu Glu Ile Leu Gln Glu Ile Glu His Val Phe Leu Val Asn Leu Trp
 75                  80                  85                  90

tac tcc ttc cag gac gag gag gac atg ttc atg gtc gtg gac ctg cta      338
Tyr Ser Phe Gln Asp Glu Glu Asp Met Phe Met Val Val Asp Leu Leu
 91                  96                 101                 106

ctg ggc ggg gac ctg cgc tac cac ctg cag cag aac gtg cag ttc tcc      386
Leu Gly Gly Asp Leu Arg Tyr His Leu Gln Gln Asn Val Gln Phe Ser
107                 112                 117                 122

gag gac acg gtg agg ctg tac atc tgc gag atg gca ctg gct ctg gac      434
Glu Asp Thr Val Arg Leu Tyr Ile Cys Glu Met Ala Leu Ala Leu Asp
123                 128                 133                 138

tac ctg cgc ggc cag cac atc atc cac aga gat gtc aag cct gac aac      482
Tyr Leu Arg Gly Gln His Ile Ile His Arg Asp Val Lys Pro Asp Asn
139                 144                 149                 154

att ctc ctg gat gag aga gga cat gca cac ctg acc gac ttc aac att      530
Ile Leu Leu Asp Glu Arg Gly His Ala His Leu Thr Asp Phe Asn Ile
155                 160                 165                 170

gcc acc atc atc aag gac ggg gag cgg gcg acg gca tta gca ggc acc      578
Ala Thr Ile Ile Lys Asp Gly Glu Arg Ala Thr Ala Leu Ala Gly Thr
171                 176                 181                 186

aag ccg tac atg gct ccg gag atc ttc cac tct ttt gtc aac gtc gtg      626
Lys Pro Tyr Met Ala Pro Glu Ile Phe His Ser Phe Val Asn Val Val
187                 192                 197                 202

acc ggc tac tcc ttc gag gtg gac tgg tgg tcg gtg ggg gtg atg gcc      674
Thr Gly Tyr Ser Phe Glu Val Asp Trp Trp Ser Val Gly Val Met Ala
203                 208                 213                 218

tat gag ctg ctg cga gga tgg agg ccc tat gac atc cac tcc agc aac      722
Tyr Glu Leu Leu Arg Gly Trp Arg Pro Tyr Asp Ile His Ser Ser Asn
219                 224                 229                 234

gcc gtg gag tcc ctg gtg cag ctg ttc agc acc gtg agc gtc cag tat      770
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Ala Val Glu Ser Leu Val Gln Leu Phe Ser Thr Val Ser Val Gln Tyr
235                 240                 245                 250

gtc ccc acg tgg tcc aag gag atg gtg gcc ttg ctg cgg aag ctc ctc      818
Val Pro Thr Trp Ser Lys Glu Met Val Ala Leu Leu Arg Lys Leu Leu
251                 256                 261                 266

act gtg aac ccc gag cac cgg ctc tcc agc ctc cag gac gtg cag gca      866
Thr Val Asn Pro Glu His Arg Leu Ser Ser Leu Gln Asp Val Gln Ala
267                 272                 277                 282

gcc ccg gcg ctg gcc ggc gtg ctg tgg gac cac ctg agc gag aag agg      914
Ala Pro Ala Leu Ala Gly Val Leu Trp Asp His Leu Ser Glu Lys Arg
283                 288                 293                 298

gtg gag ccg ggc ttc gtg ccc aac aaa ggc cgt ctg cac tgc gac ccc      962
Val Glu Pro Gly Phe Val Pro Asn Lys Gly Arg Leu His Cys Asp Pro
299                 304                 309                 314

acc ttt gag ctg gag gag atg atc ctg gag tcc agg ccc ctg cac aag     1010
Thr Phe Glu Leu Glu Glu Met Ile Leu Glu Ser Arg Pro Leu His Lys
315                 320                 325                 330

aag aag aag cgc ctg gcc aag aac aag tcc cgg gac aac agc agg gac     1058
Lys Lys Lys Arg Leu Ala Lys Asn Lys Ser Arg Asp Asn Ser Arg Asp
331                 336                 341                 346

agc tcc cag tcc gag aat gac tat ctt caa gac tgc ctc gat gcc atc     1106
Ser Ser Gln Ser Glu Asn Asp Tyr Leu Gln Asp Cys Leu Asp Ala Ile
347                 352                 357                 362

cag caa gac ttc gtg att ttt aac aga gaa aag ctg aag agg agc cag     1154
Gln Gln Asp Phe Val Ile Phe Asn Arg Glu Lys Leu Lys Arg Ser Gln
363                 368                 373                 378

gac ctc ccg agg gag cct ctc ccc gcc cct gag tcc agg gat gct gcg     1202
Asp Leu Pro Arg Glu Pro Leu Pro Ala Pro Glu Ser Arg Asp Ala Ala
379                 384                 389                 394

gag cct gtg gag gac gag gcg gaa cgc tcc gcc ctg ccc atg tgc ggc     1250
Glu Pro Val Glu Asp Glu Ala Glu Arg Ser Ala Leu Pro Met Cys Gly
395                 400                 405                 410

ccc att tgc ccc tcg gcc ggg agc ggc tag g ccgggacgcc cgtggtcctc     1301
Pro Ile Cys Pro Ser Ala Gly Ser Gly  *
411                 416

acccccttgag ctgctttgga gactcggctg ccagagggag ggccatgggc cgaggcctgg   1361

cattcacgtt cccacccagc ctggctggcg gtgcccacag tgccccggac acatttcaca   1421

cctcaggctc gtggtggtgc aggggacaag aggctgtggg tgcaggggac acctgtggag   1481

ggcatttccc gtgggccccc gagacccgcc tagatggagg aagcgctgct gggcgccctc   1541

ttaccgctca cggggagctg gggccatgga tgggacagga gtctttgtcc ctgctcagcc   1601
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cggaggctgt gcacggccct cgtcacaagg tgacccttgc agcacaggcc gcgggtgccc 1661

caggctcggc tcagttcttg gaggtcaagg gcatgggttg gggtagtggg tggggaggtg 1721

aatgttttct agagattcaa actgctccag caatttctgt atagttttca cctctgagaa 1781

ttacaatgtg agaaccgctc aaaaaaaaaa aaaaggggg gccctttaa aagaacaaat 1841

ttttactccc gggggttggc aaggtatttt ttttttttg gggccccaaa attaaattcc 1901

gggggcggtt ttttaaaaag gggggagtgg aaaaaccctg gggttaccca attttatttg 1961

ttttggagaa a 1972

<210> 167
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<212> DNA
<213> Homo sapiens

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<400> 167
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gcaccgcggc gctcgggtgt ttttgggggc ccgggtggag ggcccgggtg ccggggccca 120

aggtgcggcc tcgctagcgg gagagggagc gggatcaccg gcccggagag agctctcagg 180

gccagagcgg ggcaggagga tgctttccca gccccacc atg gag ctg cgc tgt 233
Met Glu Leu Arg Cys
1

ggg gga ttg ctg ttc agt tct cgc ttt gat tca ggg aat cta gcc cac 281
Gly Gly Leu Leu Phe Ser Ser Arg Phe Asp Ser Gly Asn Leu Ala His
6 11 16 21

gtg gag aag gtg gaa tct ttg tcc agt gat ggg gaa ggg gta gga ggt 329
Val Glu Lys Val Glu Ser Leu Ser Ser Asp Gly Glu Gly Val Gly Gly
22 27 32 37

ggg gcg tca gcc ctg acc agt ggc att gcc tct tcc cct gac tat gaa 377
Gly Ala Ser Ala Leu Thr Ser Gly Ile Ala Ser Ser Pro Asp Tyr Glu
38 43 48 53

ttc aac gtg tgg acc cga cca gac tgt gct gaa acg gaa ttt gag aat 425
Phe Asn Val Trp Thr Arg Pro Asp Cys Ala Glu Thr Glu Phe Glu Asn
54 59 64 69

ggg aac agg tca tgg ttc tac ttc agc gtc cgg gga gga atg cca gga 473
Gly Asn Arg Ser Trp Phe Tyr Phe Ser Val Arg Gly Gly Met Pro Gly
70 75 80 85

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aaa ctc atc aag atc aac att atg aac atg aac aag cag agc aag ctg      521
Lys Leu Ile Lys Ile Asn Ile Met Asn Met Asn Lys Gln Ser Lys Leu
 86                  91                  96                 101

tat tcc cag ggc atg gcc ccc ttt gtg cgc aca ctg ccc acc cgg cca      569
Tyr Ser Gln Gly Met Ala Pro Phe Val Arg Thr Leu Pro Thr Arg Pro
102                 107                 112                 117

cgc tgg gaa cgc att cga gac cgg ccc acc ttt gag atg aca gag acg      617
Arg Trp Glu Arg Ile Arg Asp Arg Pro Thr Phe Glu Met Thr Glu Thr
118                 123                 128                 133

cag ttt gtg tta tcc ttt gtt cat cgt ttc gtg gag ggc cgt ggg gcc      665
Gln Phe Val Leu Ser Phe Val His Arg Phe Val Glu Gly Arg Gly Ala
134                 139                 144                 149

acc acc ttc ttc gcc ttc tgc tac ccc ttc tcc tac agt gac tgc cag      713
Thr Thr Phe Phe Ala Phe Cys Tyr Pro Phe Ser Tyr Ser Asp Cys Gln
150                 155                 160                 165

gaa ctg cta aac cag cta gac cag cgc ttt ccg gag aac cac cct acc      761
Glu Leu Leu Asn Gln Leu Asp Gln Arg Phe Pro Glu Asn His Pro Thr
166                 171                 176                 181

cat agc agc ccc ctg gat acc atc tat tac cat cgg gag ctc ctt tgc      809
His Ser Ser Pro Leu Asp Thr Ile Tyr Tyr His Arg Glu Leu Leu Cys
182                 187                 192                 197

tat tct ctg gat gga ctt cgt gta gat ctg ctg acg atc act tcc tgc      857
Tyr Ser Leu Asp Gly Leu Arg Val Asp Leu Leu Thr Ile Thr Ser Cys
198                 203                 208                 213

cat ggg ctt cga gaa gat cga gag ccc cgt cta gag cag cta ttt cct      905
His Gly Leu Arg Glu Asp Arg Glu Pro Arg Leu Glu Gln Leu Phe Pro
214                 219                 224                 229

gat acc agc acc cct cga cca ttc cgt ttc gca ggc aag agg ata ttc      953
Asp Thr Ser Thr Pro Arg Pro Phe Arg Phe Ala Gly Lys Arg Ile Phe
230                 235                 240                 245

ttc tta agc agt aga gta cac cca ggg gag act cca tct agc ttt gtc     1001
Phe Leu Ser Ser Arg Val His Pro Gly Glu Thr Pro Ser Ser Phe Val
246                 251                 256                 261

ttc aat ggc ttt ctg gac ttc atc ctc cga cct gat gat ccc cgg gcc     1049
Phe Asn Gly Phe Leu Asp Phe Ile Leu Arg Pro Asp Asp Pro Arg Ala
262                 267                 272                 277

caa acc ctc cgt cgc ctc ttc gtc ttt aag ctg att ccc atg ttg aac     1097
Gln Thr Leu Arg Arg Leu Phe Val Phe Lys Leu Ile Pro Met Leu Asn
278                 283                 288                 293

ccc gat ggt gtg gtc cgg gga cac tac cgc aca gac tca cgt gga gtg     1145
Pro Asp Gly Val Val Arg Gly His Tyr Arg Thr Asp Ser Arg Gly Val
294                 299                 304                 309

aat ctg aac cgt cag tac ctg aag cct gat gcc gtc ctg cac ccg gcc     1193
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Asn Leu Asn Arg Gln Tyr Leu Lys Pro Asp Ala Val Leu His Pro Ala
310                 315                 320                 325

atc tat ggg gcc aaa gct gtg ctt ctc tac cac cat gtg cac tct cgt      1241
Ile Tyr Gly Ala Lys Ala Val Leu Leu Tyr His His Val His Ser Arg
326                 331                 336                 341

ctg aac tcc cag agt tcc tct gag cac cag ccc agt tcc tgt ctc cct      1289
Leu Asn Ser Gln Ser Ser Ser Glu His Gln Pro Ser Ser Cys Leu Pro
342                 347                 352                 357

cct gat gct cct gtt tct gac ctg gag aaa gcc aac aat ctc caa aat      1337
Pro Asp Ala Pro Val Ser Asp Leu Glu Lys Ala Asn Asn Leu Gln Asn
358                 363                 368                 373

gaa gct cag tgt ggg cac tca gct gac agg cat aac gct gaa gcc tgg      1385
Glu Ala Gln Cys Gly His Ser Ala Asp Arg His Asn Ala Glu Ala Trp
374                 379                 384                 389

aaa caa aca gag cca gca gaa cag aag ctc aac agt gtg tgg att atg      1433
Lys Gln Thr Glu Pro Ala Glu Gln Lys Leu Asn Ser Val Trp Ile Met
390                 395                 400                 405

cca caa cag tct gcg ggg ctt gaa gag tca gcc cct gat acc atc ccc      1481
Pro Gln Gln Ser Ala Gly Leu Glu Glu Ser Ala Pro Asp Thr Ile Pro
406                 411                 416                 421

ccc aaa gag agt ggc gtt gct tac tat gtg gac ctg cat gga cat gct      1529
Pro Lys Glu Ser Gly Val Ala Tyr Tyr Val Asp Leu His Gly His Ala
422                 427                 432                 437

tcc aaa agg ggc tgc ttc atg tac gga aac agc ttt agt gat gag agc      1577
Ser Lys Arg Gly Cys Phe Met Tyr Gly Asn Ser Phe Ser Asp Glu Ser
438                 443                 448                 453

acc cag gtg gaa aac atg cta tat cca aag ctc atc tcc ttg aat tca      1625
Thr Gln Val Glu Asn Met Leu Tyr Pro Lys Leu Ile Ser Leu Asn Ser
454                 459                 464                 469

gcc cac ttc gac ttc cag ggc tgc aat ttc tca gag aag aat atg tat      1673
Ala His Phe Asp Phe Gln Gly Cys Asn Phe Ser Glu Lys Asn Met Tyr
470                 475                 480                 485

gcc cga gac cgt aga gat ggc cag tct aaa gag gga agc ggc cgt gtt      1721
Ala Arg Asp Arg Arg Asp Gly Gln Ser Lys Glu Gly Ser Gly Arg Val
486                 491                 496                 501

gca atc tac aaa gcc tca ggg ata atc cac agc tac aca ctt gaa tgc      1769
Ala Ile Tyr Lys Ala Ser Gly Ile Ile His Ser Tyr Thr Leu Glu Cys
502                 507                 512                 517

aac tac aac act gga cgc tca gta aac agc atc cct gct gcc tgc cat      1817
Asn Tyr Asn Thr Gly Arg Ser Val Asn Ser Ile Pro Ala Ala Cys His
518                 523                 528                 533

gac aat ggg cgt gcc agc ccc cct ccc ccg ccg gct ttc ccc tcc aga      1865
Asp Asn Gly Arg Ala Ser Pro Pro Pro Pro Pro Ala Phe Pro Ser Arg
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534                 539                 544                 549

tac act gtg gaa cta ttt gag cag gtg gga cga gct atg gcc att gca     1913
Tyr Thr Val Glu Leu Phe Glu Gln Val Gly Arg Ala Met Ala Ile Ala
550                 555                 560                 565

gcc ctg gac atg gcg gaa tgt aat ccg tgg ccc cga att gta ctg tca     1961
Ala Leu Asp Met Ala Glu Cys Asn Pro Trp Pro Arg Ile Val Leu Ser
566                 571                 576                 581

gag cac agc agc ctt act aat cta cgg gcc tgg atg ctg aaa cat gta     2009
Glu His Ser Ser Leu Thr Asn Leu Arg Ala Trp Met Leu Lys His Val
582                 587                 592                 597

cgc aac agc cga ggc cta agc agc act ctg aat gtg ggt gtc aac aag     2057
Arg Asn Ser Arg Gly Leu Ser Ser Thr Leu Asn Val Gly Val Asn Lys
598                 603                 608                 613

aag agg ggc ctt cga act cca ccc aaa agt cac aat ggg ttg cct gtc     2105
Lys Arg Gly Leu Arg Thr Pro Pro Lys Ser His Asn Gly Leu Pro Val
614                 619                 624                 629

tcc tgc tcc gaa aac acc ttg agt cgg gca cga agt ttt agc acc ggc     2153
Ser Cys Ser Glu Asn Thr Leu Ser Arg Ala Arg Ser Phe Ser Thr Gly
630                 635                 640                 645

aca agt gcc ggt ggt agc agc agc agc caa caa aat tct cca cag atg     2201
Thr Ser Ala Gly Gly Ser Ser Ser Ser Gln Gln Asn Ser Pro Gln Met
646                 651                 656                 661

aag aat tcc ccc agc ttt cct ttt cat ggc agt cgg cct gca ggg ctg     2249
Lys Asn Ser Pro Ser Phe Pro Phe His Gly Ser Arg Pro Ala Gly Leu
662                 667                 672                 677

cca ggc ctg ggc tct agt acc caa aag gtc acc cac cgg gtg ctg ggc     2297
Pro Gly Leu Gly Ser Ser Thr Gln Lys Val Thr His Arg Val Leu Gly
678                 683                 688                 693

ccc gtc aga gag ccc cga agc cag gac agg aga cgg cag cag cag ccc     2345
Pro Val Arg Glu Pro Arg Ser Gln Asp Arg Arg Arg Gln Gln Gln Pro
694                 699                 704                 709

ctg aac cat cgt cct gca ggc agc ctc gct cca tcc cca gct cct act     2393
Leu Asn His Arg Pro Ala Gly Ser Leu Ala Pro Ser Pro Ala Pro Thr
710                 715                 720                 725

agt tct ggc cca gcc tcc tca cac aag ctg ggc tcc tgt cta ctg gct     2441
Ser Ser Gly Pro Ala Ser Ser His Lys Leu Gly Ser Cys Leu Leu Ala
726                 731                 736                 741

tga ttca ttcaacatac caggggagca gtggctcact cttgtccttc tggagacaaa     2498
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742

ccagagctgt catggtaatc ggga                                         2522
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gcctgagtcg cggccacccg caggtctgag ctgtgggctg aggcagcgca gccgctgccg 120

cagggtgcgc gatgctttga acctgggaaa ctatgtgaag caacactctg gattttgaaa 180

gacatctttt catc atg gga cag caa att tcg gat cag aca cag ttg gtt 230
Met Gly Gln Gln Ile Ser Asp Gln Thr Gln Leu Val
1 5 10

att aac aag tta cca gaa aaa gta gca aaa cat gtt acg ttg gtt cga 278
Ile Asn Lys Leu Pro Glu Lys Val Ala Lys His Val Thr Leu Val Arg
13 18 23 28

gag agt ggc tcc tta act tat gaa gaa ttt ctt ggg aga gta gct gag 326
Glu Ser Gly Ser Leu Thr Tyr Glu Glu Phe Leu Gly Arg Val Ala Glu
29 34 39 44

ctt aat gat gta acg gct aaa gtg gct tct ggc cag gaa aaa cat ctt 374
Leu Asn Asp Val Thr Ala Lys Val Ala Ser Gly Gln Glu Lys His Leu
45 50 55 60

ctc ttt gag gta caa cct ggg tct gat tcc tct gct ttt tgg aaa gtg 422
Leu Phe Glu Val Gln Pro Gly Ser Asp Ser Ser Ala Phe Trp Lys Val
61 66 71 76

gtt gta cgg gtg gtc tgt acc aag att aac aaa agc agt ggc att gtg 470
Val Val Arg Val Val Cys Thr Lys Ile Asn Lys Ser Ser Gly Ile Val
77 82 87 92

gag gca tca cgg atc atg aat tta tac cag ttt att caa ctt tat aaa 518
Glu Ala Ser Arg Ile Met Asn Leu Tyr Gln Phe Ile Gln Leu Tyr Lys
93 98 103 108

gat atc aca agt caa gca gca gga gta ttg gca cag agc tcc acc tct 566
Asp Ile Thr Ser Gln Ala Ala Gly Val Leu Ala Gln Ser Ser Thr Ser
109 114 119 124

gaa gaa cct gat gaa aac tca tcc tct gta aca tct tgt cag gct agt 614
Glu Glu Pro Asp Glu Asn Ser Ser Ser Val Thr Ser Cys Gln Ala Ser
125 130 135 140

ctt tgg atg gga agg gtg aag cag ctg acc gat gag gag gag tgt tgt 662
Leu Trp Met Gly Arg Val Lys Gln Leu Thr Asp Glu Glu Glu Cys Cys
141 146 151 156

```
atc tgt atg gat ggg cgg gct gac ctc atc ctg cct tgt gct cac agc      710
Ile Cys Met Asp Gly Arg Ala Asp Leu Ile Leu Pro Cys Ala His Ser
157                 162                 167                 172

ttt tgt cag aag tgt att gat aaa tgg agt gat cga cac agg aat tgc      758
Phe Cys Gln Lys Cys Ile Asp Lys Trp Ser Asp Arg His Arg Asn Cys
173                 178                 183                 188

cct att tgt cgc cta cag atg act gga gca aat gaa tct tgg gtg gta      806
Pro Ile Cys Arg Leu Gln Met Thr Gly Ala Asn Glu Ser Trp Val Val
189                 194                 199                 204

tca gat gca ccc act gaa gat gat atg gct aac tat att ctt aac atg      854
Ser Asp Ala Pro Thr Glu Asp Asp Met Ala Asn Tyr Ile Leu Asn Met
205                 210                 215                 220

gct gat gag gca ggc cag ccc cac agg cca tga ccttgaag tgaaagtctt      905
Ala Asp Glu Ala Gly Gln Pro His Arg Pro  *
221                 226                 231

ctgttgctat tgtgggctca aatatttggt catgggggaa gaatgtaggg ttgtggcact    965

ggcacagaca caggaaaatc cattttcccc actcttttat ttttgctatt ctgatcattt   1025

gtcccccttt taaaaataaa cttcccatgt cttccaaaaa aaaaa                   1070
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<213> Homo sapiens

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<222> (114)..(887)

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ccgcaaagcg aacgggggcc gcggcgcggg ccccgcgggg gttagaggtc acc   atg     116
                                                            Met
                                                              1

ctg agg gtc gcg tgg agg acg ctg agt ttg att cgg acc cgg gca gtt      164
Leu Arg Val Ala Trp Arg Thr Leu Ser Leu Ile Arg Thr Arg Ala Val
  2                   7                  12                  17

acc cag gtc cta gta ccc ggg ctg ccg ggc ggt ggg agc gcc aag ttt      212
Thr Gln Val Leu Val Pro Gly Leu Pro Gly Gly Gly Ser Ala Lys Phe
 18                  23                  28                  33

cct ttc aac cag tgg ggc ctg cag cct cga agt ctc ctc ctc cag gcc      260
Pro Phe Asn Gln Trp Gly Leu Gln Pro Arg Ser Leu Leu Leu Gln Ala
 34                  39                  44                  49
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gcg cgc gga tat gtc gtc cgg aaa cca gcc cag tct agg ctg gat gat      308
Ala Arg Gly Tyr Val Val Arg Lys Pro Ala Gln Ser Arg Leu Asp Asp
 50                  55                  60                  65

gac cca cct cct tct acg ctg ctc aaa gac tac cag aat gtc cct gga      356
Asp Pro Pro Pro Ser Thr Leu Leu Lys Asp Tyr Gln Asn Val Pro Gly
 66                  71                  76                  81

att gag aag gtt gat gat gtc gtg aaa aga ctc ttg tct ttg gaa atg      404
Ile Glu Lys Val Asp Asp Val Val Lys Arg Leu Leu Ser Leu Glu Met
 82                  87                  92                  97

gcc aac aag aag gag atg cta aaa atc aag caa gaa cag ttt atg aag      452
Ala Asn Lys Lys Glu Met Leu Lys Ile Lys Gln Glu Gln Phe Met Lys
 98                 103                 108                 113

aag att gtt gca aac cca gag gac acc aga tcc ctg gag gct cga att      500
Lys Ile Val Ala Asn Pro Glu Asp Thr Arg Ser Leu Glu Ala Arg Ile
114                 119                 124                 129

att gcc ttg tct gtc aag atc cgc agt tat gaa gaa cac ttg gag aaa      548
Ile Ala Leu Ser Val Lys Ile Arg Ser Tyr Glu Glu His Leu Glu Lys
130                 135                 140                 145

cat cga aag gac aaa gcc cac aaa cgc tat ctg cta atg agc att gac      596
His Arg Lys Asp Lys Ala His Lys Arg Tyr Leu Leu Met Ser Ile Asp
146                 151                 156                 161

cag agg aaa aag atg ctc aaa aac ctc cgt aac acc aac tat gat gtc      644
Gln Arg Lys Lys Met Leu Lys Asn Leu Arg Asn Thr Asn Tyr Asp Val
162                 167                 172                 177

ttt gag aag ata tgc tgg ggg ctg gga att gag tac acc ttc ccc cct      692
Phe Glu Lys Ile Cys Trp Gly Leu Gly Ile Glu Tyr Thr Phe Pro Pro
178                 183                 188                 193

ctg tat tac cga aga gcc cac cgc cga ttc gtg acc aag aag gct ctg      740
Leu Tyr Tyr Arg Arg Ala His Arg Arg Phe Val Thr Lys Lys Ala Leu
194                 199                 204                 209

tgc att cgg gtt ttc cag gag act caa aag ctg aag aag cga aga aga      788
Cys Ile Arg Val Phe Gln Glu Thr Gln Lys Leu Lys Lys Arg Arg Arg
210                 215                 220                 225

gcc tta aag gct gca gca gca gcc caa aaa caa gca aag cgg agg aac      836
Ala Leu Lys Ala Ala Ala Ala Ala Gln Lys Gln Ala Lys Arg Arg Asn
226                 231                 236                 241

cca gac agc cct gcc aaa gcc ata cca aag aca ctc aaa gac agc caa      884
Pro Asp Ser Pro Ala Lys Ala Ile Pro Lys Thr Leu Lys Asp Ser Gln
242                 247                 252                 257

taa attc tgttcaatca tttctttctg tcttgaagaa tgataggaga gatgatgggg      941
 *
258
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ctctttttgg cctgaagagg agaaggaatt tattctttca ttcagctctg agatcccaga 1001

gttttctgag gcagagtccc tgcctcaccc accagaggat acacactcat gacatgcctc 1061

ccacacactc atacaaacaa gtacctgtca tccaggtgat gtgtgtcagt ggaggcaaga 1121

cagagcatgt gacagcacag tggaagtgtg gccggctggg taggaaga 1169

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<213> Homo sapiens

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<222> (292)..(2871)

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ctgttctgtg gtattctttg ttcttctcta ggtgggagca actgtgtgat agccatcttt 180

gtatcctcag ttctttgtct cgaggatccg aattcgcggc cgcgtcgacg cggtttctga 240

ggttcttcac tcgcgactga cggagctgcg gtggcgtctc cacacgcaac c atg aag 297
Met Lys
1

ttg aag gac aca aaa tca agg cca aag cag tca agc tgt ggc aaa ttt 345
Leu Lys Asp Thr Lys Ser Arg Pro Lys Gln Ser Ser Cys Gly Lys Phe
3 8 13 18

cag aca aag gga atc aaa gtt gtg gga aaa tgg aag gaa gtg aag att 393
Gln Thr Lys Gly Ile Lys Val Val Gly Lys Trp Lys Glu Val Lys Ile
19 24 29 34

gac cca aat atg ttt gca gat gga cag atg gat gac ttg gtg tgc ttt 441
Asp Pro Asn Met Phe Ala Asp Gly Gln Met Asp Asp Leu Val Cys Phe
35 40 45 50

gag gaa ttg aca gat tac cag ttg gtc tcc cct gcc aag aat ccc tcc 489
Glu Glu Leu Thr Asp Tyr Gln Leu Val Ser Pro Ala Lys Asn Pro Ser
51 56 61 66

agt ctc ttc tca aag gaa gca ccc aag aga aag gca caa gct gtt tca 537
Ser Leu Phe Ser Lys Glu Ala Pro Lys Arg Lys Ala Gln Ala Val Ser
67 72 77 82

gaa gaa gag gag gag gag gag gga aag tct agc tca cca aag aaa aag 585
Glu Glu Glu Glu Glu Glu Glu Gly Lys Ser Ser Ser Pro Lys Lys Lys
83 88 93 98

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atc aag ttg aag aaa agt aaa aat gta gca act gaa gga acc agt acc      633
Ile Lys Leu Lys Lys Ser Lys Asn Val Ala Thr Glu Gly Thr Ser Thr
 99                 104                 109                 114

cag aaa gaa ttt gaa gtg aaa gat cct gag ctg gag gcc cag gga gat      681
Gln Lys Glu Phe Glu Val Lys Asp Pro Glu Leu Glu Ala Gln Gly Asp
115                 120                 125                 130

gac atg gtt tgt gat gat ccg gag gct ggg gag atg aca tca gaa aac      729
Asp Met Val Cys Asp Asp Pro Glu Ala Gly Glu Met Thr Ser Glu Asn
131                 136                 141                 146

ctg gtc caa act gct cca aaa aag aag aaa aat aaa ggg aaa aaa ggg      777
Leu Val Gln Thr Ala Pro Lys Lys Lys Lys Asn Lys Gly Lys Lys Gly
147                 152                 157                 162

ttg gag cct tct cag agc act gct gcc aag gtg ccc aaa aaa gcg aag      825
Leu Glu Pro Ser Gln Ser Thr Ala Ala Lys Val Pro Lys Lys Ala Lys
163                 168                 173                 178

aca tgg att cct gaa gtt cat gat cag aaa gca gat gtg tca gct tgg      873
Thr Trp Ile Pro Glu Val His Asp Gln Lys Ala Asp Val Ser Ala Trp
179                 184                 189                 194

aag gac ctg ttt gtt ccc agg ccg gtt ctc cga gca ctc agc ttt cta      921
Lys Asp Leu Phe Val Pro Arg Pro Val Leu Arg Ala Leu Ser Phe Leu
195                 200                 205                 210

ggc ttc tct gca ccc aca cca atc caa gcc ctg acc ttg gca cct gcc      969
Gly Phe Ser Ala Pro Thr Pro Ile Gln Ala Leu Thr Leu Ala Pro Ala
211                 216                 221                 226

atc cgt gac aaa ctg gac atc ctt ggg gct gct gag aca gga agt ggg     1017
Ile Arg Asp Lys Leu Asp Ile Leu Gly Ala Ala Glu Thr Gly Ser Gly
227                 232                 237                 242

aaa act ctt gcc ttt gcc atc cca atg att cat gcg gtg ttg cag tgg     1065
Lys Thr Leu Ala Phe Ala Ile Pro Met Ile His Ala Val Leu Gln Trp
243                 248                 253                 258

cag aag agg aat gct gcc cct cct cca agt aac acc gaa gca cca cct     1113
Gln Lys Arg Asn Ala Ala Pro Pro Pro Ser Asn Thr Glu Ala Pro Pro
259                 264                 269                 274

gga gag acc aga act gag gcc gga gct gag act aga tca cca ggc aag     1161
Gly Glu Thr Arg Thr Glu Ala Gly Ala Glu Thr Arg Ser Pro Gly Lys
275                 280                 285                 290

gct gaa gct gag tct gat gca ttg cct gac gat act gta att gag agt     1209
Ala Glu Ala Glu Ser Asp Ala Leu Pro Asp Asp Thr Val Ile Glu Ser
291                 296                 301                 306

gaa gca ctg ccc agt gat att gca gcc gag gcc aga gcc aag act gga     1257
Glu Ala Leu Pro Ser Asp Ile Ala Ala Glu Ala Arg Ala Lys Thr Gly
307                 312                 317                 322

ggc act gtc tca gac cag gcg ttg ctc ttt ggt gac gat gat gct ggt     1305
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Gly Thr Val Ser Asp Gln Ala Leu Leu Phe Gly Asp Asp Asp Ala Gly
323                 328                 333                 338

gaa ggg cct tct tcc ctg atc agg gag aaa cct gtt ccc aaa cag aat     1353
Glu Gly Pro Ser Ser Leu Ile Arg Glu Lys Pro Val Pro Lys Gln Asn
339                 344                 349                 354

gag aat gag gag gaa aat ctt gat aaa gag cag act gga aat cta aaa     1401
Glu Asn Glu Glu Glu Asn Leu Asp Lys Glu Gln Thr Gly Asn Leu Lys
355                 360                 365                 370

cag gag ttg gat gac aaa agc gcc acc tgt aag gca tat cca aag cgt     1449
Gln Glu Leu Asp Asp Lys Ser Ala Thr Cys Lys Ala Tyr Pro Lys Arg
371                 376                 381                 386

cct ctg ctt gga ctg gtt ctg act ccc act cga gag ctg gcc gtc cag     1497
Pro Leu Leu Gly Leu Val Leu Thr Pro Thr Arg Glu Leu Ala Val Gln
387                 392                 397                 402

gtc aaa cag cac att gat gct gtg gcc agg ttt aca gga att aaa act     1545
Val Lys Gln His Ile Asp Ala Val Ala Arg Phe Thr Gly Ile Lys Thr
403                 408                 413                 418

gct att ttg gtt ggt gga atg tcc acg cag aaa cag cag agg atg ctg     1593
Ala Ile Leu Val Gly Gly Met Ser Thr Gln Lys Gln Gln Arg Met Leu
419                 424                 429                 434

aac cgt cgt cct gag att gtg gtt gct act cca ggc cgg ctg tgg gaa     1641
Asn Arg Arg Pro Glu Ile Val Val Ala Thr Pro Gly Arg Leu Trp Glu
435                 440                 445                 450

tta att aaa gaa aag cat tat cat ttg agg aac ctt cgg cag ctc agg     1689
Leu Ile Lys Glu Lys His Tyr His Leu Arg Asn Leu Arg Gln Leu Arg
451                 456                 461                 466

tgc ctg gta gtg gat gag gct gac cgg atg gtt gag aaa ggc cat ttt     1737
Cys Leu Val Val Asp Glu Ala Asp Arg Met Val Glu Lys Gly His Phe
467                 472                 477                 482

gct gag ctc tca cag ctg cta gag atg ctc aat gac tcc caa tac aac     1785
Ala Glu Leu Ser Gln Leu Leu Glu Met Leu Asn Asp Ser Gln Tyr Asn
483                 488                 493                 498

cca aag aga caa acg ctt gtt ttt tct gcc aca ctc acc ctg gtg cat     1833
Pro Lys Arg Gln Thr Leu Val Phe Ser Ala Thr Leu Thr Leu Val His
499                 504                 509                 514

cag gct cct gct cga atc ctt cat aag aag cac acc aag aaa atg gat     1881
Gln Ala Pro Ala Arg Ile Leu His Lys Lys His Thr Lys Lys Met Asp
515                 520                 525                 530

aaa aca gcc aaa ctt gac ctc ctt atg cag aaa att ggc atg agg ggc     1929
Lys Thr Ala Lys Leu Asp Leu Leu Met Gln Lys Ile Gly Met Arg Gly
531                 536                 541                 546

aag ccc aag gtc att gac ctc aca agg aat gag gcc acg gtg gag acg     1977
Lys Pro Lys Val Ile Asp Leu Thr Arg Asn Glu Ala Thr Val Glu Thr
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547                 552                 557                 562

cta aca gag acc aag atc cat tgt gag act gat gag aaa gac ttc tac     2025
Leu Thr Glu Thr Lys Ile His Cys Glu Thr Asp Glu Lys Asp Phe Tyr
563                 568                 573                 578

ttg tac tac ttc ctg atg cag tat cca ggc cgc agc tta gtg ttt gcc     2073
Leu Tyr Tyr Phe Leu Met Gln Tyr Pro Gly Arg Ser Leu Val Phe Ala
579                 584                 589                 594

aac agt atc tcc tgc atc aaa cgc ctc tct ggg ctc ctc aaa gtc ctt     2121
Asn Ser Ile Ser Cys Ile Lys Arg Leu Ser Gly Leu Leu Lys Val Leu
595                 600                 605                 610

gat atc atg ccc ttg acc ctg cat gcc tgt atg cac cag aag cag agg     2169
Asp Ile Met Pro Leu Thr Leu His Ala Cys Met His Gln Lys Gln Arg
611                 616                 621                 626

ctc aga aac ctg gag cag ttt gcc cgt ctg gaa gac tgt gtt ctc ttg     2217
Leu Arg Asn Leu Glu Gln Phe Ala Arg Leu Glu Asp Cys Val Leu Leu
627                 632                 637                 642

gca aca gat gtg gca gct cgg ggt ctg gat att cct aaa gtc cag cat     2265
Ala Thr Asp Val Ala Ala Arg Gly Leu Asp Ile Pro Lys Val Gln His
643                 648                 653                 658

gtc atc cat tac cag gtc cca cgt acc tcg gag att tat gtc cac cga     2313
Val Ile His Tyr Gln Val Pro Arg Thr Ser Glu Ile Tyr Val His Arg
659                 664                 669                 674

agt ggt cga act gct cga gct acc aat gaa ggc ctc agt ctg atg ctc     2361
Ser Gly Arg Thr Ala Arg Ala Thr Asn Glu Gly Leu Ser Leu Met Leu
675                 680                 685                 690

att ggg cct gag gat gtg atc aac ttt aag aag att tac aaa acg ctc     2409
Ile Gly Pro Glu Asp Val Ile Asn Phe Lys Lys Ile Tyr Lys Thr Leu
691                 696                 701                 706

aag aaa gat gag gat atc cca ctg ttc ccc gtg cag aca aaa tac atg     2457
Lys Lys Asp Glu Asp Ile Pro Leu Phe Pro Val Gln Thr Lys Tyr Met
707                 712                 717                 722

gat gtg gtc aag gag cga atc cgt tta gct cga cag att gag aaa tct     2505
Asp Val Val Lys Glu Arg Ile Arg Leu Ala Arg Gln Ile Glu Lys Ser
723                 728                 733                 738

gag tat cgg aac ttc cag gct tgc ctg cac aac tct tgg att gag cag     2553
Glu Tyr Arg Asn Phe Gln Ala Cys Leu His Asn Ser Trp Ile Glu Gln
739                 744                 749                 754

gca gca gct gcc ctg gag att gag ctg gaa gaa gac atg tat aag gga     2601
Ala Ala Ala Ala Leu Glu Ile Glu Leu Glu Glu Asp Met Tyr Lys Gly
755                 760                 765                 770

gga aaa gct gac cag caa gaa gaa cgt cgg aga caa aag cag atg aag     2649
Gly Lys Ala Asp Gln Gln Glu Glu Arg Arg Arg Gln Lys Gln Met Lys
771                 776                 781                 786
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gtt ctg aag aag gag ctg cgc cac ctg ctg tcc cag cca ctg ttt acg     2697
Val Leu Lys Lys Glu Leu Arg His Leu Leu Ser Gln Pro Leu Phe Thr
787                 792                 797                 802

gag agc cag aaa acc aag tat ccc act cag tct ggc aag ccg ccc ctg     2745
Glu Ser Gln Lys Thr Lys Tyr Pro Thr Gln Ser Gly Lys Pro Pro Leu
803                 808                 813                 818

ctt gtg tct gcc cca agt aag agc gag tct gct ttg agc tgt ctc tcc     2793
Leu Val Ser Ala Pro Ser Lys Ser Glu Ser Ala Leu Ser Cys Leu Ser
819                 824                 829                 834

aag cag aag aag aag aag aca aag aag ccg aag gag cca cag ccg gaa     2841
Lys Gln Lys Lys Lys Lys Thr Lys Lys Pro Lys Glu Pro Gln Pro Glu
835                 840                 845                 850

cag cca cag cca agt aca agt gca aat taa c tgccgtggtc aagtgtgtca     2892
Gln Pro Gln Pro Ser Thr Ser Ala Asn  *
851                 856

gtgactgcac attggtttct gttctctggc tatttgcaaa acctctccca cccttgtgtt   2952

tcactccacc accaacccca ggtaaaaaag tatccctctc ttccactcac acccatagcg   3012

ggagagacct catgcagatt tgcattgttt tggagtaaga attcaatgca gcagcttaat   3072

ttttctgtat tgcagtgttt ataggcttct tgtgtgttaa acttgatttc ataaattaaa   3132

aacaatggtc agctcgtgcc gaattcttgg cctcgagggc caaat                   3177
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<213> Homo sapiens

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<222> (42)..(938)

<400> 171

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cgacccacgc gtccgctggc cctttccttt ccgcgtgtag a    atg tgg ggc gcc      53
                                                 Met Trp Gly Ala
                                                   1

tgt aaa gtt aag gtt cac gat tcc ttg gcc acc att tcc atc act ctg     101
Cys Lys Val Lys Val His Asp Ser Leu Ala Thr Ile Ser Ile Thr Leu
  5                  10                  15                  20

aga cgg tac ctg aga ttg ggg gcg acc atg gca aaa agc aag ttc gag     149
Arg Arg Tyr Leu Arg Leu Gly Ala Thr Met Ala Lys Ser Lys Phe Glu
 21                  26                  31                  36

tac gtg agg gac ttc gag gct gac gac acc tgc ctg gca cac tgc tgg     197
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Tyr Val Arg Asp Phe Glu Ala Asp Asp Thr Cys Leu Ala His Cys Trp
 37                  42                  47                  52

gtg gta gtg cgg ctg gac ggc cgg aat ttc cat cgg ttt gct gag aag      245
Val Val Val Arg Leu Asp Gly Arg Asn Phe His Arg Phe Ala Glu Lys
 53                  58                  63                  68

cac aac ttt gca aaa ccc aat gac agc cgt gct ctc cag ctg atg acc      293
His Asn Phe Ala Lys Pro Asn Asp Ser Arg Ala Leu Gln Leu Met Thr
 69                  74                  79                  84

aaa tgt gcg cag act gtg atg gaa gaa cta gag gat att gtg atc gcg      341
Lys Cys Ala Gln Thr Val Met Glu Glu Leu Glu Asp Ile Val Ile Ala
 85                  90                  95                 100

tat gga cag agt gat gag tac agc ttt gtg ttc aag cgg aaa acc aat      389
Tyr Gly Gln Ser Asp Glu Tyr Ser Phe Val Phe Lys Arg Lys Thr Asn
101                 106                 111                 116

tgg ttt aaa aga aga gcc agt aag ttc atg act cac gtg gcc tcc cag      437
Trp Phe Lys Arg Arg Ala Ser Lys Phe Met Thr His Val Ala Ser Gln
117                 122                 127                 132

ttt gcc tcc agc tat gtg ttt tat tgg cgg gat tac ttt gag gac cag      485
Phe Ala Ser Ser Tyr Val Phe Tyr Trp Arg Asp Tyr Phe Glu Asp Gln
133                 138                 143                 148

ccc ctt ctg tat ccc cca ggc ttt gac gga aga gtc gtg gtg tat ccc      533
Pro Leu Leu Tyr Pro Pro Gly Phe Asp Gly Arg Val Val Val Tyr Pro
149                 154                 159                 164

agc aac cag act tta aag gac tac ctc agc tgg cga caa gca gat tgt      581
Ser Asn Gln Thr Leu Lys Asp Tyr Leu Ser Trp Arg Gln Ala Asp Cys
165                 170                 175                 180

cac atc aat aat ctt tat aat aca gtt ttc tgg gca ctt ata caa caa      629
His Ile Asn Asn Leu Tyr Asn Thr Val Phe Trp Ala Leu Ile Gln Gln
181                 186                 191                 196

tct gga cta aca cca gta caa gcc caa ggg aga tta cag gga act ctt      677
Ser Gly Leu Thr Pro Val Gln Ala Gln Gly Arg Leu Gln Gly Thr Leu
197                 202                 207                 212

gca gca gac aag aat gag att ttg ttt tct gaa ttc aac atc aac tat      725
Ala Ala Asp Lys Asn Glu Ile Leu Phe Ser Glu Phe Asn Ile Asn Tyr
213                 218                 223                 228

aat aat gag ctg ccg atg tat agg aaa ggg act gtg ttg ata tgg cag      773
Asn Asn Glu Leu Pro Met Tyr Arg Lys Gly Thr Val Leu Ile Trp Gln
229                 234                 239                 244

aag gtg gat gaa gtg atg aca aaa gaa att aag ctg cca aca gaa atg      821
Lys Val Asp Glu Val Met Thr Lys Glu Ile Lys Leu Pro Thr Glu Met
245                 250                 255                 260

gaa gga aaa aag atg gca gtg acc cgg acc agg aca aag cca gtg ccc      869
Glu Gly Lys Lys Met Ala Val Thr Arg Thr Arg Thr Lys Pro Val Pro
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261                 266                 271                 276

ttg cac tgc gat atc atc ggg gat gct ttc tgg aag gaa cat cca gag      917
Leu His Cys Asp Ile Ile Gly Asp Ala Phe Trp Lys Glu His Pro Glu
277                 282                 287                 292

att cta gat gaa gac agc tga cc cttttgcgct tcagttctgg tgtgcttaac      970
Ile Leu Asp Glu Asp Ser  *
293                 298

catgcaagcc ctcccacctc ccagggctcc ttgccttagg tggctgtagc atccctacca   1030

cccaggacac tggtgcgaat gacacaactc aagttgggag gggaacaggg aaggaaggga   1090

tggatggggg tggtgtatct tactctgttt aagcagaaca ccttgtttgc ggtgttggaa   1150

catggttcct ttggcagaag tgctttttt ttaatcgcag tactattttt ataaagcaag   1210

aactattcca aaaaaaaaaa a                                           1231
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US 20050059026 A1

<210> 172
<211> 1040
<212> DNA
<213> Homo sapiens

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<222> (182)..(664)

<400> 172

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gctctcctga acctttaggc ttgtctcggc ccatttgaag accaggaagt tgatcaatcc    120

cgaggctgct gagagacggt ggcgcgattg ggacagtcgc cagggatggc tgagcgtgaa    180

g    atg cag cgg gtg tcc ggg ctg ctc tcc tgg acg ctg agc aga gtc      226
     Met Gln Arg Val Ser Gly Leu Leu Ser Trp Thr Leu Ser Arg Val
       1               5                  10

ctg tgg ctc tcc ggc ctc tct gag ccg gga gct gcc cgg cag ccc cgg      274
Leu Trp Leu Ser Gly Leu Ser Glu Pro Gly Ala Ala Arg Gln Pro Arg
 16                  21                  26                  31

atc atg gaa gag aaa gcg cta gag gtt tat gat ttg att aga act atc      322
Ile Met Glu Glu Lys Ala Leu Glu Val Tyr Asp Leu Ile Arg Thr Ile
 32                  37                  42                  47

cgg gac cca gaa aag ccc aat act tta gaa gaa ctg gaa gtg gtc tcg      370
Arg Asp Pro Glu Lys Pro Asn Thr Leu Glu Glu Leu Glu Val Val Ser
 48                  53                  58                  63

gaa agt tgt gtg gaa gtt cag gag ata aat gaa gaa gaa tat ctg gtt      418
Glu Ser Cys Val Glu Val Gln Glu Ile Asn Glu Glu Glu Tyr Leu Val
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 64                  69                  74                  79

att atc agg ttc acg cca aca gta cct cat tgc tct ttg gcg act ctt      466
Ile Ile Arg Phe Thr Pro Thr Val Pro His Cys Ser Leu Ala Thr Leu
 80                  85                  90                  95

att ggg ctg tgc tta aga gta aaa ctt cag cga tgt tta cca ttt aaa      514
Ile Gly Leu Cys Leu Arg Val Lys Leu Gln Arg Cys Leu Pro Phe Lys
 96                 101                 106                 111

cat aag ttg gaa atc tac att tct gaa gga acc cac tca aca gaa gaa      562
His Lys Leu Glu Ile Tyr Ile Ser Glu Gly Thr His Ser Thr Glu Glu
112                 117                 122                 127

gac atc aat aag cag ata aat gac aaa gag cga gtg gca gct gca atg      610
Asp Ile Asn Lys Gln Ile Asn Asp Lys Glu Arg Val Ala Ala Ala Met
128                 133                 138                 143

gaa aac ccc aac tta cgg gaa att gtg gaa cag tgt gtc ctt gaa cct      658
Glu Asn Pro Asn Leu Arg Glu Ile Val Glu Gln Cys Val Leu Glu Pro
144                 149                 154                 159

gac tga tagctgtttt aagagccact ggcctgtaat tgtttgatat atttgtttaa      714
Asp  *
160

actctttgta taatgtcaga gactcatgtt taatacatag gtgatttgta cctcagagca    774

ttttttaaag gattctttcc aagcgagatt taattataag gtagtaccta atttgttcaa    834

tgtataacat tctcaggatt tgtaacactt aaatgatcag acagaataat attttctagt    894

tattatgtgt aagatgagtt gctatttttc tgatgctcat tctgatacaa ctatttttcg    954

tgtcaaatat ctactgtgcc caaatgtact caatttaaat cattactctg taaaataaat   1014

aagcagatga ttcttaaaaa aaaaaa                                        1040
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<213> Homo sapiens

<220>
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<222> (266)..(1945)

<400> 173

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agacttaaaa ccagagaatg tagtcttctt tgaaaaacaa ggtcttgtaa agttgacaga    120

ctttgggttc agcaacaaat ttcaaccagg gaagaagctc actacaagct gtggatctct    180
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tgcatattcc gctccagaaa ttctgcttgg tgatgagtat gatgcacctg cagtagatat     240

ttggagtctg ggagtgatcc ttttc  atg ttg gtg tgt ggg cag ccg ccc ttt      292
                             Met Leu Val Cys Gly Gln Pro Pro Phe
                               1               5

caa gaa gcc aat gac agt gaa aca ctg aca atg atc atg gat tgc aaa       340
Gln Glu Ala Asn Asp Ser Glu Thr Leu Thr Met Ile Met Asp Cys Lys
 10                  15                  20                  25

tat aca gta cca tcc cat gtg tct aaa gag tgt aaa gac cta atc aca       388
Tyr Thr Val Pro Ser His Val Ser Lys Glu Cys Lys Asp Leu Ile Thr
 26                  31                  36                  41

cgg atg cta cag aga gat ccc aag aga agg gct tct tta gaa gag att       436
Arg Met Leu Gln Arg Asp Pro Lys Arg Arg Ala Ser Leu Glu Glu Ile
 42                  47                  52                  57

gaa aat cat cct tgg ctt cag gga gtg gac cct tca cca gct aca aag       484
Glu Asn His Pro Trp Leu Gln Gly Val Asp Pro Ser Pro Ala Thr Lys
 58                  63                  68                  73

tat aac att ccc ctt gtg tca tac aaa aat ctc tcg gaa gag gag cac       532
Tyr Asn Ile Pro Leu Val Ser Tyr Lys Asn Leu Ser Glu Glu Glu His
 74                  79                  84                  89

aac agc atc att cag cgc atg gtg ctt ggg gac ata gcg gat cga gac       580
Asn Ser Ile Ile Gln Arg Met Val Leu Gly Asp Ile Ala Asp Arg Asp
 90                  95                 100                 105

gcc att gta gaa gcc ctg gaa acc aac agg tat aac cat atc aca gcc       628
Ala Ile Val Glu Ala Leu Glu Thr Asn Arg Tyr Asn His Ile Thr Ala
106                 111                 116                 121

aca tac ttc ctg ctg gct gaa agg atc ctg aga gaa aag caa gag aaa       676
Thr Tyr Phe Leu Leu Ala Glu Arg Ile Leu Arg Glu Lys Gln Glu Lys
122                 127                 132                 137

gaa ata cag acc aga tct gca agc ccg agc aat atc aag gcc cag ttt       724
Glu Ile Gln Thr Arg Ser Ala Ser Pro Ser Asn Ile Lys Ala Gln Phe
138                 143                 148                 153

agg cag tca tgg cca acc aaa att gat gta ccc cag gac ctt gag gat       772
Arg Gln Ser Trp Pro Thr Lys Ile Asp Val Pro Gln Asp Leu Glu Asp
154                 159                 164                 169

gac ctc acg gcc act cct ttg tcc cac gcg act gtc cct cag tct cct       820
Asp Leu Thr Ala Thr Pro Leu Ser His Ala Thr Val Pro Gln Ser Pro
170                 175                 180                 185

gct cgg gct gct gac agt gtc ctc aat ggc cac agg agc aaa ggc ctg       868
Ala Arg Ala Ala Asp Ser Val Leu Asn Gly His Arg Ser Lys Gly Leu
186                 191                 196                 201

tgt gac tca gct aag aaa gat gac ctc cct gag ttg gct gga cca gca       916
Cys Asp Ser Ala Lys Lys Asp Asp Leu Pro Glu Leu Ala Gly Pro Ala
202                 207                 212                 217
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ctc tct acg gtg cca ccc gca agc tta aaa ccc aca gcc agt ggg cgg      964
Leu Ser Thr Val Pro Pro Ala Ser Leu Lys Pro Thr Ala Ser Gly Arg
218                 223                 228                 233

aag tgt ctg ttc agg gtg gaa gaa gat gaa gag gaa gat gag gag gac     1012
Lys Cys Leu Phe Arg Val Glu Glu Asp Glu Glu Glu Asp Glu Glu Asp
234                 239                 244                 249

aag aaa ccc atg tcc ctc tca aca caa gtg gtt ttg cgc cgg aag cca     1060
Lys Lys Pro Met Ser Leu Ser Thr Gln Val Val Leu Arg Arg Lys Pro
250                 255                 260                 265

tct gta acc aac cgc ctg aca tcc agg aag agt gcg ccc gtc ctc aac     1108
Ser Val Thr Asn Arg Leu Thr Ser Arg Lys Ser Ala Pro Val Leu Asn
266                 271                 276                 281

cag atc ttt gag gaa ggg gaa tct gat gat gag ttt gac atg gat gag     1156
Gln Ile Phe Glu Glu Gly Glu Ser Asp Asp Glu Phe Asp Met Asp Glu
282                 287                 292                 297

aat ctg cct ccc aag ttg agc agg tta aag atg aat ata gct tct cca     1204
Asn Leu Pro Pro Lys Leu Ser Arg Leu Lys Met Asn Ile Ala Ser Pro
298                 303                 308                 313

ggt aca gtt cac aaa cgc tac cac cgg agg aaa agt cag ggc cgg ggc     1252
Gly Thr Val His Lys Arg Tyr His Arg Arg Lys Ser Gln Gly Arg Gly
314                 319                 324                 329

tcc agc tgc agt agt tcg gag acc agt gat gat gat tct gaa agc cgg     1300
Ser Ser Cys Ser Ser Ser Glu Thr Ser Asp Asp Asp Ser Glu Ser Arg
330                 335                 340                 345

cgg cgg ctc gat aaa gat agc ggg ttc acc tac tcc tgg cac cga cgg     1348
Arg Arg Leu Asp Lys Asp Ser Gly Phe Thr Tyr Ser Trp His Arg Arg
346                 351                 356                 361

gat agc agc gag ggg ccc cct ggc agt gag ggg gat ggc ggg ggc cag     1396
Asp Ser Ser Glu Gly Pro Pro Gly Ser Glu Gly Asp Gly Gly Gly Gln
362                 367                 372                 377

agc aag cca agc aat gcc agt gga ggg gtg gac aag gcc agc ccc agt     1444
Ser Lys Pro Ser Asn Ala Ser Gly Gly Val Asp Lys Ala Ser Pro Ser
378                 383                 388                 393

gag aac aat gct ggt ggg ggc agt ccc tcc agc ggc tcg ggt ggc aac     1492
Glu Asn Asn Ala Gly Gly Gly Ser Pro Ser Ser Gly Ser Gly Gly Asn
394                 399                 404                 409

ccc acc aat aca tcg ggt acc aca cgc cgc tgt gcc ggc ccc agc aac     1540
Pro Thr Asn Thr Ser Gly Thr Thr Arg Arg Cys Ala Gly Pro Ser Asn
410                 415                 420                 425

tcc atg cag ctg gcc tct cgc agt gct ggg gag ctc gtt gag agc ctc     1588
Ser Met Gln Leu Ala Ser Arg Ser Ala Gly Glu Leu Val Glu Ser Leu
426                 431                 436                 441
```

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aaa ctc atg agc ctc tgc ctc ggc tcc cag ctt cat ggg agc acc aag      1636
Lys Leu Met Ser Leu Cys Leu Gly Ser Gln Leu His Gly Ser Thr Lys
442                 447                 452                 457

tac att att gat cca cag aat ggc ttg tca ttt tcc agt gtg aaa gtc      1684
Tyr Ile Ile Asp Pro Gln Asn Gly Leu Ser Phe Ser Ser Val Lys Val
458                 463                 468                 473

caa gag aaa tct acg tgg aaa atg tgc att agc tcc aca ggg aat gca      1732
Gln Glu Lys Ser Thr Trp Lys Met Cys Ile Ser Ser Thr Gly Asn Ala
474                 479                 484                 489

ggg cag gtc cct gca gtg ggc ggc ata aag ttt ttc tct gac cac atg      1780
Gly Gln Val Pro Ala Val Gly Gly Ile Lys Phe Phe Ser Asp His Met
490                 495                 500                 505

gca gat acc acc act gaa ttg gaa cgg ata aag agc aag aac ctg aaa      1828
Ala Asp Thr Thr Thr Glu Leu Glu Arg Ile Lys Ser Lys Asn Leu Lys
506                 511                 516                 521

aat aac gtg ctg cag cta cct ctg tgc gaa aag acc atc tct gtg aac      1876
Asn Asn Val Leu Gln Leu Pro Leu Cys Glu Lys Thr Ile Ser Val Asn
522                 527                 532                 537

atc cag cgg aac cct aag gag ggg ctg ctg tgc gca tcc agc cca gcc      1924
Ile Gln Arg Asn Pro Lys Glu Gly Leu Leu Cys Ala Ser Ser Pro Ala
538                 543                 548                 553

agc tgt tgc cat gtc atc tga ct gtggccccat ctggccgcta gcacgcttcc      1977
Ser Cys Cys His Val Ile  *
554                 559

tgctcagagc agtgaagacc ggctcacttc actgttccat ttggttttac tattttaaag   2037

tgggcgttag gagcaattat ttattacctt tccatttgtt cgcctgatga tgtgacaatg   2097

catggtcttt gtgcatgctg ctagacactt ttctttccca gccgaaaagc ctattatgta   2157

atttttacat tcataatttt aatgtggatg atcaggatta aatcaagata tatatctgga   2217

acctcttata aatggagcac ttagaaattt gttgttctgc acttaaccta gagagagaaa   2277

aaatgctttt tctttgtgaa aaatctgaat tcctgtcctg accttctgtg atgtggaaac   2337

cctaggctct gagacacact ctctggtgtc tgagacagaa ccaaagcaat aacgttgtga   2397

tgcccacagg cctggagcca gctagcgacc ttgtgccgcc cagctgtcca tggcccgtgc   2457

agagcagagg acagtgagtg tctgcactga gaaccttaaa ccacagttga acatacccac   2517

acctgtttgt cttaagctat agtgtaaaaa caaagtttgg gctctgaaaa tttaactgaa   2577

aaagatttcc ttgtttttgt aataggtgag ataaagtact tagatttata agggcagctt   2637

cccctgtagt gataaattac aagcagacaa tcttattttg taatgtgatg aagtgatgat   2697

gtcttaactc tacttagaga gtgtatgtct gtctaacaga acaaaaagat gctctgtgta   2757
```

Sequence Listing

aattccttcc tgtagggcac actgcaggat ttccatgtag atagaagaac tatagggcct 2817

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ggaatttggt ttttaggagt ttggtaatta gattatctct tttgttattt tcattcagtt 2937

atatcctttg ggctcagcta gctttgaaat tggctgatga aaaaatatac ataaaagggt 2997

aaaattcaca catacagcaa acaaaaatgc acaaagcctg cttcgtaact ttttttctg 3057

gaattgtttt tcactttgcc tttttctgcc aaaacaataa tcaaagaact cttgctttaa 3117

cctattcctg tacaaagact gtttttgacc agataatcat ctgttgtggc attctatctt 3177

gtaggacact gtatattgca aattgctgat tatggaaggg gccagttgct gttttttcat 3237

gcagtgccct gggagtctta aaagcagtgc ttagcaacat tggtgatagc atgtggctgg 3297

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acgcatctgg tcctgtaatt cagagagtgg gcacatcacc aaagaactgc attgctgtgg 3417

tcactgtttc ttcaagtaca cactgactct gctactttag gataaatata ttttactcag 3477

aactctgaat ttcacagtat acttactaaa ctaagtaaaa atgatactta aaatacttat 3537

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ataatttgaa agctatgaga atagatgtgt gggtgaagcc atagaacata tttgcttgaa 3657

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attatagcct tattagttgt gtggttgacc cttggggtat acaaatgtca gtctgagtgg 4017

tgtcttactc ctttgtttat aagtgaatga ttgtgcatgt tttgtatgtc atagtatgtc 4077

gtcacataaa agggagggag cgaaaaacca ttacattaag ataatattgg accaaactac 4137

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acagtagtgt ataaattaaa tattgtggaa aaacagtctt gtatttttct gtatgtgtgt 4257

atatatatat ataattatgt acttctggca attctatctg tatttaaaga tgtgacaatc 4317

ttgacaccaa ttttaagaat agctgtgaga ccgaattaaa gataatccct accaagtgaa 4377

aattgatgtg tgttaagagg gtacagaatt atcaactgat ttggtcagtt gcttccaatg 4437

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ctggttgatt tccctcattg tgtaaacatt gacaggtatg tgacaaatgg gaaaaaaaat   4497

ccaaataata aagtgacata ttggtgttca gcaataaaaa aaaaaa                  4543
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<213> Homo sapiens

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<222> (62)..(517)

<400> 174

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c    atg gag cgc ccg gag ccc gag ctg atc cgg cag agc tgg cgg gca      106
     Met Glu Arg Pro Glu Pro Glu Leu Ile Arg Gln Ser Trp Arg Ala
       1               5                  10

gtg agc cgc agc ccg ctg gag cac ggc acc gtc ctg ttt gcc agg ctg      154
Val Ser Arg Ser Pro Leu Glu His Gly Thr Val Leu Phe Ala Arg Leu
 16                  21                  26                  31

ttt gcc ctg gag cct gac ctg ctg ccc ctc ttc cag tac aac tgc cgc      202
Phe Ala Leu Glu Pro Asp Leu Leu Pro Leu Phe Gln Tyr Asn Cys Arg
 32                  37                  42                  47

cag ttc tcc agc cca gag gac tgt ctc tcc tcg cct gag ttc ctg gac      250
Gln Phe Ser Ser Pro Glu Asp Cys Leu Ser Ser Pro Glu Phe Leu Asp
 48                  53                  58                  63

cac atc agg aag gtg atg ctc gtg att gat gct gca gtg acc aat gtg      298
His Ile Arg Lys Val Met Leu Val Ile Asp Ala Ala Val Thr Asn Val
 64                  69                  74                  79

gaa gac ctg tcc tca ctg gag gag tac ctt gcc agc ctg ggc agg aag      346
Glu Asp Leu Ser Ser Leu Glu Glu Tyr Leu Ala Ser Leu Gly Arg Lys
 80                  85                  90                  95

cac cgg gca gtg ggt gtg aag ctc agc tcc ttc tcg aca gtg ggt gag      394
His Arg Ala Val Gly Val Lys Leu Ser Ser Phe Ser Thr Val Gly Glu
 96                 101                 106                 111

tct ctg ctc tac atg ctg gag aag tgt ctg ggc cct gcc ttc aca cca      442
Ser Leu Leu Tyr Met Leu Glu Lys Cys Leu Gly Pro Ala Phe Thr Pro
112                 117                 122                 127

gcc aca cgg gct gcc tgg agc caa ctc tac ggg gcc gta gtg cag gcc      490
Ala Thr Arg Ala Ala Trp Ser Gln Leu Tyr Gly Ala Val Val Gln Ala
128                 133                 138                 143

atg agt cga ggc tgg gat ggc gag taa gaggc gaccccgccc ggcagccccc      542
Met Ser Arg Gly Trp Asp Gly Glu  *
```

```
144                 149

atccatctgt gtctgtctgt tggcctgtat ctgttgtagc ccaggctccc caagcttccc    602

tgcatcttgg tccttgtccc cttggccaca ctggagagg                           641
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<210> 175
<211> 3423
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (62)..(2047)

<400> 175

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aattgacatc gtcggcctcg cccggaattc ccgggtcgac ccacgcgtcc ggagcgattg     60

g    atg gtg gtg gga aag aga aag atg att att gaa gat gaa aca gag     106
     Met Val Val Gly Lys Arg Lys Met Ile Ile Glu Asp Glu Thr Glu
       1               5                  10

ttt tgt ggg gaa gag ctg ctt cac agt gtg ttg cag tgt aag agc gtg     154
Phe Cys Gly Glu Glu Leu Leu His Ser Val Leu Gln Cys Lys Ser Val
 16                  21                  26                  31

ttt gat gtc ttg gat ggg gaa gag atg cgg cga gct cgg act cgg gcc     202
Phe Asp Val Leu Asp Gly Glu Glu Met Arg Arg Ala Arg Thr Arg Ala
 32                  37                  42                  47

aat ccc tat gag atg atc cga gga gtc ttc ttt cta aac agg gca gca     250
Asn Pro Tyr Glu Met Ile Arg Gly Val Phe Phe Leu Asn Arg Ala Ala
 48                  53                  58                  63

atg aag atg gct aac atg gat ttt gta ttt gat cgc atg ttc aca aat     298
Met Lys Met Ala Asn Met Asp Phe Val Phe Asp Arg Met Phe Thr Asn
 64                  69                  74                  79

ccg cgg gac tct tat ggg aag cca ctg gtg aag gac cgg gaa gct gag     346
Pro Arg Asp Ser Tyr Gly Lys Pro Leu Val Lys Asp Arg Glu Ala Glu
 80                  85                  90                  95

ctt ctg tac ttt gct gat gtc tgc gca ggc cca ggt ggc ttc tca gag     394
Leu Leu Tyr Phe Ala Asp Val Cys Ala Gly Pro Gly Gly Phe Ser Glu
 96                 101                 106                 111

tat gtg ctg tgg agg aag aag tgg cat gca aag ggc ttt gga atg act     442
Tyr Val Leu Trp Arg Lys Lys Trp His Ala Lys Gly Phe Gly Met Thr
112                 117                 122                 127

ttg aag ggc cct aat gac ttc aag ctg gag gac ttc tac tct gct tcc     490
Leu Lys Gly Pro Asn Asp Phe Lys Leu Glu Asp Phe Tyr Ser Ala Ser
128                 133                 138                 143
```

```
agt gaa ctc ttc gaa ccc tac tat ggt gag ggt ggg att gat gga gat      538
Ser Glu Leu Phe Glu Pro Tyr Tyr Gly Glu Gly Gly Ile Asp Gly Asp
144                 149                 154                 159

gga gat atc acc cgc cca gag aac atc tct gct ttt cgg aat ttt gtc      586
Gly Asp Ile Thr Arg Pro Glu Asn Ile Ser Ala Phe Arg Asn Phe Val
160                 165                 170                 175

ctg gat aac aca gat cgc aag ggt gtc cat ttt ctg atg gct gat ggg      634
Leu Asp Asn Thr Asp Arg Lys Gly Val His Phe Leu Met Ala Asp Gly
176                 181                 186                 191

ggt ttc tcg gtg gag ggg cag gag aac ctg cag gag atc ctc agc aag      682
Gly Phe Ser Val Glu Gly Gln Glu Asn Leu Gln Glu Ile Leu Ser Lys
192                 197                 202                 207

cag ctg ctt ctg tgt cag ttc ctc atg gcg ctg tcc att gtc cgg aca      730
Gln Leu Leu Leu Cys Gln Phe Leu Met Ala Leu Ser Ile Val Arg Thr
208                 213                 218                 223

gga ggc cac ttc atc tgt aaa acc ttt gac ctg ttc aca ccg ttt agt      778
Gly Gly His Phe Ile Cys Lys Thr Phe Asp Leu Phe Thr Pro Phe Ser
224                 229                 234                 239

gtg ggg ctt gtc tac ctg ctg tac tgc tgc ttt gaa cga gtt tgt ctc      826
Val Gly Leu Val Tyr Leu Leu Tyr Cys Cys Phe Glu Arg Val Cys Leu
240                 245                 250                 255

ttc aag cct att acc agc cgt cct gcc aac tca gag agg tat gtg gtg      874
Phe Lys Pro Ile Thr Ser Arg Pro Ala Asn Ser Glu Arg Tyr Val Val
256                 261                 266                 271

tgc aag ggc ctg aag gtg ggc ata gat gat gtt cgg gat tac ctc ttc      922
Cys Lys Gly Leu Lys Val Gly Ile Asp Asp Val Arg Asp Tyr Leu Phe
272                 277                 282                 287

gca gtg aat att aaa ctc aat cag ctg cgg aac acg gat tcc gac gtc      970
Ala Val Asn Ile Lys Leu Asn Gln Leu Arg Asn Thr Asp Ser Asp Val
288                 293                 298                 303

aac ttg gtg gtc ccc ctg gag gtg atc aag gga gac cat gaa ttt act     1018
Asn Leu Val Val Pro Leu Glu Val Ile Lys Gly Asp His Glu Phe Thr
304                 309                 314                 319

gac tac atg ata cgg tcc aat gag agc cac tgt agt ctg cag atc aaa     1066
Asp Tyr Met Ile Arg Ser Asn Glu Ser His Cys Ser Leu Gln Ile Lys
320                 325                 330                 335

gct ctg gcg aaa atc cat gcc ttt gtt caa gac acg aca ctg agt gag     1114
Ala Leu Ala Lys Ile His Ala Phe Val Gln Asp Thr Thr Leu Ser Glu
336                 341                 346                 351

cct cga cag gca gag ata cgg aag gag tgc ctc cga ctc tgg ggg atc     1162
Pro Arg Gln Ala Glu Ile Arg Lys Glu Cys Leu Arg Leu Trp Gly Ile
352                 357                 362                 367

cca gac cag gct cgt gtg gct cct tct tcc tcc gac cct aaa tcg aag     1210
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Pro Asp Gln Ala Arg Val Ala Pro Ser Ser Ser Asp Pro Lys Ser Lys
368                 373                 378                 383

ttc ttt gag cta atc cag ggc act gag att gac atc ttc agc tac aag     1258
Phe Phe Glu Leu Ile Gln Gly Thr Glu Ile Asp Ile Phe Ser Tyr Lys
384                 389                 394                 399

ccc aca ctg ctc acc tct aaa acc ctg gag aag atc cgc cct gtg ttt     1306
Pro Thr Leu Leu Thr Ser Lys Thr Leu Glu Lys Ile Arg Pro Val Phe
400                 405                 410                 415

gac tac cgc tgc atg gta tct ggc agt gag cag aag ttc ctc atc ggc     1354
Asp Tyr Arg Cys Met Val Ser Gly Ser Glu Gln Lys Phe Leu Ile Gly
416                 421                 426                 431

ctg ggg aaa tcc cag atc tac aca tgg gat ggc cgc cag tca gac cgc     1402
Leu Gly Lys Ser Gln Ile Tyr Thr Trp Asp Gly Arg Gln Ser Asp Arg
432                 437                 442                 447

tgg atc aag cta gac ctg aag aca gag ctg ccc cgg gac act ctg cta     1450
Trp Ile Lys Leu Asp Leu Lys Thr Glu Leu Pro Arg Asp Thr Leu Leu
448                 453                 458                 463

tct gtg gaa att gtg cat gag ctg aaa ggg gag ggg aag gcc cag agg     1498
Ser Val Glu Ile Val His Glu Leu Lys Gly Glu Gly Lys Ala Gln Arg
464                 469                 474                 479

aag atc agt gcc atc cac atc ctc gat gtc ctt gtg ctg aat ggc acc     1546
Lys Ile Ser Ala Ile His Ile Leu Asp Val Leu Val Leu Asn Gly Thr
480                 485                 490                 495

gac gtt cgg gag cag cac ttt aac cag cga att cag ctt gcc gag aaa     1594
Asp Val Arg Glu Gln His Phe Asn Gln Arg Ile Gln Leu Ala Glu Lys
496                 501                 506                 511

ttt gtg aaa gcc gtt tcc aag cct agt cga ccc gac atg aat ccc atc     1642
Phe Val Lys Ala Val Ser Lys Pro Ser Arg Pro Asp Met Asn Pro Ile
512                 517                 522                 527

agg gtg aag gag gtg tac aga ctg gaa gag atg gag aag att ttt gtc     1690
Arg Val Lys Glu Val Tyr Arg Leu Glu Glu Met Glu Lys Ile Phe Val
528                 533                 538                 543

agg ttg gag atg aag atc atc aag ggc tcc agt ggc acc cca aag ctc     1738
Arg Leu Glu Met Lys Ile Ile Lys Gly Ser Ser Gly Thr Pro Lys Leu
544                 549                 554                 559

agc tac aca ggg cgt gat gac cgg cac ttt gta ccc atg ggc ctc tac     1786
Ser Tyr Thr Gly Arg Asp Asp Arg His Phe Val Pro Met Gly Leu Tyr
560                 565                 570                 575

atc gtc agg aca gtg aat gag ccc tgg act atg gga ttc agc aaa agc     1834
Ile Val Arg Thr Val Asn Glu Pro Trp Thr Met Gly Phe Ser Lys Ser
576                 581                 586                 591

ttc aag aag aag ttc ttc tac aac aag aaa acc aag gac tct act ttt     1882
Phe Lys Lys Lys Phe Phe Tyr Asn Lys Lys Thr Lys Asp Ser Thr Phe
```

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592                 597                 602                 607

gac ctc cct gca gac tcc att gcc cca ttt cac att tgc tac tat ggc     1930
Asp Leu Pro Ala Asp Ser Ile Ala Pro Phe His Ile Cys Tyr Tyr Gly
608                 613                 618                 623

cgg ctc ttc tgg gag tgg ggg gat ggc att cgt gtg cat gac tcc cag     1978
Arg Leu Phe Trp Glu Trp Gly Asp Gly Ile Arg Val His Asp Ser Gln
624                 629                 634                 639

aag ccc cag gac cag gac aag ctg tcc aag gag gac gtc ctc tcc ttc     2026
Lys Pro Gln Asp Gln Asp Lys Leu Ser Lys Glu Asp Val Leu Ser Phe
640                 645                 650                 655

atc cag atg cac agg gcc taa ga gcctcagaat gtgccacccc tgcagaatgc     2079
Ile Gln Met His Arg Ala  *
656                 661

cctgtcattc ctgagatggg gccacctggg gcccacagtg ctggcttctt ccccctcttg   2139

aaaagggact ggggagcatt gcacctggca tgaggagtgg gtggcctcct ctccatcccc   2199

tgaagagctc aggcagggcc ctgcagagaa cactcatgtt ccttctggga cacctgcctg   2259

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agctccctta ctacccttcc ccttcctttt tcttccctaa taggaggtac aatctgcttt   3039

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tacctctcag agatgttcat gcaggctccc tagggcccca tcccagtgcc caggctggtt   3219

tccatggaga tagggcactg aggctcccgt gaggttggaa tcgacttcac catgggggtc   3279
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cttcagccag catccagctc cccaccccca ggctggcagt agcactgctg agatgctgta   3339

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acatattttt aaaaaaaaaa aaaa                                          3423
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<210> 176
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<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (100)..(798)

<400> 176

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cttctgaatc gaagttcaag tcccgcggac actgcaacc   atg aag gag aga cgg     114
                                             Met Lys Glu Arg Arg
                                               1

gcc ccc cag cca gtc gtg gcc aga tgt aag ctc gtt ctg gtc ggg gac     162
Ala Pro Gln Pro Val Val Ala Arg Cys Lys Leu Val Leu Val Gly Asp
  6                  11                  16                  21

gtg cag tgt ggg aag acc gcg atg ttg caa gtg tta gcg aag gat tgc     210
Val Gln Cys Gly Lys Thr Ala Met Leu Gln Val Leu Ala Lys Asp Cys
 22                  27                  32                  37

tat cca gag acc tat gtg ccc acc gtg ttc gaa aat tac aca gcc tgt     258
Tyr Pro Glu Thr Tyr Val Pro Thr Val Phe Glu Asn Tyr Thr Ala Cys
 38                  43                  48                  53

ttg gag aca gag gaa cag agg gtg gag ctt agt ctc tgg gat acc tca     306
Leu Glu Thr Glu Glu Gln Arg Val Glu Leu Ser Leu Trp Asp Thr Ser
 54                  59                  64                  69

gga tct ccc tac tac gat aat gtc cgt cca ctc tgc tac agc gac tcg     354
Gly Ser Pro Tyr Tyr Asp Asn Val Arg Pro Leu Cys Tyr Ser Asp Ser
 70                  75                  80                  85

gat gca gta tta cta tgt ttt gac atc agc cgt cca gag aca gtg gac     402
Asp Ala Val Leu Leu Cys Phe Asp Ile Ser Arg Pro Glu Thr Val Asp
 86                  91                  96                 101

agc gca ctc aag aag tgg agg aca gaa atc cta gat tat tgt ccc agc     450
Ser Ala Leu Lys Lys Trp Arg Thr Glu Ile Leu Asp Tyr Cys Pro Ser
102                 107                 112                 117

acc cgc gtt ttg ctc att ggc tgc aag aca gac ctg cga aca gac ctg     498
Thr Arg Val Leu Leu Ile Gly Cys Lys Thr Asp Leu Arg Thr Asp Leu
118                 123                 128                 133
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agt act ctg atg gag ctg tcc cac cag aag cag gcg ccc atc tcc tat      546
Ser Thr Leu Met Glu Leu Ser His Gln Lys Gln Ala Pro Ile Ser Tyr
134                 139                 144                 149

gag cag ggt tgt gca ata gca aag cag ctg ggt gca gaa atc tac ctg      594
Glu Gln Gly Cys Ala Ile Ala Lys Gln Leu Gly Ala Glu Ile Tyr Leu
150                 155                 160                 165

gaa ggc tca gct ttc acc tca gaa aag agc atc cac agc atc ttt cgg      642
Glu Gly Ser Ala Phe Thr Ser Glu Lys Ser Ile His Ser Ile Phe Arg
166                 171                 176                 181

acg gca tcc atg ctg tgt ctg aac aag cct agc cca ctg ccc cag aag      690
Thr Ala Ser Met Leu Cys Leu Asn Lys Pro Ser Pro Leu Pro Gln Lys
182                 187                 192                 197

agc cct gtc cga agc ctc tcc aaa cga ctg ctc cac ctc ccc agt cgc      738
Ser Pro Val Arg Ser Leu Ser Lys Arg Leu Leu His Leu Pro Ser Arg
198                 203                 208                 213

tct gaa ctc atc tct tct acc ttc aag aag gaa aag gcc aaa agc tgt      786
Ser Glu Leu Ile Ser Ser Thr Phe Lys Lys Glu Lys Ala Lys Ser Cys
214                 219                 224                 229

tcc att atg tga agt ggaaattgga ggggggagac aacccccctac ttcctccctt      841
Ser Ile Met  *
230

ggggtgcaga ggcacgggga gagggaggat gagacaattt aggacactgg acatgagttt    901

ttcaaatggc cacggtgagg gcttggaagg agacaggaat ggggcgagga aggagccagg    961

cccggcatga ggacctgacg ctgagagaga accatcatac cccaagccag gcactagatt   1021

ttggaggggg cgactacccc agtgcccccc cccgctccag aggaaggaaa gctgtggggg   1081

acgggggggca tgctggcctc atgggcttgg gggcctacag cagcctcacc ttcagcttca  1141

tgcctcttcc acacagcgtt tccatgcagg tcaggggatg ggaggggtcc ctgagccctt   1201

cccttcccct ctaaggaggc agcaacggca gagtggggaa gtggagcggc agctcccttg   1261

ggggcttagc ccaggtgctt cgtaactgca atcggaagtg caggagctgg tcagagccaa   1321

tgagaaggaa acctcatctt tgcatagccc atgcctcatg gagaggtgac atcatacatt   1381

cacatgcttc tcacctaagt ccccagggtc caagggagaa gccccagacc cccttctctt   1441

gcagagtgtg ggggtggtgg tgctgcaggg gcagggctgg gtgggggtca ccagactttt   1501

tctgccctta gggtagtaca gctggcattt gttttataga ctcttgtctt tggaattggg   1561

gggaggggggg gagtgtttca atctgttata tgttctgtgt ttaatgaaga aaacctattt   1621

attaatgaaa aatataatac atataaagaa aaaaaaaa                           1659
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US 9,550,838 B2

<210> 177
<211> 1382
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (103)..(657)

<400> 177
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aatgaaatcg atgacatccg cgccggaatt cccgggtcga cccacgcgtc cgccctggtc     60

cgcgggcgag ctcgagcagc caaccccggg cgcgtcgggg cc   atg gac ggc ctg     114
                                                 Met Asp Gly Leu
                                                   1

agg cag cgc gtg gag cac ttc ctg gag caa agg aac ctg gtc acc gaa      162
Arg Gln Arg Val Glu His Phe Leu Glu Gln Arg Asn Leu Val Thr Glu
  5                  10                  15                  20

gtg ctg ggg gcg ctg gag gcc aag acc ggg gtg gag aag cgg tat ctg      210
Val Leu Gly Ala Leu Glu Ala Lys Thr Gly Val Glu Lys Arg Tyr Leu
 21                  26                  31                  36

gct gca gga gcc gtc act ctg cta agc ctg tat ctg ctg ttc ggc tac      258
Ala Ala Gly Ala Val Thr Leu Leu Ser Leu Tyr Leu Leu Phe Gly Tyr
 37                  42                  47                  52

gga gcg tct ctg ctg tgc aat ctc atc gga ttt gtg tac ccc gca tat      306
Gly Ala Ser Leu Leu Cys Asn Leu Ile Gly Phe Val Tyr Pro Ala Tyr
 53                  58                  63                  68

gcc tca atc aaa gct atc gag agc cca agc aag gac gac gac act gtg      354
Ala Ser Ile Lys Ala Ile Glu Ser Pro Ser Lys Asp Asp Asp Thr Val
 69                  74                  79                  84

tgg ctc acc tac tgg gtg gtg tac gcc ctg ttt ggg ctg gcc gag ttc      402
Trp Leu Thr Tyr Trp Val Val Tyr Ala Leu Phe Gly Leu Ala Glu Phe
 85                  90                  95                 100

ttc agc gat cta ctc ctg tcc tgg ttc cct ttc tac tac gtg ggc aag      450
Phe Ser Asp Leu Leu Leu Ser Trp Phe Pro Phe Tyr Tyr Val Gly Lys
101                 106                 111                 116

tgc gcc ttc ctg ttg ttc tgc atg gct ccc agg ccc tgg aac ggg gct      498
Cys Ala Phe Leu Leu Phe Cys Met Ala Pro Arg Pro Trp Asn Gly Ala
117                 122                 127                 132

ctc atg ctg tat cag cgc gtc gtg cgt ccg ctg ttc cta agg cac cac      546
Leu Met Leu Tyr Gln Arg Val Val Arg Pro Leu Phe Leu Arg His His
133                 138                 143                 148

ggg gcc gta gac aga atc atg aac gac ctc agc ggg cga gcc ctg gac      594
Gly Ala Val Asp Arg Ile Met Asn Asp Leu Ser Gly Arg Ala Leu Asp
```

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149                 154                 159                 164

gcg gcg gcc gga ata acc agg aac gtc aag cca agc cag acc ccg cag      642
Ala Ala Ala Gly Ile Thr Arg Asn Val Lys Pro Ser Gln Thr Pro Gln
165                 170                 175                 180

ccg aag gac aag tga agcagccccc tgagcctcac aaggacctcc tggctggtga      697
Pro Lys Asp Lys  *
181

ggaggggcc gcgccaggct cccaggcctc cacagagtct tcagcgcatc ccccaacagc    757

agcccctgcc agtccctcgg gtccaggcaa ggccctgggg gtctccttaa atgccacctc    817

gggcaagtcc cagtcccagt cctcggccac ccccagctct ggatcccagg gccagctgcc    877

ctctggctct ggctgtggct cccgcctgtc cggcagggcc cagggccagc gtcgggcaca    937

gggcagctcc cactggtctc ggcaacacac ccagccgcct ggtacttcct ccagcccctc    997

ccagtcagcc ctcccgtcct cggggcccct gcagccaccc aacgtcacct ccagcccggt   1057

ctcacccatg gtccagtctc ccagcagcag caacatcccc acgcagcccc ccagcaagtc   1117

ctctggcaag ccggaggacg cagcccccaa gaccagcgga cagcgccaga aggaatcgtc   1177

gaaacagcct gccagcagcg cctcagtgcc cgagctggtc ccctgccatt ccgggacctc   1237

tctggagtac acttcggagt ccaccaccga gatcacctgc agctggccac accacaggcc   1297

cccgtgcctg cagcactact ggtgcctgaa acacctggcc tgctaggagg ctccaataaa   1357

gctaacccgg accagaaaaa aaaaa                                         1382
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<210> 178
<211> 1365
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (348)..(1037)

<400> 178

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acccacgcgt ccggacttct tcagctaaag aaaattgtgg agacgggcca gatgccagga     60

tccctgaaaa gagaccatat actgtaccat ttgatactca tttggggcat tatatttata    120

tcccatcaag acaagattcc aggaggggga atcacttgca aggtccacac aagtccgcct    180

atgtactctc tggatcgaat atttgctgga tttcgaacac aaagtcagat gctgttggat    240

cacgtagaag aacgagatga ggtcctccac tgccaatttt ctgataacag tgatgatgaa    300
```

```
gaatcagaag gccaagagaa atctggaact agatgtagaa gtcgttc  atg gat tca     356
                                                      Met Asp Ser
                                                        1

gaa gcc aga ctc tgt tcc ctt gtt gaa ttg agt gat act cag gat gaa     404
Glu Ala Arg Leu Cys Ser Leu Val Glu Leu Ser Asp Thr Gln Asp Glu
  4                   9                  14                  19

aca caa aag tca gat tcg gag aat gaa gat tta aag att gat tgt ctc     452
Thr Gln Lys Ser Asp Ser Glu Asn Glu Asp Leu Lys Ile Asp Cys Leu
 20                  25                  30                  35

cag gag agt caa gaa ttg aat ttg caa aaa tta aag aat tca gaa cgc     500
Gln Glu Ser Gln Glu Leu Asn Leu Gln Lys Leu Lys Asn Ser Glu Arg
 36                  41                  46                  51

ata ctt act gaa gcc aaa caa aaa atg aga gaa ctt aca gtt aac atc     548
Ile Leu Thr Glu Ala Lys Gln Lys Met Arg Glu Leu Thr Val Asn Ile
 52                  57                  62                  67

aag atg aag gaa gat ctg att aaa gaa tta ata aaa aca ggt aac gat     596
Lys Met Lys Glu Asp Leu Ile Lys Glu Leu Ile Lys Thr Gly Asn Asp
 68                  73                  78                  83

gcc aag tct gta agc aag cag tat act ttg aaa gta aca aag cta gag     644
Ala Lys Ser Val Ser Lys Gln Tyr Thr Leu Lys Val Thr Lys Leu Glu
 84                  89                  94                  99

cat gat gca gaa cag gca aaa gtc gaa cta act gaa aca caa aag cag     692
His Asp Ala Glu Gln Ala Lys Val Glu Leu Thr Glu Thr Gln Lys Gln
100                 105                 110                 115

cta cag gag ctg gaa aac aaa gat ctt tct gat gtt gca atg aag gta     740
Leu Gln Glu Leu Glu Asn Lys Asp Leu Ser Asp Val Ala Met Lys Val
116                 121                 126                 131

aaa tta cag aaa gag ttt cgt aaa aag gtg gat gct gca aag ctg aga     788
Lys Leu Gln Lys Glu Phe Arg Lys Lys Val Asp Ala Ala Lys Leu Arg
132                 137                 142                 147

gtt cag gtc tta cag aag aag caa caa gat agt aag aaa ctg gca tca     836
Val Gln Val Leu Gln Lys Lys Gln Gln Asp Ser Lys Lys Leu Ala Ser
148                 153                 158                 163

ctg tca atc caa aat gag aaa cgt gct aat gaa cta gag cag agt gta     884
Leu Ser Ile Gln Asn Glu Lys Arg Ala Asn Glu Leu Glu Gln Ser Val
164                 169                 174                 179

gat cac atg aaa tat caa aag ata cag cta caa aga aaa cta caa gaa     932
Asp His Met Lys Tyr Gln Lys Ile Gln Leu Gln Arg Lys Leu Gln Glu
180                 185                 190                 195

gaa aat gaa aaa agg aag caa ctg gat gca gta att aag cgg gac cag     980
Glu Asn Glu Lys Arg Lys Gln Leu Asp Ala Val Ile Lys Arg Asp Gln
196                 201                 206                 211

caa aaa atc aaa gta ata ttg tca tac att cct gct aag tat aat atg    1028
```

```
Gln Lys Ile Lys Val Ile Leu Ser Tyr Ile Pro Ala Lys Tyr Asn Met
212                 217                 222                 227

aaa tgt taa acggctc agagctaacg aatccatggt cttcattcag ttggcttgtg     1084
Lys Cys  *
228

aagtatctat ccttgacttg cccttcactg ctgtccttat tcactttaaa gctttgttca   1144

tctacatagt aaaacctatt tattgaattt tgagtactgt cttgaaggct ttgacttcac   1204

aaaagaaggt acaatgataa tttctcttag gaggatccta actttaattg aagctgccaa   1264

aaacatgcat ttataaagcc agctttctaa ataataccta tcatttgaat aggattttct   1324

gttttcaaag tgctttgaca tgcattggcc atgtggctac c                       1365
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<210> 179
<211> 956
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (142)..(678)

<400> 179

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cgacccacgc gtccggacgc agcagccacc gccgcgtccc tctctccacg aggctgccgg     60

cttaggaccc ccagctccga cgtaagtccc tctcgcgcgc cacctccatc cgctgccccct    120

ctgcccacgg gccgggctca g  atg tcg ccc tct ggt cgc ctg tgt ctt ctc      171
                        Met Ser Pro Ser Gly Arg Leu Cys Leu Leu
                          1               5

acc atc gtt ggc ctg att ctc ccc acc aga gga cag acg ttg aaa gat      219
Thr Ile Val Gly Leu Ile Leu Pro Thr Arg Gly Gln Thr Leu Lys Asp
 11                  16                  21                  26

acc acg tcc agt tct tca gca gac gca act atc atg gac att cag gtc      267
Thr Thr Ser Ser Ser Ser Ala Asp Ala Thr Ile Met Asp Ile Gln Val
 27                  32                  37                  42

ccg aca cga gcc cca gat gca gtc tac aca gaa ctc cag ccc acc tct      315
Pro Thr Arg Ala Pro Asp Ala Val Tyr Thr Glu Leu Gln Pro Thr Ser
 43                  48                  53                  58

cca acc cca acc tgg cct gct gat gaa aca cca caa ccc cag acc cag      363
Pro Thr Pro Thr Trp Pro Ala Asp Glu Thr Pro Gln Pro Gln Thr Gln
 59                  64                  69                  74

acc cag caa ctg gaa gga acg gat ggg cct cta gtg aca gat cca gag      411
Thr Gln Gln Leu Glu Gly Thr Asp Gly Pro Leu Val Thr Asp Pro Glu
 75                  80                  85                  90
```

```
aca cac aag agc acc aaa gca gct cat ccc act gat gac acc acg acg      459
Thr His Lys Ser Thr Lys Ala Ala His Pro Thr Asp Asp Thr Thr Thr
 91                  96                  101                 106

ctc tct gag aga cca tcc cca agc aca gac gtc cag aca gac ccc cag      507
Leu Ser Glu Arg Pro Ser Pro Ser Thr Asp Val Gln Thr Asp Pro Gln
107                 112                 117                 122

acc ctc aag cca tct ggt ttt cat gag gat gac ccc ttc ttc tat gat      555
Thr Leu Lys Pro Ser Gly Phe His Glu Asp Asp Pro Phe Phe Tyr Asp
123                 128                 133                 138

gaa cac acc ctc cgg aaa cgg ggg ctg ttg gtc gca gct gtg ctg ttc      603
Glu His Thr Leu Arg Lys Arg Gly Leu Leu Val Ala Ala Val Leu Phe
139                 144                 149                 154

atc aca ggc atc atc atc ctc acc agt ggc aag tgc agg cag ctg tcc      651
Ile Thr Gly Ile Ile Ile Leu Thr Ser Gly Lys Cys Arg Gln Leu Ser
155                 160                 165                 170

cgg tta tgc cgg aat cat tgc agg tga gtcca tcagaaacag gagctgacaa      703
Arg Leu Cys Arg Asn His Cys Arg  *
171                 176

cccgctgggc acccgaagac caagcccccc gccagctcac cgtgcccagc ctcctgcatc    763

ccctcgaaga gcctggccag agagggaaga cacagatgat gaagctggag ccagggctgc    823

cggtccgagt ctcctacctc ccccaaccct gcccgccccc gaaggctacc tggcgccttg    883

ggggctgtcc ctcaagttat ctcctctgtt aagacaaaaa gtaaagcact gtggtctttg    943

ctaaaaaaaa aaa                                                       956
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<210> 180
<211> 1748
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (189)..(506)

<400> 180

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aattggaagc cttgagttga gacccgtgtt gcagggtcga cccacgcgtg cgcccacgcg     60

tccggtgagc ttcctggagc ccagagatga gaagataaag atgccgctcc tacgaggact    120

gctgtggctc caggtgctgt gtgcgggccc tctccataca gaggctgtgg tacttctggt    180

tccttctg atg atg ggc gtg ctt ttc tgc tgc gga gcc ggc ttc ttc atc     230
         Met Met Gly Val Leu Phe Cys Cys Gly Ala Gly Phe Phe Ile
           1               5                  10
```

```
cgg agg cgc atg tac ccc ccg ccg ctg atc gag gag cca gcc ttc aat      278
Arg Arg Arg Met Tyr Pro Pro Pro Leu Ile Glu Glu Pro Ala Phe Asn
 15                  20                  25                  30

gtg tcc tac acc agg cag ccc cca aat ccc ggc cca gga gcc cag cag      326
Val Ser Tyr Thr Arg Gln Pro Pro Asn Pro Gly Pro Gly Ala Gln Gln
 31                  36                  41                  46

ccg ggg ccg ccc tat tac acc gac cca gga gga ccg ggg atg aac cct      374
Pro Gly Pro Pro Tyr Tyr Thr Asp Pro Gly Gly Pro Gly Met Asn Pro
 47                  52                  57                  62

gtc ggg aat tcc atg gca atg gct ttc cag gtc cca ccc aac tca ccc      422
Val Gly Asn Ser Met Ala Met Ala Phe Gln Val Pro Pro Asn Ser Pro
 63                  68                  73                  78

cag ggg agt gtg gcc tgc ccg ccc cct cca gcc tac tgc aac acg cct      470
Gln Gly Ser Val Ala Cys Pro Pro Pro Pro Ala Tyr Cys Asn Thr Pro
 79                  84                  89                  94

ccg ccc ccg tac gaa cag gta gtg aag gcc aag tag tggg gtgcccacgt      520
Pro Pro Pro Tyr Glu Gln Val Val Lys Ala Lys  *
 95                 100                 105

gcaagaggag agacaggaga gggcctttcc ctggcctttc tgtcttcgtt gatgttcact    580

tccaggaacg gtctcgtggg ctgctaaggg cagttcctct gatatcctca cagcaagcac    640

agctctcttt caggctttcc atggagtaca atatatgaac tcacactttg tctcctctgt    700

tgcttctgtt tctgacgcag tctgtgctct cacatggtag tgtggtgaca gtccccgagg    760

gctgacgtcc ttacggtggc gtgaccagat ctacaggaga gagactgaga ggaagaaggc    820

agtgctggag gtgcaggtgg catgtagagg ggccaggccg agcatcccag gcaagcatcc    880

ttctgcccgg gtattaatag gaagccccat gccgggcggc tcagccgatg aagcagcagc    940

cgactgagct gagcccagca ggtcatctgc tccagcctgt cctctcgtca gccttcctct   1000

tccagaagct gttggagaga cattcaggag agagcaagcc ccttgtcatg tttctgtctc   1060

tgttcatatc ctaaagatag acttctcctg caccgccagg gaagggtagc acgtgcagct   1120

ctcaccgcag gatggggcct agaatcaggc ttgccttgga ggcctgacag tgatctgaca   1180

tccactaagc aaatttattt aaattcatgg gaaatcactt cctgccccaa actgagacat   1240

tgcattttgt gagctcttgg tctgatttgg agaaaggact gttacccatt tttttggtgt   1300

gtttatggaa gtgcatgtag agcgtcctgc cctttgaaat cagactgggt gtgtgtcttc   1360

cctggacatc actgcctctc cagggcattc tcaggcccgg gggtctcctt ccctcaggca   1420

gctccagtgg tgggttctga agggtgcttt caaaacgggg cacatctggc tgggaagtca   1480
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Docket No. 2006-0660.00

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catggactct tccagggaga gagaccagct gaggcgtctc tctctgaggt tgtgttgggt   1540

ctaagcgggt gtgtgctggg ctccaaggag gaggagcttg ctgggaaaag acaggagaag   1600

tactgactca actgcactga ccatgttgtc ataattagaa taaagaagaa gtggtcggaa   1660

atgcacattc ctggatagga atcacagctc accccaggat ctcacaggta gtctcctgag   1720

tagttgacgg ctagcggggg agctagtt                                      1748
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<210> 181
<211> 2736
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (212)..(2443)

<400> 181

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cttgatcgcc tgcggtaccg gtccggaatt cccgggtcga cccacgcgtc cggttagagc     60

tcgggtctcc tcgccacagc tccgagtctt tcgttctggg aggcccaggc ggcttcgcgt    120

tctgagaata aacagaacct ctgttgctct gcgacttgca ggcactggga gattcgtagc    180

taagacgcca gggcatcccg gaagctggga a   atg gga ctg ttg aca ttc agg      232
                                     Met Gly Leu Leu Thr Phe Arg
                                       1               5

gat gtg gcc gta gaa ttc tct ttg gag gag tgg gaa cac ctg gaa cca      280
Asp Val Ala Val Glu Phe Ser Leu Glu Glu Trp Glu His Leu Glu Pro
  8                  13                  18                  23

gct cag aag aat ttg tat cag gat gtg atg tta gaa aac tac aga aac      328
Ala Gln Lys Asn Leu Tyr Gln Asp Val Met Leu Glu Asn Tyr Arg Asn
 24                  29                  34                  39

ctg gtc tct ctg ggt ctt gtt gtc tct aag ccg gac ctg atc acc ttt      376
Leu Val Ser Leu Gly Leu Val Val Ser Lys Pro Asp Leu Ile Thr Phe
 40                  45                  50                  55

ttg gaa caa agg aaa gag cct tgg aat gtg aag agt gag gag aca gta      424
Leu Glu Gln Arg Lys Glu Pro Trp Asn Val Lys Ser Glu Glu Thr Val
 56                  61                  66                  71

gcc atc cag cca gat gtg ttt tcg cat tat aac aag gac ctg ttg aca      472
Ala Ile Gln Pro Asp Val Phe Ser His Tyr Asn Lys Asp Leu Leu Thr
 72                  77                  82                  87

gag cac tgc aca gaa gct tca ttc caa aaa gtg ata tcg agg aga cat      520
Glu His Cys Thr Glu Ala Ser Phe Gln Lys Val Ile Ser Arg Arg His
 88                  93                  98                 103
```

```
ggg agc tgt gat ctt gag aat tta cat tta aga aaa agg tgg aaa agg      568
Gly Ser Cys Asp Leu Glu Asn Leu His Leu Arg Lys Arg Trp Lys Arg
104                 109                 114                 119

gag gag tgt gaa ggg cac aat gga tgt tat gat gaa aag act ttt aaa      616
Glu Glu Cys Glu Gly His Asn Gly Cys Tyr Asp Glu Lys Thr Phe Lys
120                 125                 130                 135

tat gat caa ttt gat gaa tcc tct gtt gaa agt ttg ttt cac cag caa      664
Tyr Asp Gln Phe Asp Glu Ser Ser Val Glu Ser Leu Phe His Gln Gln
136                 141                 146                 151

ata ctt tct tct tgt gcc aaa agc tat aac ttt gat caa tat agg aag      712
Ile Leu Ser Ser Cys Ala Lys Ser Tyr Asn Phe Asp Gln Tyr Arg Lys
152                 157                 162                 167

gtc ttt act cat tca tca ttg ctt aat caa caa gag gaa ata gat att      760
Val Phe Thr His Ser Ser Leu Leu Asn Gln Gln Glu Glu Ile Asp Ile
168                 173                 178                 183

tgg gga aaa cat cac ata tat gat aaa act tca gtg tta ttt agg cag      808
Trp Gly Lys His His Ile Tyr Asp Lys Thr Ser Val Leu Phe Arg Gln
184                 189                 194                 199

gtc tct act cta aat agt tac cga aat gtt ttt att gga gag aaa aat      856
Val Ser Thr Leu Asn Ser Tyr Arg Asn Val Phe Ile Gly Glu Lys Asn
200                 205                 210                 215

tat cat tgc aat aat tct gaa aaa acc ttg aac caa agc tca agc cct      904
Tyr His Cys Asn Asn Ser Glu Lys Thr Leu Asn Gln Ser Ser Ser Pro
216                 221                 226                 231

aaa aat cat cag gaa aat tat ttt cta gaa aaa caa tac aaa tgt aaa      952
Lys Asn His Gln Glu Asn Tyr Phe Leu Glu Lys Gln Tyr Lys Cys Lys
232                 237                 242                 247

gaa ttt gag gaa gtc ttt ctt cag agt atg cat ggg caa gag aaa caa     1000
Glu Phe Glu Glu Val Phe Leu Gln Ser Met His Gly Gln Glu Lys Gln
248                 253                 258                 263

gaa cag tct tac aaa tgt aat aaa tgt gta gaa gtt tgt acc cag tca     1048
Glu Gln Ser Tyr Lys Cys Asn Lys Cys Val Glu Val Cys Thr Gln Ser
264                 269                 274                 279

tta aaa cat att caa cat cag acc atc cat atc aga gaa aac tca tat     1096
Leu Lys His Ile Gln His Gln Thr Ile His Ile Arg Glu Asn Ser Tyr
280                 285                 290                 295

agc tat aac aaa tat gat aaa gat ctt agt cag tca tca aat ctt aga     1144
Ser Tyr Asn Lys Tyr Asp Lys Asp Leu Ser Gln Ser Ser Asn Leu Arg
296                 301                 306                 311

aag cag ata atc cat aat gaa gag aaa cca tac aaa tgt gaa aaa tgt     1192
Lys Gln Ile Ile His Asn Glu Glu Lys Pro Tyr Lys Cys Glu Lys Cys
312                 317                 322                 327

ggg gat agc tta aac cat agt ttg cac ctt act caa cat cag atc att     1240
```

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Gly Asp Ser Leu Asn His Ser Leu His Leu Thr Gln His Gln Ile Ile
328                 333                 338                 343

cct acc gaa gag aaa ccc tat aaa tgg aaa gaa tgt ggc aag gtc ttt     1288
Pro Thr Glu Glu Lys Pro Tyr Lys Trp Lys Glu Cys Gly Lys Val Phe
344                 349                 354                 359

aac ctt aac tgt agt tta tac ctt act aaa cag cag caa att gat act     1336
Asn Leu Asn Cys Ser Leu Tyr Leu Thr Lys Gln Gln Gln Ile Asp Thr
360                 365                 370                 375

gga gaa aac ctt tac aaa tgt aaa gca tgt agc aaa tct ttt act cgt     1384
Gly Glu Asn Leu Tyr Lys Cys Lys Ala Cys Ser Lys Ser Phe Thr Arg
376                 381                 386                 391

tcc tcc aat ctt att gtg cat cag aga att cac act gga gag aaa cca     1432
Ser Ser Asn Leu Ile Val His Gln Arg Ile His Thr Gly Glu Lys Pro
392                 397                 402                 407

tac aaa tgt aaa gaa tgt ggc aaa gcc ttt cgc tgt agt tca tac ctt     1480
Tyr Lys Cys Lys Glu Cys Gly Lys Ala Phe Arg Cys Ser Ser Tyr Leu
408                 413                 418                 423

act aaa cat aag cga att cat act gga gag aaa cct tat aaa tgt aaa     1528
Thr Lys His Lys Arg Ile His Thr Gly Glu Lys Pro Tyr Lys Cys Lys
424                 429                 434                 439

gaa tgt gga aaa gct ttt aac cgt agt tca tgc ctt act caa cat cag     1576
Glu Cys Gly Lys Ala Phe Asn Arg Ser Ser Cys Leu Thr Gln His Gln
440                 445                 450                 455

aca act cat aca gga gaa aaa ctt tac aaa tgt aaa gta tgt agc aaa     1624
Thr Thr His Thr Gly Glu Lys Leu Tyr Lys Cys Lys Val Cys Ser Lys
456                 461                 466                 471

tct tat gct cgt tct tca aat ctt att atg cat cag aga gtt cat act     1672
Ser Tyr Ala Arg Ser Ser Asn Leu Ile Met His Gln Arg Val His Thr
472                 477                 482                 487

gga gag aag cct tat aaa tgt aaa gaa tgt ggc aaa gtc ttt agc cgt     1720
Gly Glu Lys Pro Tyr Lys Cys Lys Glu Cys Gly Lys Val Phe Ser Arg
488                 493                 498                 503

agt tct tgc ctt act caa cat cgg aaa att cat act gga gaa aat ctt     1768
Ser Ser Cys Leu Thr Gln His Arg Lys Ile His Thr Gly Glu Asn Leu
504                 509                 514                 519

tac aaa tgc aaa gta tgt gct aaa cct ttt act tgt ttc tca aat ctt     1816
Tyr Lys Cys Lys Val Cys Ala Lys Pro Phe Thr Cys Phe Ser Asn Leu
520                 525                 530                 535

att gtg cat gag aga att cat act gga gag aaa ccc tat aaa tgt aaa     1864
Ile Val His Glu Arg Ile His Thr Gly Glu Lys Pro Tyr Lys Cys Lys
536                 541                 546                 551

gaa tgt ggc aaa gcc ttt cct tat agt tca cac ctt att cga cat cat     1912
Glu Cys Gly Lys Ala Phe Pro Tyr Ser Ser His Leu Ile Arg His His
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552                 557                 562                 567

cga att cat act gga gaa aaa cca tac aaa tgt aaa gca tgt agc aaa     1960
Arg Ile His Thr Gly Glu Lys Pro Tyr Lys Cys Lys Ala Cys Ser Lys
568                 573                 578                 583

tct ttt agt gac tcc tca ggt ctt act gtg cat cgg cga act cat act     2008
Ser Phe Ser Asp Ser Ser Gly Leu Thr Val His Arg Arg Thr His Thr
584                 589                 594                 599

gga gag aaa ccc tat aca tgt aaa gaa tgt ggc aaa gcc ttt agt tat     2056
Gly Glu Lys Pro Tyr Thr Cys Lys Glu Cys Gly Lys Ala Phe Ser Tyr
600                 605                 610                 615

agt tca gat gtt att cag cat cgg aga att cat act ggc cag aga ccc     2104
Ser Ser Asp Val Ile Gln His Arg Arg Ile His Thr Gly Gln Arg Pro
616                 621                 626                 631

tac aaa tgt gaa gaa tgt ggc aaa gcc ttc aac tat agg tca tac ctc     2152
Tyr Lys Cys Glu Glu Cys Gly Lys Ala Phe Asn Tyr Arg Ser Tyr Leu
632                 637                 642                 647

act aca cat cag aga agt cat act gga gag aga ccc tac aaa tgt gaa     2200
Thr Thr His Gln Arg Ser His Thr Gly Glu Arg Pro Tyr Lys Cys Glu
648                 653                 658                 663

gaa tgt ggc aaa gcc ttc aac tct agg tca tac ctc act aca cat cgg     2248
Glu Cys Gly Lys Ala Phe Asn Ser Arg Ser Tyr Leu Thr Thr His Arg
664                 669                 674                 679

aga aga cat act gga gag aga ccc tac aaa tgt gat gaa tgt ggt aaa     2296
Arg Arg His Thr Gly Glu Arg Pro Tyr Lys Cys Asp Glu Cys Gly Lys
680                 685                 690                 695

gcc ttc agc tat agg tca tac ctc act aca cat cgg aga agt cat agt     2344
Ala Phe Ser Tyr Arg Ser Tyr Leu Thr Thr His Arg Arg Ser His Ser
696                 701                 706                 711

gga gag aga ccc tac aaa tgt gaa gaa tgt ggc aaa gcc ttt aac tct     2392
Gly Glu Arg Pro Tyr Lys Cys Glu Glu Cys Gly Lys Ala Phe Asn Ser
712                 717                 722                 727

agg tca tac ctc att gca cat cag aga agt cat act aga gaa aaa ctt     2440
Arg Ser Tyr Leu Ile Ala His Gln Arg Ser His Thr Arg Glu Lys Leu
728                 733                 738                 743

taa aaat gtaaaacatg gagcagattt tttacttgtt acccatgtct tattgtgcat     2497
 *
744

cagataattt atatgggagt gaaaccctac aaatgttaag aatgtggcat aacctttaac   2557

tattttcaag ccttacacaa tagcagagaa tataaactga aaaaatccat acaaatatta   2617

aaaatgtggc aaattatttt aaactgtgct caacccttac tcaagataat ccatactaga   2677

gaaacactat agatgtaaaa atgtgaaaag ttttattcaa aatatcaaac ttatgagtc    2736
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<213> Homo sapiens

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atccactagt ccagtgtggt ggaattcccc ggctcctggt cccactgctg ctcagcccag 120

tggcctcaca ggacaccagc ttcccaggag gcgtctgaca cagt atg atg atg aag 176
Met Met Met Lys
1

atc cca tgg ggc agc atc cca gta ctg atg ttg ctc ctg ctc ctg ggc 224
Ile Pro Trp Gly Ser Ile Pro Val Leu Met Leu Leu Leu Leu Leu Gly
5 10 15 20

cta atc gat atc tcc cag gcc cag ctc agc tgc acc ggg ccc cca gcc 272
Leu Ile Asp Ile Ser Gln Ala Gln Leu Ser Cys Thr Gly Pro Pro Ala
21 26 31 36

atc cct ggc atc ccg ggt atc cct ggg aca cct ggc ccc gat ggc caa 320
Ile Pro Gly Ile Pro Gly Ile Pro Gly Thr Pro Gly Pro Asp Gly Gln
37 42 47 52

cct ggg acc cca ggg ata aaa gga gag aaa ggg ctt cca ggg ctg gct 368
Pro Gly Thr Pro Gly Ile Lys Gly Glu Lys Gly Leu Pro Gly Leu Ala
53 58 63 68

gga gac cat ggt gag ttc gga gag aag gga gac cca ggg att cct ggg 416
Gly Asp His Gly Glu Phe Gly Glu Lys Gly Asp Pro Gly Ile Pro Gly
69 74 79 84

aat cca gga aaa gtc ggc ccc aag ggc ccc atg ggc cct aaa ggt ggc 464
Asn Pro Gly Lys Val Gly Pro Lys Gly Pro Met Gly Pro Lys Gly Gly
85 90 95 100

cca ggg gcc cct gga gcc cca ggc ccc aaa ggt gaa tcg gga gac tac 512
Pro Gly Ala Pro Gly Ala Pro Gly Pro Lys Gly Glu Ser Gly Asp Tyr
101 106 111 116

aag gcc acc cag aaa atc gcc ttc tct gcc aca aga acc atc aac gtc 560
Lys Ala Thr Gln Lys Ile Ala Phe Ser Ala Thr Arg Thr Ile Asn Val
117 122 127 132

ccc ctg cgc cgg gac cag acc atc cgc ttc gac cac gtg atc acc aac 608
Pro Leu Arg Arg Asp Gln Thr Ile Arg Phe Asp His Val Ile Thr Asn
133 138 143 148

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atg aac aac aat tat gag ccc cgc agt ggc aag ttc acc tgc aag gtg      656
Met Asn Asn Asn Tyr Glu Pro Arg Ser Gly Lys Phe Thr Cys Lys Val
149                 154                 159                 164

ccc ggt ctc tac tac ttc acc tac cac gcc agc tct cga ggg aac ctg      704
Pro Gly Leu Tyr Tyr Phe Thr Tyr His Ala Ser Ser Arg Gly Asn Leu
165                 170                 175                 180

tgc gtg aac ctc atg cgt ggc cgg gag cgt gca cag aag gtg gtc acc      752
Cys Val Asn Leu Met Arg Gly Arg Glu Arg Ala Gln Lys Val Val Thr
181                 186                 191                 196

ttc tgt gac tat gcc tac aac acc ttc cag gtc acc acc ggt ggc atg      800
Phe Cys Asp Tyr Ala Tyr Asn Thr Phe Gln Val Thr Thr Gly Gly Met
197                 202                 207                 212

gtc ctc aag ctg gag cag ggg gag aac gtc ttc ctg cag gcc acc gac      848
Val Leu Lys Leu Glu Gln Gly Glu Asn Val Phe Leu Gln Ala Thr Asp
213                 218                 223                 228

aag aac tca cta ctg ggc atg gag ggt gcc aac agc atc ttt tcc ggg      896
Lys Asn Ser Leu Leu Gly Met Glu Gly Ala Asn Ser Ile Phe Ser Gly
229                 234                 239                 244

ttc ctg ctc ttt cca gat atg gag gcc tga c ctgtgggctg cttcacatcc      947
Phe Leu Leu Phe Pro Asp Met Glu Ala  *
245                 250

accccggctc cccctgccag caacgctcac tctaccccca acaccacccc ttgcccagcc   1007

aatgcacaca gtagggcttg gtgaatgctg ctgagtgaat gagtaaataa actcttcaag   1067

gccaagggac agtggtctaa ttcaactctg tgtcccagca cctggcacac cagaagtgcc   1127

atgctcagaa atgttggtta catgaatgaa tgaaccatga atgaatgaaa aaaaaaaa     1185
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<210> 183
<211> 1704
<212> DNA
<213> Homo sapiens

<220>
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<222> (131)..(1258)

<400> 183

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ttgacgctgc tgaatccgcc gagcaccccct ggcgtaacac cgcgggccgt caggggctgc     60

ggccccgggc tgcgccctcc cccgcggcca ggctctggag ggacccagga gctgccgccg    120

gcctcagccc   atg gcc cgg agg tat gat gag ctg ccg cac tac cca ggc     169
             Met Ala Arg Arg Tyr Asp Glu Leu Pro His Tyr Pro Gly
               1               5                  10
```

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atc gtg gat ggc ccc gca gcc ctg gct agc ttc cca gag aca gtg ccc      217
Ile Val Asp Gly Pro Ala Ala Leu Ala Ser Phe Pro Glu Thr Val Pro
 14                  19                  24                  29

gca gta cca ggg ccc tat ggc ccg cac cgg cct ccc cag ccc ctg ccc      265
Ala Val Pro Gly Pro Tyr Gly Pro His Arg Pro Pro Gln Pro Leu Pro
 30                  35                  40                  45

cca ggc ttg gac agc gac ggc ctg aag agg gag aag gat gag atc tat      313
Pro Gly Leu Asp Ser Asp Gly Leu Lys Arg Glu Lys Asp Glu Ile Tyr
 46                  51                  56                  61

gga cac ccg ctc ttc ccc ctc ttg gcc ctg gtc ttt gag aaa tgt gaa      361
Gly His Pro Leu Phe Pro Leu Leu Ala Leu Val Phe Glu Lys Cys Glu
 62                  67                  72                  77

ctg gct aca tgc tct ccc cgt gac ggg gcc gga gct ggg ctg ggg aca      409
Leu Ala Thr Cys Ser Pro Arg Asp Gly Ala Gly Ala Gly Leu Gly Thr
 78                  83                  88                  93

ccc cct gga ggt gac gtc tgc tcc tct gat tcc ttc aac gag gac atc      457
Pro Pro Gly Gly Asp Val Cys Ser Ser Asp Ser Phe Asn Glu Asp Ile
 94                  99                  104                 109

gct gcc ttt gcc aag cag gtt cgc tct gag agg ccc ctc ttc tcc tcc      505
Ala Ala Phe Ala Lys Gln Val Arg Ser Glu Arg Pro Leu Phe Ser Ser
110                 115                 120                 125

aac cca gaa ctg gac aat ctg gtg atc cag gcc atc cag gtg ctg cgg      553
Asn Pro Glu Leu Asp Asn Leu Val Ile Gln Ala Ile Gln Val Leu Arg
126                 131                 136                 141

ttc cac ctg ctg gag ctg gag aag gtc cac gac ctg tgc gac aac ttc      601
Phe His Leu Leu Glu Leu Glu Lys Val His Asp Leu Cys Asp Asn Phe
142                 147                 152                 157

tgt cac cgc tac atc acc tgc ctc aag gga aag atg ccc atc gac ctg      649
Cys His Arg Tyr Ile Thr Cys Leu Lys Gly Lys Met Pro Ile Asp Leu
158                 163                 168                 173

gtc atc gag gat cgg gac ggc ggc tgc agg gag gac ttc gag gac tac      697
Val Ile Glu Asp Arg Asp Gly Gly Cys Arg Glu Asp Phe Glu Asp Tyr
174                 179                 184                 189

cca gcc tcc tgc ccc agc ctc cca gac cag aat aat atg tgg att cga      745
Pro Ala Ser Cys Pro Ser Leu Pro Asp Gln Asn Asn Met Trp Ile Arg
190                 195                 200                 205

gac cat gag gat agt ggg tct gta cat ttg ggg acc cca ggt cca tcc      793
Asp His Glu Asp Ser Gly Ser Val His Leu Gly Thr Pro Gly Pro Ser
206                 211                 216                 221

agt ggg ggc ctg gcc tcc cag agt ggg gac aac tcc agt gac caa gga      841
Ser Gly Gly Leu Ala Ser Gln Ser Gly Asp Asn Ser Ser Asp Gln Gly
222                 227                 232                 237
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gac ggg ctg gac acc agc gtg gcc tct ccc agt tct ggt gga gaa gat      889
Asp Gly Leu Asp Thr Ser Val Ala Ser Pro Ser Ser Gly Gly Glu Asp
238                 243                 248                 253

gag gac ttg gac cag gag cga cgg cga aac aag aag agg ggg atc ttc      937
Glu Asp Leu Asp Gln Glu Arg Arg Arg Asn Lys Lys Arg Gly Ile Phe
254                 259                 264                 269

ccc aag gtg gcc acc aac atc atg cga gcc tgg ttg ttc cag cac ctc      985
Pro Lys Val Ala Thr Asn Ile Met Arg Ala Trp Leu Phe Gln His Leu
270                 275                 280                 285

tcg cac ccg tac ccc tcg gag gag cag aag aaa cag ctg gcg cag gac     1033
Ser His Pro Tyr Pro Ser Glu Glu Gln Lys Lys Gln Leu Ala Gln Asp
286                 291                 296                 301

acg ggg ctc acc atc ctg caa gtc aac aac tgg ttc att aac gcc cgg     1081
Thr Gly Leu Thr Ile Leu Gln Val Asn Asn Trp Phe Ile Asn Ala Arg
302                 307                 312                 317

aga cgc atc gtg caa cct atg atc gat caa tcc aac cgc aca ggg cag     1129
Arg Arg Ile Val Gln Pro Met Ile Asp Gln Ser Asn Arg Thr Gly Gln
318                 323                 328                 333

ggt gca gcc ttc agc cca gag ggc cag ccc atc ggg ggc tat acc gag     1177
Gly Ala Ala Phe Ser Pro Glu Gly Gln Pro Ile Gly Gly Tyr Thr Glu
334                 339                 344                 349

acg cag cca cac gtg gcc gtc cgg cct ccg gga tca gtg ggg atg agt     1225
Thr Gln Pro His Val Ala Val Arg Pro Pro Gly Ser Val Gly Met Ser
350                 355                 360                 365

ttg aac ttg gaa gga gaa tgg cat tat cta tag aggctgat gcaggagaga     1276
Leu Asn Leu Glu Gly Glu Trp His Tyr Leu  *
366                 371                 376

cccagcctcc ggctgtgacc cccagcctca cacctgcctc tggttcccgc ctggtcctcc   1336

agcttcagga ccccacctcc aaaggcccct ctgctcaatg cctacctccc tagggccctg   1396

ctgggacatg ggggcctgag tgcccatcca agggctctca aggacaccgg caaggcctcc   1456

aggccctgag ccccacttct gccttcacct ctgcctggga cccgagctgg gctcctgggc   1516

cttggtcccc agaagatggc ggctagggcc tcgccgccag gacagagaag ggacggggtg   1576

gctgggcagt cagggaagga gggtcgcccg gatccgacat tttggagaga ttccttcact   1636

ctcctgtccc ccctacctcc cttctctaat ttcttctttt ttttaatgat aaagtcttaa   1696

aaacacgg                                                            1704
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<212> DNA
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gacgggggg gcccagagaa gggggcctcg ggcgccccgc ctgcgcctgc tgccccgcc 120

ccggcggtaa tgcgctcctg cccgtgaccc ccgctggggg cgggggccgg ggtccatgcg 180

cggagtcccc acccggcccg gcgcctgccg ctaacgacgg cgggggtggg ggggcgcgcg 240

cctgacctcc tgcccacacc ctggcgtcaa caccgcgggc cgtcaggggc tgcggccccg 300

ggctgcgccc tcccccgcgg ccaggctctg gagggaccca ggagctgccg ccggcctcag 360

ccc atg gcc cgg agg tat gat gag ctg ccg cac tac cca ggc atc gtg 408
Met Ala Arg Arg Tyr Asp Glu Leu Pro His Tyr Pro Gly Ile Val
1 5 10

gat ggc ccc gca gcc ctg gct agc ttc cca gag aca gtg ccc gca gta 456
Asp Gly Pro Ala Ala Leu Ala Ser Phe Pro Glu Thr Val Pro Ala Val
16 21 26 31

cca ggg ccc tat ggc ccg cac cgg cct ccc cag ccc ctg ccc cca ggc 504
Pro Gly Pro Tyr Gly Pro His Arg Pro Pro Gln Pro Leu Pro Pro Gly
32 37 42 47

ttg gac agc gac ggc ctg aag agg gag aag gat gag atc tat gga cac 552
Leu Asp Ser Asp Gly Leu Lys Arg Glu Lys Asp Glu Ile Tyr Gly His
48 53 58 63

ccg ctc ttc ccc ctc ttg gcc ctg gtc ttt gag aaa tgt gaa ctg gct 600
Pro Leu Phe Pro Leu Leu Ala Leu Val Phe Glu Lys Cys Glu Leu Ala
64 69 74 79

aca tgc tct ccc cgt gac ggg gcc gga gct ggg ctg ggg aca ccc cct 648
Thr Cys Ser Pro Arg Asp Gly Ala Gly Ala Gly Leu Gly Thr Pro Pro
80 85 90 95

gga ggt gac gtc tgc tcc tct gat tcc ttc aac gag gac atc gct gcc 696
Gly Gly Asp Val Cys Ser Ser Asp Ser Phe Asn Glu Asp Ile Ala Ala
96 101 106 111

ttt gcc aag cag gtt cgc tct gag agg ccc ctc ttc tcc tcc aac cca 744
Phe Ala Lys Gln Val Arg Ser Glu Arg Pro Leu Phe Ser Ser Asn Pro
112 117 122 127

gaa ctg gac aat ctg atg atc cag gcc atc caa gtg ctg cgg ttc cac 792
Glu Leu Asp Asn Leu Met Ile Gln Ala Ile Gln Val Leu Arg Phe His
128 133 138 143

ctg ctg gag ctg gag aag gga aag atg ccc atc gac ctg gtc atc gag 840

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Leu Leu Glu Leu Glu Lys Gly Lys Met Pro Ile Asp Leu Val Ile Glu
144                 149                 154                 159

gat cgg gat ggc ggc tgc agg gag gac ttc gag gac tac cca gcc tcc      888
Asp Arg Asp Gly Gly Cys Arg Glu Asp Phe Glu Asp Tyr Pro Ala Ser
160                 165                 170                 175

tgc ccc agc ctc cca gac cag aat aat ata tgg att cga gac cat gag      936
Cys Pro Ser Leu Pro Asp Gln Asn Asn Ile Trp Ile Arg Asp His Glu
176                 181                 186                 191

gat agc ggg tct gta cat ttg ggg acc cca ggt cca tcc agc ggg ggg      984
Asp Ser Gly Ser Val His Leu Gly Thr Pro Gly Pro Ser Ser Gly Gly
192                 197                 202                 207

ctg gcc tcc cag agt ggg gac aac tcc agt gac caa gga gtc ggg ctg     1032
Leu Ala Ser Gln Ser Gly Asp Asn Ser Ser Asp Gln Gly Val Gly Leu
208                 213                 218                 223

gac acc agc gtg gcc tct ccc agt tct ggt gga gaa gat gag gac ttg     1080
Asp Thr Ser Val Ala Ser Pro Ser Ser Gly Gly Glu Asp Glu Asp Leu
224                 229                 234                 239

gac cag gag cca cgg cga aac aag aag agg ggg atc ttc ccc aag gtg     1128
Asp Gln Glu Pro Arg Arg Asn Lys Lys Arg Gly Ile Phe Pro Lys Val
240                 245                 250                 255

gcc acc aac atc atg cga gcc tgg ttg ttc cag cac ctc tca cac ccg     1176
Ala Thr Asn Ile Met Arg Ala Trp Leu Phe Gln His Leu Ser His Pro
256                 261                 266                 271

tac ccc tcg gag gag cag aag aaa cag ctg gcg cag gac acg ggg ctt     1224
Tyr Pro Ser Glu Glu Gln Lys Lys Gln Leu Ala Gln Asp Thr Gly Leu
272                 277                 282                 287

acc atc ctg caa gtc aac aac tgg ttc att aat gcc cgg aga cgc atc     1272
Thr Ile Leu Gln Val Asn Asn Trp Phe Ile Asn Ala Arg Arg Arg Ile
288                 293                 298                 303

gtg caa cct atg atc gat caa tcc aac cgc aca ggg cag ggt gca gcc     1320
Val Gln Pro Met Ile Asp Gln Ser Asn Arg Thr Gly Gln Gly Ala Ala
304                 309                 314                 319

ttc agc cca gag ggc cag ccc atc ggg ggc tat acc gag aca gag cca     1368
Phe Ser Pro Glu Gly Gln Pro Ile Gly Gly Tyr Thr Glu Thr Glu Pro
320                 325                 330                 335

cac gtg gcc ttc cgg gct cca gca tca gtg ggg gat gag ttt gga act     1416
His Val Ala Phe Arg Ala Pro Ala Ser Val Gly Asp Glu Phe Gly Thr
336                 341                 346                 351

cgg aag gag gaa tgg cat tat cta tag aggct gatgcgggag agacccagcc     1468
Arg Lys Glu Glu Trp His Tyr Leu  *
352                 357

tccggctgtg acccccagcc tcacacctgg ctctggttcc cgcctggtcc tctggcttca   1528
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ggatcccacc tccaaaggcc tctccgctca acgcctacct ccctagggcc ctgctgggac 1588

atgggggcct gagtgcccac ccaaggggct ctcaaggaca ccggcaaggc ctccaggctc 1648

tgagccccgc ttctgccttc acctctgcct gggacccgag ctgggctcct gggccttggt 1708

ccccagaaga tggcagctag ggcctcgccg cgaggacaga gaagggacag ggtggctggg 1768

cagtcaggga aggagggtcg cccggatccg acattttgga gagattcttt caccctcctg 1828

tccccccccac ctcccttctc taatttcttc ttttttttaat gataaagtct taaaacacag 1888

aaaaaaaaaa gacttcagag aattaggtag atgaagcact ttatacagta tatatcttca 1948

gcttaaattt gttttgagta tttttttttat ttttaagtag gcaaagattt aaaatttttt 2008

atttttagta aatgtttgaa gcaaactaaa aagacgtggg caatatttac cacaaccaaa 2068

cagaacccac aaaattgtac atcttgatct tagcaaatat ccttattgta gagacactta 2128

ataaagagat ggtattttaa tatctccagt tctgaggtag ggtgtaactt agttctacat 2188

tgtgatttag gaatttttaa acctttcttc ttcaggggag aagtgaccca ggcctcgagt 2248

ttagtgctaa agccactagt gtacttatgc tgtcacctaa ccaccacatg cgacatggag 2308

gcagaggcta aatatagggg ctttcttaag aaagtgagag gaaattagca agcattatta 2368

gtgtttgact actgctatca agtgaattca aaggaaacag gtttttatgt catatttaag 2428

ttacagaaac caggcatgct tagaatagtt tctaaggtga cagagcggcc gc 2480

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<211> 2531
<212> DNA
<213> Homo sapiens

<220>
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<222> (364)..(1494)

<400> 185
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gacgggggg gcccagagaa gggggcctcg ggcgccccgc ctgcgcctgc tgccccgcc 120

ccggcggtaa tgcgctcctg cccgtgaccc ccgctggggg cgggggccgg ggtccatgcg 180

cggagtcccc acccggcccg gcgcctgccg ctaacgacgg cgggggtggg ggggcgcgcg 240

cctgacctcc tgcccacacc ctggcgtcaa caccgcgggc cgtcaggggc tgcggccccg 300

ggctgcgccc tcccccgcgg ccaggctctg gagggaccca ggagctgccg ccggcctcag 360

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ccc  atg gcc cgg agg tat gat gag ctg ccg cac tac cca ggc atc gtg      408
     Met Ala Arg Arg Tyr Asp Glu Leu Pro His Tyr Pro Gly Ile Val
       1               5                  10

gat ggc ccc gca gcc ctg gct agc ttc cca gag aca gtg ccc gca gta      456
Asp Gly Pro Ala Ala Leu Ala Ser Phe Pro Glu Thr Val Pro Ala Val
 16                  21                  26                  31

cca ggg ccc tat ggc ccg cac cgg cct ccc cag ccc ctg ccc cca ggc      504
Pro Gly Pro Tyr Gly Pro His Arg Pro Pro Gln Pro Leu Pro Pro Gly
 32                  37                  42                  47

ttg gac agc gac ggc ctg aag agg gag aag gat gag atc tat gga cac      552
Leu Asp Ser Asp Gly Leu Lys Arg Glu Lys Asp Glu Ile Tyr Gly His
 48                  53                  58                  63

ccg ctc ttc ccc ctc ttg gcc ctg gtc ttt gag aaa tgt gaa ctg gct      600
Pro Leu Phe Pro Leu Leu Ala Leu Val Phe Glu Lys Cys Glu Leu Ala
 64                  69                  74                  79

aca tgc tct ccc cgt gac ggg gcc gga gct ggg ctg ggg aca ccc cct      648
Thr Cys Ser Pro Arg Asp Gly Ala Gly Ala Gly Leu Gly Thr Pro Pro
 80                  85                  90                  95

gga ggt gac gtc tgc tcc tct gat tcc ttc aac gag gac atc gct gcc      696
Gly Gly Asp Val Cys Ser Ser Asp Ser Phe Asn Glu Asp Ile Ala Ala
 96                 101                 106                 111

ttt gcc aag cag gtt cgc tct gag agg ccc ctc ttc tcc tcc aac cca      744
Phe Ala Lys Gln Val Arg Ser Glu Arg Pro Leu Phe Ser Ser Asn Pro
112                 117                 122                 127

gaa ctg gac aat ctg atg atc cag gcc atc caa gtg ctg cgg ttc cac      792
Glu Leu Asp Asn Leu Met Ile Gln Ala Ile Gln Val Leu Arg Phe His
128                 133                 138                 143

ctg ctg gag ctg gag aag gtc cac gac ctg tgc gac aac ttc tgt cac      840
Leu Leu Glu Leu Glu Lys Val His Asp Leu Cys Asp Asn Phe Cys His
144                 149                 154                 159

cgc tac atc acc tgc ctc aag gga aag atg ccc atc gac ctg gtc atc      888
Arg Tyr Ile Thr Cys Leu Lys Gly Lys Met Pro Ile Asp Leu Val Ile
160                 165                 170                 175

gag gat cgg gat ggc ggc tgc agg gag gac ttc gag gac tac cca gcc      936
Glu Asp Arg Asp Gly Gly Cys Arg Glu Asp Phe Glu Asp Tyr Pro Ala
176                 181                 186                 191

tcc tgc ccc agc ctc cca gac cag aat aat ata tgg att cga gac cat      984
Ser Cys Pro Ser Leu Pro Asp Gln Asn Asn Ile Trp Ile Arg Asp His
192                 197                 202                 207

gag gat agc ggg tct gta cat ttg ggg acc cca ggt cca tcc agc ggg     1032
Glu Asp Ser Gly Ser Val His Leu Gly Thr Pro Gly Pro Ser Ser Gly
208                 213                 218                 223

ggg ctg gcc tcc cag agt ggg gac aac tcc agt gac caa gga gtc ggg     1080
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Gly Leu Ala Ser Gln Ser Gly Asp Asn Ser Ser Asp Gln Gly Val Gly
224                 229                 234                 239

ctg gac acc agc gtg gcc tct ccc agt tct ggt gga gaa gat gag gac     1128
Leu Asp Thr Ser Val Ala Ser Pro Ser Ser Gly Gly Glu Asp Glu Asp
240                 245                 250                 255

ttg gac cag gag cca cgg cga aac aag aag agg ggg atc ttc ccc aag     1176
Leu Asp Gln Glu Pro Arg Arg Asn Lys Lys Arg Gly Ile Phe Pro Lys
256                 261                 266                 271

gtg gcc acc aac atc atg cga gcc tgg ttg ttc cag cac ctc tca cac     1224
Val Ala Thr Asn Ile Met Arg Ala Trp Leu Phe Gln His Leu Ser His
272                 277                 282                 287

ccg tac ccc tcg gag gag cag aag aaa cag ctg gcg cag gac acg ggg     1272
Pro Tyr Pro Ser Glu Glu Gln Lys Lys Gln Leu Ala Gln Asp Thr Gly
288                 293                 298                 303

ctt acc atc ctg caa gtc aac aac tgg ttc att aat gcc cgg aga cgc     1320
Leu Thr Ile Leu Gln Val Asn Asn Trp Phe Ile Asn Ala Arg Arg Arg
304                 309                 314                 319

atc gtg caa cct atg atc gat caa tcc aac cgc aca ggg cag ggt gca     1368
Ile Val Gln Pro Met Ile Asp Gln Ser Asn Arg Thr Gly Gln Gly Ala
320                 325                 330                 335

gcc ttc agc cca gag ggc cag ccc atc ggg ggc tat acc gag aca gag     1416
Ala Phe Ser Pro Glu Gly Gln Pro Ile Gly Gly Tyr Thr Glu Thr Glu
336                 341                 346                 351

cca cac gtg gcc ttc cgg gct cca gca tca gtg ggg gat gag ttt gga     1464
Pro His Val Ala Phe Arg Ala Pro Ala Ser Val Gly Asp Glu Phe Gly
352                 357                 362                 367

act cgg aag gag gaa tgg cat tat cta tag a ggctgatgcg ggagagaccc     1515
Thr Arg Lys Glu Glu Trp His Tyr Leu  *
368                 373

agcctccggc tgtgaccccc agcctcacac ctggctctgg ttcccgcctg gtcctctggc   1575

ttcaggatcc cacctccaaa ggcctctccg ctcaacgcct acctccctag ggccctgctg   1635

ggacatgggg gcctgagtgc ccacccaagg ggctctcaag gacaccggca aggcctccag   1695

gctctgagcc ccgcttctgc cttcacctct gcctgggacc cgagctgggc tcctgggcct   1755

tggtccccag aagatggcag ctagggcctc gccgcgagga cagagaaggg acagggtggc   1815

tgggcagtca gggaaggagg gtcgcccgga tccgacattt tggagagatt ctttcaccct   1875

cctgtccccc ccacctccct tctctaattt cttctttttt taatgataaa gtcttaaaac   1935

acagaaaaaa aaaagacttc agagaattag gtagatgaag cactttatac agtatatatc   1995

ttcagcttaa atttgttttg agtatttttt ttatttttaa gtaggcaaag atttaaaatt   2055
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Confidential - Subject to Protective Order

ttttatttt agtaaatgtt tgaagcaaac taaaaagacg tgggcaatat ttaccacaac 2115

caaacagaac ccacaaaatt gtacatcttg atcttagcaa atatccttat tgtagagaca 2175

cttaataaag agatggtatt ttaatatctc cagttctgag gtagggtgta acttagttct 2235

acattgtgat ttaggaattt ttaaaccttt cttcttcagg ggagaagtga cccaggcctc 2295

gagtttagtg ctaaagccac tagtgtactt atgctgtcac ctaaccacca catgcgacat 2355

ggaggcagag gctaaatata ggggctttct taagaaagtg agaggaaatt agcaagcatt 2415

attagtgttt gactactgct atcaagtgaa ttcaaaggaa acaggttttt atgtcatatt 2475

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<400> 186
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gacgggggg gcccagagaa gggggcctcg ggcgccccgc ctgcgcctgc tgccccgcc 120

ccggcggtaa tgcgctcctg cccgtgaccc ccgctggggg cgggggccgg ggtccatgcg 180

cggagtcccc acccggcccg gcgcctgccg ctaacgacgg cgggggtggg ggggcgcgcg 240

cctgacctcc tgcccacacc ctggcgtcaa caccgcgggc cgtcaggggc tgcggccccg 300

ggctgcgccc tcccccgcgg ccaggctctg gagggaccca ggagctgccg ccggcctcag 360

ccc atg gcc cgg agg tat gat gag ctg ccg cac tac cca ggc atc gtg 408
Met Ala Arg Arg Tyr Asp Glu Leu Pro His Tyr Pro Gly Ile Val
1 5 10

gat ggc ccc gca gcc ctg gct agc ttc cca gag aca gtg ccc gca gta 456
Asp Gly Pro Ala Ala Leu Ala Ser Phe Pro Glu Thr Val Pro Ala Val
16 21 26 31

cca ggg ccc tat ggc ccg cac cgg cct ccc cag ccc ctg ccc cca ggc 504
Pro Gly Pro Tyr Gly Pro His Arg Pro Pro Gln Pro Leu Pro Pro Gly
32 37 42 47

ttg gac agc gac ggc ctg aag agg gag aag gat gag atc tat gga cac 552
Leu Asp Ser Asp Gly Leu Lys Arg Glu Lys Asp Glu Ile Tyr Gly His
48 53 58 63

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ccg ctc ttc ccc ctc ttg gcc ctg gtc ttt gag aaa tgt gaa ctg gct      600
Pro Leu Phe Pro Leu Leu Ala Leu Val Phe Glu Lys Cys Glu Leu Ala
 64                  69                  74                  79

aca tgc tct ccc cgt gac ggg gcc gga gct ggg ctg ggg aca ccc cct      648
Thr Cys Ser Pro Arg Asp Gly Ala Gly Ala Gly Leu Gly Thr Pro Pro
 80                  85                  90                  95

gga ggt gac gtc tgc tcc tct gat tcc ttc aac gag gac atc gct gcc      696
Gly Gly Asp Val Cys Ser Ser Asp Ser Phe Asn Glu Asp Ile Ala Ala
 96                 101                 106                 111

ttt gcc aag cag gtt cgc tct gag agg ccc ctc ttc tcc tcc aac cca      744
Phe Ala Lys Gln Val Arg Ser Glu Arg Pro Leu Phe Ser Ser Asn Pro
112                 117                 122                 127

gaa ctg gac aat ctg gtc cac gac ctg tgc gac aac ttc tgt cac cgc      792
Glu Leu Asp Asn Leu Val His Asp Leu Cys Asp Asn Phe Cys His Arg
128                 133                 138                 143

tac atc acc tgc ctc aag gga aag atg ccc atc gac ctg gtc atc gag      840
Tyr Ile Thr Cys Leu Lys Gly Lys Met Pro Ile Asp Leu Val Ile Glu
144                 149                 154                 159

gat cgg gat ggc ggc tgc agg gag gac ttc gag gac tac cca gcc tcc      888
Asp Arg Asp Gly Gly Cys Arg Glu Asp Phe Glu Asp Tyr Pro Ala Ser
160                 165                 170                 175

tgc ccc agc ctc cca gac cag aat aat ata tgg att cga gac cat gag      936
Cys Pro Ser Leu Pro Asp Gln Asn Asn Ile Trp Ile Arg Asp His Glu
176                 181                 186                 191

gat agc ggg tct gta cat ttg ggg acc cca ggt cca tcc agc ggg ggg      984
Asp Ser Gly Ser Val His Leu Gly Thr Pro Gly Pro Ser Ser Gly Gly
192                 197                 202                 207

ctg gcc tcc cag agt ggg gac aac tcc agt gac caa gga gtc ggg ctg     1032
Leu Ala Ser Gln Ser Gly Asp Asn Ser Ser Asp Gln Gly Val Gly Leu
208                 213                 218                 223

gac acc agc gtg gcc tct ccc agt tct ggt gga gaa gat gag gac ttg     1080
Asp Thr Ser Val Ala Ser Pro Ser Ser Gly Gly Glu Asp Glu Asp Leu
224                 229                 234                 239

gac cag gag cca cgg cga aac aag aag agg ggg atc ttc ccc aag gtg     1128
Asp Gln Glu Pro Arg Arg Asn Lys Lys Arg Gly Ile Phe Pro Lys Val
240                 245                 250                 255

gcc acc aac atc atg cga gcc tgg ttg ttc cag cac ctc tca cac ccg     1176
Ala Thr Asn Ile Met Arg Ala Trp Leu Phe Gln His Leu Ser His Pro
256                 261                 266                 271

tac ccc tcg gag gag cag aag aaa cag ctg gcg cag gac acg ggg ctt     1224
Tyr Pro Ser Glu Glu Gln Lys Lys Gln Leu Ala Gln Asp Thr Gly Leu
272                 277                 282                 287

acc atc ctg caa gtc aac aac tgg ttc att aat gcc cgg aga cgc atc     1272
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Thr Ile Leu Gln Val Asn Asn Trp Phe Ile Asn Ala Arg Arg Arg Ile
288                 293                 298                 303

gtg caa cct atg atc gat caa tcc aac cgc aca ggg cag ggt gca gcc     1320
Val Gln Pro Met Ile Asp Gln Ser Asn Arg Thr Gly Gln Gly Ala Ala
304                 309                 314                 319

ttc agc cca gag ggc cag ccc atc ggg ggc tat acc gag aca gag cca     1368
Phe Ser Pro Glu Gly Gln Pro Ile Gly Gly Tyr Thr Glu Thr Glu Pro
320                 325                 330                 335

cac gtg gcc ttc cgg gct cca gca tca gtg ggg gat gag ttt gga act     1416
His Val Ala Phe Arg Ala Pro Ala Ser Val Gly Asp Glu Phe Gly Thr
336                 341                 346                 351

cgg aag gag gaa tgg cat tat cta tag aggct gatgcgggag agacccagcc     1468
Arg Lys Glu Glu Trp His Tyr Leu  *
352                 357

tccggctgtg acccccagcc tcacacctgg ctctggttcc cgcctggtcc tctggcttca   1528

ggatcccacc tccaaaggcc tctccgctca acgcctacct ccctagggcc ctgctgggac   1588

atgggggcct gagtgcccac ccaaggggct ctcaaggaca ccggcaaggc ctccaggctc   1648

tgagccccgc ttctgccttc acctctgcct gggacccgag ctgggctcct gggccttggt   1708

ccccagaaga tggcagctag ggcctcgccg cgaggacaga gaagggacag ggtggctggg   1768

cagtcaggga aggagggtcg cccggatccg acattttgga gagattcttt caccctcctg   1828

tccccccccac ctcccttctc taatttcttc ttttttttaat gataaagtct taaaacacag   1888

aaaaaaaaaa gacttcagag aattaggtag atgaagcact ttatacagta tatatcttca   1948

gcttaaattt gttttgagta tttttttttat ttttaagtag gcaaagattt aaaatttttt   2008

atttttagta aatgtttgaa gcaaactaaa aagacgtggg caatatttac cacaaccaaa   2068

cagaacccac aaaattgtac atcttgatct tagcaaatat ccttattgta gagacactta   2128

ataaagagat ggtattttaa tatctccagt tctgaggtag ggtgtaactt agttctacat   2188

tgtgatttag gaatttttaa acctttcttc ttcaggggag aagtgaccca ggcctcgagt   2248

ttagtgctaa agccactagt gtacttatgc tgtcacctaa ccaccacatg cgacatggag   2308

gcagaggcta aatatagggg ctttcttaag aaagtgagag gaaattagca agcattatta   2368

gtgtttgact actgctatca agtgaattca aaggaaacag gtttttatgt catatttaag   2428

ttacagaaac caggcatgct tagaatagtt tctaaggtga cagagcggcc gc           2480
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<210> 187

<211> 1964
<212> DNA
<213> Homo sapiens

<220>
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<222> (300)..(1742)

<220>
<221> misc_feature
<222> (1)...(1964)
<223> n = a,t,c or g

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gctgcggccc ttcccaggcc cccgaggcgt ttcgccgttc ccgaagcccg actgggggaa 120

gagtccagca ccaaagcggc cgttctcgga ttccggagcg ttctggagcc ccgagagacg 180

ccccggggtt ctagaagctc cccggcggcg cccagtcccg gcttcattcg ggcgtccctc 240

cgaaacccac tcgggtgcac gggtcgtcgg cgagccgcga ccgggtcctg gcgcgcacc 299

atg atc gtg gcg gac tcc gag tgc cgc gca gag ctc aag gac tac ctg 347
Met Ile Val Ala Asp Ser Glu Cys Arg Ala Glu Leu Lys Asp Tyr Leu
1 5 10 15

cgg ttc gcc ccg ggc ggc gtc ggc gac tcg ggc ccc gga gag gag cag 395
Arg Phe Ala Pro Gly Gly Val Gly Asp Ser Gly Pro Gly Glu Glu Gln
17 22 27 32

agg gag agc cgg gct cgg cga ggc cct cga ggg ccc agc gcc ttc atc 443
Arg Glu Ser Arg Ala Arg Arg Gly Pro Arg Gly Pro Ser Ala Phe Ile
33 38 43 48

ccc gtg gag gag gtc ctt cgg gag ggg gct gag agc ctc gag cag cac 491
Pro Val Glu Glu Val Leu Arg Glu Gly Ala Glu Ser Leu Glu Gln His
49 54 59 64

ctg ggg ctg gag gca ctg atg tcc tct ggg cga gta gac aac ctg gca 539
Leu Gly Leu Glu Ala Leu Met Ser Ser Gly Arg Val Asp Asn Leu Ala
65 70 75 80

gtg gtg atg ggc ctg cac cct gac tac ttt acc agc ttc tgg cgc ctg 587
Val Val Met Gly Leu His Pro Asp Tyr Phe Thr Ser Phe Trp Arg Leu
81 86 91 96

cac tac ctg ctg ctg cac acg gat ggt ccc ttg gcc agc tcc tgg cgc 635
His Tyr Leu Leu Leu His Thr Asp Gly Pro Leu Ala Ser Ser Trp Arg
97 102 107 112

cac tac att gcc atc atg gct gcc gcc cgc cat cag tgt tct tac ctg 683
His Tyr Ile Ala Ile Met Ala Ala Ala Arg His Gln Cys Ser Tyr Leu
113 118 123 128

gta ggc tcc cac atg gcc gag ttt ctg cag act ggt ggt gac cct gag 731

```
Val Gly Ser His Met Ala Glu Phe Leu Gln Thr Gly Gly Asp Pro Glu
129                 134                 139                 144

tgg ctg ctg ggc ctc cac cgg gcc ccc gag aag ctg cgc aaa ctc agc      779
Trp Leu Leu Gly Leu His Arg Ala Pro Glu Lys Leu Arg Lys Leu Ser
145                 150                 155                 160

gag atc aac aag ttg ctg gcg cat cgg cca tgg ctc atc acc aag gaa      827
Glu Ile Asn Lys Leu Leu Ala His Arg Pro Trp Leu Ile Thr Lys Glu
161                 166                 171                 176

cac atc cag gcc ttg ctg aag acc ggc gag cac act tgg tcc ctg gcc      875
His Ile Gln Ala Leu Leu Lys Thr Gly Glu His Thr Trp Ser Leu Ala
177                 182                 187                 192

gag ctc att cag gct ctg gtc ctg ctc acc cac tgc cac tcg ctc tcc      923
Glu Leu Ile Gln Ala Leu Val Leu Leu Thr His Cys His Ser Leu Ser
193                 198                 203                 208

tcc ttc gtg ttt ggc tgt ggc atc ctc cct gag ggg gat gca gat ggc      971
Ser Phe Val Phe Gly Cys Gly Ile Leu Pro Glu Gly Asp Ala Asp Gly
209                 214                 219                 224

agc cct gcc ccc cag gca cct aca ccc cct agt gaa cag agc agc ccc     1019
Ser Pro Ala Pro Gln Ala Pro Thr Pro Pro Ser Glu Gln Ser Ser Pro
225                 230                 235                 240

cca agc agg gac ccg ttg aac aac tct ggg ggc ttt gag tct gcc cgc     1067
Pro Ser Arg Asp Pro Leu Asn Asn Ser Gly Gly Phe Glu Ser Ala Arg
241                 246                 251                 256

gac gtg gag gcg ctg atg gag cgc atg cag cag ctg cag gag agc ctg     1115
Asp Val Glu Ala Leu Met Glu Arg Met Gln Gln Leu Gln Glu Ser Leu
257                 262                 267                 272

ctg cgg gat gag ggg acg tcc cag gag gag atg gag agc cgc ttt gag     1163
Leu Arg Asp Glu Gly Thr Ser Gln Glu Glu Met Glu Ser Arg Phe Glu
273                 278                 283                 288

ctg gag aag tca gag agc ctg ctg gtg acc ccc tca gct gac atc ctg     1211
Leu Glu Lys Ser Glu Ser Leu Leu Val Thr Pro Ser Ala Asp Ile Leu
289                 294                 299                 304

gag ccc tct cca cac cca gac atg ctg tgc ttt gtg gaa gac cct act     1259
Glu Pro Ser Pro His Pro Asp Met Leu Cys Phe Val Glu Asp Pro Thr
305                 310                 315                 320

ttc gga tat gag gac ttc act cgg aga ggg gct cag gca ccc cct acc     1307
Phe Gly Tyr Glu Asp Phe Thr Arg Arg Gly Ala Gln Ala Pro Pro Thr
321                 326                 331                 336

ttc cgg gcc cag gat tat acc tgg gaa gac cat ggc tac tcg ctg atc     1355
Phe Arg Ala Gln Asp Tyr Thr Trp Glu Asp His Gly Tyr Ser Leu Ile
337                 342                 347                 352

cag cgg ctt tac cct gag ggt ggg cag ctg ctg gat gag aag ttc cag     1403
Gln Arg Leu Tyr Pro Glu Gly Gly Gln Leu Leu Asp Glu Lys Phe Gln
```

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353                 358                 363                 368

gca gcc tat agc ctc acc tac aat acc atc gcc atg cac agt ggt gtg     1451
Ala Ala Tyr Ser Leu Thr Tyr Asn Thr Ile Ala Met His Ser Gly Val
369                 374                 379                 384

gac acc tcc gtg ctc cgc agg gcc atc tgg aac tat atc cac tgc gtc     1499
Asp Thr Ser Val Leu Arg Arg Ala Ile Trp Asn Tyr Ile His Cys Val
385                 390                 395                 400

ttt ggc atc aga tat gat gac tat gat tat ggg gag gtg aac cag ctc     1547
Phe Gly Ile Arg Tyr Asp Asp Tyr Asp Tyr Gly Glu Val Asn Gln Leu
401                 406                 411                 416

ctg gag cgg aac ctc aag gtc tat atc aag aca gtg gcc tgc tac cca     1595
Leu Glu Arg Asn Leu Lys Val Tyr Ile Lys Thr Val Ala Cys Tyr Pro
417                 422                 427                 432

gag aag acc acc cga aga atg tac aac ctc ttc tgg agg cac ttc cgc     1643
Glu Lys Thr Thr Arg Arg Met Tyr Asn Leu Phe Trp Arg His Phe Arg
433                 438                 443                 448

cac tca gag aag gtc cac gtg aac ttg ctg ctc ctg gag gcg cgc atg     1691
His Ser Glu Lys Val His Val Asn Leu Leu Leu Leu Glu Ala Arg Met
449                 454                 459                 464

caa gcc gct ctg ctg tac gcc ctc cgt gcc atc acc cgc tac atg acc     1739
Gln Ala Ala Leu Leu Tyr Ala Leu Arg Ala Ile Thr Arg Tyr Met Thr
465                 470                 475                 480

tga ctcc tgagcaggac ctgggcccgg ttcagcttcc cacaaggact tctctgtctg     1796
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481

gagacagccc cagacccttt tgtgtnccat gcccaccctc cccacgctgc agtgggcttg   1856

tgtgtgatgt gcagtcccga agccacaccc ttccttttttc tcactggaat ggacaagtca   1916

ttgcactgac tcttggatct caccctgct cctgggagct gaagagca                 1964
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<213> Homo sapiens

<220>
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<222> (42)..(1385)

<400> 188

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                                                  Met Gly Ala Gly
                                                    1
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cgg ctc ggc gcg ccc atg gag cgc cac ggc agg gct tcc gcc acc tcc      101
Arg Leu Gly Ala Pro Met Glu Arg His Gly Arg Ala Ser Ala Thr Ser
  5                  10                  15                  20

gtc tcg tcg gct ggg gag cag gcg gcc ggg gac ccc gaa ggg cgg cgg      149
Val Ser Ser Ala Gly Glu Gln Ala Ala Gly Asp Pro Glu Gly Arg Arg
 21                  26                  31                  36

cag gag cca ctg cgg cgc cgg gcg agc agc gcg tcg gtg ccc gcg gtc      197
Gln Glu Pro Leu Arg Arg Arg Ala Ser Ser Ala Ser Val Pro Ala Val
 37                  42                  47                  52

ggg gcc tcg gct gag ggc acg agg cgg gat cga ctg ggc tct tac agc      245
Gly Ala Ser Ala Glu Gly Thr Arg Arg Asp Arg Leu Gly Ser Tyr Ser
 53                  58                  63                  68

ggc ccc acc tcg gtc tcc cgc cag cgc gtc gaa agc ctg agg aaa aag      293
Gly Pro Thr Ser Val Ser Arg Gln Arg Val Glu Ser Leu Arg Lys Lys
 69                  74                  79                  84

cgg ccg ctt ttt cca tgg ttt gga ctg gat atc ggt gga act ctg gtc      341
Arg Pro Leu Phe Pro Trp Phe Gly Leu Asp Ile Gly Gly Thr Leu Val
 85                  90                  95                 100

aag ctg gta tat ttt gaa ccc aaa gac atc act gct gaa gaa gaa gag      389
Lys Leu Val Tyr Phe Glu Pro Lys Asp Ile Thr Ala Glu Glu Glu Glu
101                 106                 111                 116

gaa gaa gtg gaa agt ctt aaa agc att cgg aag tac ctg acc tcc aat      437
Glu Glu Val Glu Ser Leu Lys Ser Ile Arg Lys Tyr Leu Thr Ser Asn
117                 122                 127                 132

gtg gct tat ggg tct aca ggc att cgg gac gtg cac ctc gag ctg aag      485
Val Ala Tyr Gly Ser Thr Gly Ile Arg Asp Val His Leu Glu Leu Lys
133                 138                 143                 148

gac ctg act ctg tgt gga cgc aaa ggc aat ctg cac ttt ata cgc ttt      533
Asp Leu Thr Leu Cys Gly Arg Lys Gly Asn Leu His Phe Ile Arg Phe
149                 154                 159                 164

ccc act cat gac atg cct gct ttt att caa atg ggc aga gat aaa aac      581
Pro Thr His Asp Met Pro Ala Phe Ile Gln Met Gly Arg Asp Lys Asn
165                 170                 175                 180

ttc tcg agt ctc cac act gtc ttt tgt gcc act gga ggt gga gcg tac      629
Phe Ser Ser Leu His Thr Val Phe Cys Ala Thr Gly Gly Gly Ala Tyr
181                 186                 191                 196

aaa ttt gag cag gat ttt ctc aca ata ggt gat ctt cag ctt tgc aaa      677
Lys Phe Glu Gln Asp Phe Leu Thr Ile Gly Asp Leu Gln Leu Cys Lys
197                 202                 207                 212

ctg gat gaa cta gat tgc ttg atc aaa gga att tta tac att gac tca      725
Leu Asp Glu Leu Asp Cys Leu Ile Lys Gly Ile Leu Tyr Ile Asp Ser
213                 218                 223                 228

gtc gga ttc aat gga cgg tca cag tgc tat tac ttt gaa aac cct gct      773
```

```
Val Gly Phe Asn Gly Arg Ser Gln Cys Tyr Tyr Phe Glu Asn Pro Ala
229                 234                 239                 244

gat tct gaa aag tgt cag aag tta cca ttt gat ttg aaa aat ccg tat      821
Asp Ser Glu Lys Cys Gln Lys Leu Pro Phe Asp Leu Lys Asn Pro Tyr
245                 250                 255                 260

cct ctg ctt ctg gtg aac att ggc tca ggg gtt agc atc tta gca gta      869
Pro Leu Leu Leu Val Asn Ile Gly Ser Gly Val Ser Ile Leu Ala Val
261                 266                 271                 276

tat tcc aaa gat aat tac aaa cgg gtc aca ggt act agt ctt gga gga      917
Tyr Ser Lys Asp Asn Tyr Lys Arg Val Thr Gly Thr Ser Leu Gly Gly
277                 282                 287                 292

gga act ttt ttt ggt ctc tgc tgt ctt ctt act ggc tgt acc act ttt      965
Gly Thr Phe Phe Gly Leu Cys Cys Leu Leu Thr Gly Cys Thr Thr Phe
293                 298                 303                 308

gaa gaa gct ctt gaa atg gca tct cgt gga gat agc acc aaa gtg gat     1013
Glu Glu Ala Leu Glu Met Ala Ser Arg Gly Asp Ser Thr Lys Val Asp
309                 314                 319                 324

aaa cta gta cga gat att tat gga ggg gac tat gag agg ttt gga ctg     1061
Lys Leu Val Arg Asp Ile Tyr Gly Gly Asp Tyr Glu Arg Phe Gly Leu
325                 330                 335                 340

cca ggc tgg gct gtg gct tca agc ttt gga aac atg atg agc aag gag     1109
Pro Gly Trp Ala Val Ala Ser Ser Phe Gly Asn Met Met Ser Lys Glu
341                 346                 351                 356

aag cga gag gct gtc agt aaa gag gac ctg gcc aga gcg act ttg atc     1157
Lys Arg Glu Ala Val Ser Lys Glu Asp Leu Ala Arg Ala Thr Leu Ile
357                 362                 367                 372

acc atc acc aac aac att ggc tca ata gca aga atg tgt gcc ctt aat     1205
Thr Ile Thr Asn Asn Ile Gly Ser Ile Ala Arg Met Cys Ala Leu Asn
373                 378                 383                 388

gaa aac att aac cag gtg gta ttt gtt gga aat ttc ttg aga att aat     1253
Glu Asn Ile Asn Gln Val Val Phe Val Gly Asn Phe Leu Arg Ile Asn
389                 394                 399                 404

acg atc gcc atg cgg ctt ttg gca tat gct ttg gat tat tgg tcc aag     1301
Thr Ile Ala Met Arg Leu Leu Ala Tyr Ala Leu Asp Tyr Trp Ser Lys
405                 410                 415                 420

ggg cag ttg aaa gca ctt ttt tcg gaa cac gag ggt tat ttt gga gct     1349
Gly Gln Leu Lys Ala Leu Phe Ser Glu His Glu Gly Tyr Phe Gly Ala
421                 426                 431                 436

gtt gga gca ctc ctt gag ctg ttg aag atc ccg tga tcat tacctgggga     1399
Val Gly Ala Leu Leu Glu Leu Leu Lys Ile Pro  *
437                 442                 447

ggggttcctg aaaccttcca caatgggatc tgtggacttt catttttta agagacttac   1459
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tcaatttcat gactgtacta cctgaaacaa agtgagaaag gacaggtgta tttttctaag   1519

tcatcaagat aaatccttaa gaattcagtc t                                  1550
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<210> 189
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<213> Homo sapiens

<220>
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<222> (73)..(738)

<220>
<221> misc_feature
<222> (1)...(956)
<223> n = a,t,c or g

<400> 189

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aggatggctc ncatagatcg ccttgngttg agcccggtat tcccgggtcg acccacgcgt     60

ccggccgggg cg    atg tgg agc gcg ggc cgc ggc ggg gct gcc tgg ccg     108
                 Met Trp Ser Ala Gly Arg Gly Gly Ala Ala Trp Pro
                   1               5                  10

gtg ctg ttg ggg ctg ctg ctg gcg ctg tta gtg ccg ggc ggt ggt gcc     156
Val Leu Leu Gly Leu Leu Leu Ala Leu Leu Val Pro Gly Gly Gly Ala
 13                  18                  23                  28

gcc aag acc ggt gcg gag ctc gtg acc tgc ggg tcg gtg ctg aag ctg     204
Ala Lys Thr Gly Ala Glu Leu Val Thr Cys Gly Ser Val Leu Lys Leu
 29                  34                  39                  44

ctc aat acg cac cac cgc gtg cgg ctg cac tcg cac gac atc aaa tac     252
Leu Asn Thr His His Arg Val Arg Leu His Ser His Asp Ile Lys Tyr
 45                  50                  55                  60

gga tcc ggc agc ggc cag caa tcg gtg acc ggc gta gag gcg tcg gac     300
Gly Ser Gly Ser Gly Gln Gln Ser Val Thr Gly Val Glu Ala Ser Asp
 61                  66                  71                  76

gac gcc aat agc tac tgg cgg atc cgc ggc ggc tcg gag ggc ggg tgc     348
Asp Ala Asn Ser Tyr Trp Arg Ile Arg Gly Gly Ser Glu Gly Gly Cys
 77                  82                  87                  92

ccg cgc ggg tcc ccg gtg cgc tgc ggg cag gcg gtg agg ctc acg cat     396
Pro Arg Gly Ser Pro Val Arg Cys Gly Gln Ala Val Arg Leu Thr His
 93                  98                 103                 108

gtg ctt acg ggc aag aac ctg cac acg cac cac ttc ccg tcg ccg ctg     444
Val Leu Thr Gly Lys Asn Leu His Thr His His Phe Pro Ser Pro Leu
109                 114                 119                 124

tcc aac aac cag gag gtg agt gcc ttt ggg gaa gac ggc gag ggc gac     492
```

```
Ser Asn Asn Gln Glu Val Ser Ala Phe Gly Glu Asp Gly Glu Gly Asp
125                 130                 135                 140

gac ctg gac cta tgg aca gtg cgc tgc tct gga cag cac tgg gag cgt      540
Asp Leu Asp Leu Trp Thr Val Arg Cys Ser Gly Gln His Trp Glu Arg
141                 146                 151                 156

gag gct gct gtg cgc ttc cag cat gtg ggc acc tct gtg ttc ctg tca      588
Glu Ala Ala Val Arg Phe Gln His Val Gly Thr Ser Val Phe Leu Ser
157                 162                 167                 172

gtc acg ggt gag cag tat gga agc ccc atc cgt ggg cag cat gag gtc      636
Val Thr Gly Glu Gln Tyr Gly Ser Pro Ile Arg Gly Gln His Glu Val
173                 178                 183                 188

cac ggc atg ccc agt gcc aac acg cac aat acg tgg aag gcc atg gaa      684
His Gly Met Pro Ser Ala Asn Thr His Asn Thr Trp Lys Ala Met Glu
189                 194                 199                 204

ggc atc ttc atc aag cct agt gtg gag ccc tct gca ggt cac gat gaa      732
Gly Ile Phe Ile Lys Pro Ser Val Glu Pro Ser Ala Gly His Asp Glu
205                 210                 215                 220

ctc tga gtgtgtggat ggatgggtgg atggagggtg gcaggtgggg cgtctgcagg       788
Leu  *
221

gccactcttg gcagagactt tgggtttgta ggggtcctca agtgcctttg tgattaaaga    848

atgttggtct aaaaaaaatc gacgcggccg cgaattcgga tcctcgagag atctcttttt    908

ttgggtttgg tggggtatct tcatcatcga atagatagtt atatacat                 956
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<210> 190
<211> 2300
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (97)..(1518)

<220>
<221> misc_feature
<222> (1)...(2300)
<223> n = a,t,c or g

<400> 190

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tggcncnnna attggacctt gaaagctgca cgcctgcagg taccggtccg gaatgcccgg     60

gtcgacgatt tcgtgcctcg tggaggacac agcagc  atg gga cag tca ggg agg     114
                                        Met Gly Gln Ser Gly Arg
                                          1
```

```
tcc cgg cac cag aag cgc gcc cgc gcc cag gcg cag ctc cgc aac ctc      162
Ser Arg His Gln Lys Arg Ala Arg Ala Gln Ala Gln Leu Arg Asn Leu
  7                  12                  17                  22

gag gcc tat gcc gcg aac ccg cac tcg ttc gtg ttc acg cga ggc tgc      210
Glu Ala Tyr Ala Ala Asn Pro His Ser Phe Val Phe Thr Arg Gly Cys
 23                  28                  33                  38

acg ggt cgc aac atc cgg cag ctc agc ctg gac gtg cgg cgg gtc atg      258
Thr Gly Arg Asn Ile Arg Gln Leu Ser Leu Asp Val Arg Arg Val Met
 39                  44                  49                  54

gag ccg ctc act gcc agc cgt ctg cag gtt cgt aag aag aac tcg ctg      306
Glu Pro Leu Thr Ala Ser Arg Leu Gln Val Arg Lys Lys Asn Ser Leu
 55                  60                  65                  70

aag gac tgc gtg gca gtg gct ggg ccc ctc ggg gtc aca cac ttt ctg      354
Lys Asp Cys Val Ala Val Ala Gly Pro Leu Gly Val Thr His Phe Leu
 71                  76                  81                  86

atc ctg agc aaa aca gag acc aat gtc tac ttt aag ctg atg cgc ctc      402
Ile Leu Ser Lys Thr Glu Thr Asn Val Tyr Phe Lys Leu Met Arg Leu
 87                  92                  97                 102

cca gga ggc ccc acc ttg acc ttc cag gtg aag aag tac tcg ctg gtg      450
Pro Gly Gly Pro Thr Leu Thr Phe Gln Val Lys Lys Tyr Ser Leu Val
103                 108                 113                 118

cgt gat gtg gtc tcc tca ctg cgc cgg cac cgc atg cac gag cag cag      498
Arg Asp Val Val Ser Ser Leu Arg Arg His Arg Met His Glu Gln Gln
119                 124                 129                 134

ttt gcc cac cca ccc ctc ctg gta ctc aac agc ttt ggc ccc cat ggt      546
Phe Ala His Pro Pro Leu Leu Val Leu Asn Ser Phe Gly Pro His Gly
135                 140                 145                 150

atg cat gtg aag ctc atg gcc acc atg ttc cag aac ctg ttc ccc tcc      594
Met His Val Lys Leu Met Ala Thr Met Phe Gln Asn Leu Phe Pro Ser
151                 156                 161                 166

atc aac gtg cac aag gtg aac ctg aac acc atc aag cgc tgc ctc ctc      642
Ile Asn Val His Lys Val Asn Leu Asn Thr Ile Lys Arg Cys Leu Leu
167                 172                 177                 182

atc gac tac aac ccc gac tcc cag gag ctg gac ttc cgc cac tat agc      690
Ile Asp Tyr Asn Pro Asp Ser Gln Glu Leu Asp Phe Arg His Tyr Ser
183                 188                 193                 198

atc aaa gtt gtt cct gtg ggc gcg agt cgc ggg atg aag aag ctg ctc      738
Ile Lys Val Val Pro Val Gly Ala Ser Arg Gly Met Lys Lys Leu Leu
199                 204                 209                 214

cag gag aag ttc ccc aac atg agc cgc ctg cag gac atc agc gag ctg      786
Gln Glu Lys Phe Pro Asn Met Ser Arg Leu Gln Asp Ile Ser Glu Leu
215                 220                 225                 230

ctg gcc acg ggc gcg ggg ctg tcg gag agc gag gca gag cct gac ggc      834
```

```
Leu Ala Thr Gly Ala Gly Leu Ser Glu Ser Glu Ala Glu Pro Asp Gly
231                 236                 241                 246

gac cac aac atc aca gag ctg cct cag gct gtc gct ggc cgt ggc aac      882
Asp His Asn Ile Thr Glu Leu Pro Gln Ala Val Ala Gly Arg Gly Asn
247                 252                 257                 262

atg cgg gcc cag cag agt gca gtg cgg ctc acc gag atc ggc ccg cgg      930
Met Arg Ala Gln Gln Ser Ala Val Arg Leu Thr Glu Ile Gly Pro Arg
263                 268                 273                 278

atg aca ctg cag ctc atc aag gtc cag gag ggc gtc ggg gag ggc aaa      978
Met Thr Leu Gln Leu Ile Lys Val Gln Glu Gly Val Gly Glu Gly Lys
279                 284                 289                 294

gtg atg ttc cac agt ttt gtg agc aag acg gag gag gag ctg cag gcc     1026
Val Met Phe His Ser Phe Val Ser Lys Thr Glu Glu Glu Leu Gln Ala
295                 300                 305                 310

atc ctg gaa gcc aag gag aag aag ctg cgg ctg aag gcg cag agg cag     1074
Ile Leu Glu Ala Lys Glu Lys Lys Leu Arg Leu Lys Ala Gln Arg Gln
311                 316                 321                 326

gcc cag cag gcc cag aat gtg cag cgc aag cag gag cag cgg gag gcc     1122
Ala Gln Gln Ala Gln Asn Val Gln Arg Lys Gln Glu Gln Arg Glu Ala
327                 332                 337                 342

cac aga aag aag agc ctg gag ggc atg aag aag gca cgg gtc ggg ggt     1170
His Arg Lys Lys Ser Leu Glu Gly Met Lys Lys Ala Arg Val Gly Gly
343                 348                 353                 358

agt gat gaa gag gcc tct ggg atc cct tca agg acg gcg agc ctg gag     1218
Ser Asp Glu Glu Ala Ser Gly Ile Pro Ser Arg Thr Ala Ser Leu Glu
359                 364                 369                 374

ttg ggt gag gac gat gat gaa cag gaa gat gat gac atc gag tat ttc     1266
Leu Gly Glu Asp Asp Asp Glu Gln Glu Asp Asp Asp Ile Glu Tyr Phe
375                 380                 385                 390

tgc cag gcg gtg ggc gag gcg ccc agt gag gac ctg ttc ccc gag gcc     1314
Cys Gln Ala Val Gly Glu Ala Pro Ser Glu Asp Leu Phe Pro Glu Ala
391                 396                 401                 406

aag cag aaa cgg ctt gcc aag tct cca ggg cgg aag cgg aag cgg tgg     1362
Lys Gln Lys Arg Leu Ala Lys Ser Pro Gly Arg Lys Arg Lys Arg Trp
407                 412                 417                 422

gaa atg gat cga ggc agg ggt cgc ctt tgt gac cag aag ttt ccc aag     1410
Glu Met Asp Arg Gly Arg Gly Arg Leu Cys Asp Gln Lys Phe Pro Lys
423                 428                 433                 438

acc aag gac aag tcc cag gga gcc cag gcc agg cgg ggg ccc aga ggg     1458
Thr Lys Asp Lys Ser Gln Gly Ala Gln Ala Arg Arg Gly Pro Arg Gly
439                 444                 449                 454

gct tcc cgg gat ggt ggg cga ggc cgg ggc cgg ggc cgc cca ggg aag     1506
Ala Ser Arg Asp Gly Gly Arg Gly Arg Gly Arg Gly Arg Pro Gly Lys
```

```
455                 460                 465                 470

aga gtg gcc tga gcc caagccgcac cggagcagcg gctggattga acgccccaga     1561
Arg Val Ala  *
471

ttggggcccg agatgtggcc ctcggtttcc tttcataaag gagttgtgtc cccagccctt   1621

ccactccagt aaagaactga attggccagg ggtccacgtc agcntttggg atgggggatt   1681

ctggagccat acaaagcaac ccagagagtc ctgggccggc cacacccgag agtccctccc   1741

acctggtttc ttcctggaag ctgggtctnt cccctaccct gcacggggtt ggtttcattg   1801

gtggcagcag cagccatgag tggcccctnc ccccagtccc accaaagagc cgtgcaagca   1861

gacaggtcac actttcagca aatgagcttg aacctcagga gggttgtggc acaatgagga   1921

aggaaacgtg ggtggaaagg cacgctggcc tgctctgctg gctgggccag taactgggga   1981

tggggctggg gcagggccca ctaagccact ggtgactggg ggaggggctg nggaactggg   2041

tagcagacac aggctgagga tcggcacggg agcatggcag ccaacgtctc gggtaaggaa   2101

aaggcatgtt ggctgtctct gggggtctgc agattgtcag gaggtggggg tagtgggtat   2161

tggtaaaaca cctaggtctg gggctgggca cggtggctca cgcctgtaat cccagcactt   2221

tgggaggtcg agggggggtgg aacacgaggt caggggttcg agaccaccct gaccaacaag   2281

gagaaacccc gtctctact                                               2300
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<210> 191
<211> 2240
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (97)..(1458)

<220>
<221> misc_feature
<222> (1)...(2240)
<223> n = a,t,c or g

<400> 191

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tggcncnnna attggacctt gaaagctgca cgcctgcagg taccggtccg gaatgcccgg     60

gtcgacgatt tcgtgcctcg tggaggacac agcagc  atg gga cag tca ggg agg     114
                                        Met Gly Gln Ser Gly Arg
                                          1

tcc cgg cac cag aag cgc gcc cgc gcc cag gcg cag ctc cgc aac ctc      162
```

```
Ser Arg His Gln Lys Arg Ala Arg Ala Gln Ala Gln Leu Arg Asn Leu
  7                  12                  17                  22

gag gcc tat gcc gcg aac ccg cac tcg ttc gtg ttc acg cga ggc tgc      210
Glu Ala Tyr Ala Ala Asn Pro His Ser Phe Val Phe Thr Arg Gly Cys
 23                  28                  33                  38

acg ggt cgc aac atc cgg cag ctc agc ctg gac gtg cgg cgg gtc atg      258
Thr Gly Arg Asn Ile Arg Gln Leu Ser Leu Asp Val Arg Arg Val Met
 39                  44                  49                  54

gag ccg ctc act gcc agc cgt ctg cag gtt cgt aag aag aac tcg ctg      306
Glu Pro Leu Thr Ala Ser Arg Leu Gln Val Arg Lys Lys Asn Ser Leu
 55                  60                  65                  70

aag gac tgc gtg gca gtg gct ggg ccc ctc ggg gtc aca cac ttt ctg      354
Lys Asp Cys Val Ala Val Ala Gly Pro Leu Gly Val Thr His Phe Leu
 71                  76                  81                  86

atc ctg agc aaa aca gag acc aat gtc tac ttt aag ctg atg cgc ctc      402
Ile Leu Ser Lys Thr Glu Thr Asn Val Tyr Phe Lys Leu Met Arg Leu
 87                  92                  97                 102

cca gga ggc ccc acc ttg acc ttc cag gtg aag aag tac tcg ctg gtg      450
Pro Gly Gly Pro Thr Leu Thr Phe Gln Val Lys Lys Tyr Ser Leu Val
103                 108                 113                 118

cgt gat gtg gtc tcc tca ctg cgc cgg cac cgc atg cac gag cag cag      498
Arg Asp Val Val Ser Ser Leu Arg Arg His Arg Met His Glu Gln Gln
119                 124                 129                 134

ttt gcc cac cca ccc ctc ctg gta ctc aac agc ttt ggc ccc cat ggt      546
Phe Ala His Pro Pro Leu Leu Val Leu Asn Ser Phe Gly Pro His Gly
135                 140                 145                 150

atg cat gtg aag ctc atg gcc acc atg ttc cag aac ctg ttc ccc tcc      594
Met His Val Lys Leu Met Ala Thr Met Phe Gln Asn Leu Phe Pro Ser
151                 156                 161                 166

atc aac gtg cac aag gtg aac ctg aac acc atc aag cgc tgc ctc ctc      642
Ile Asn Val His Lys Val Asn Leu Asn Thr Ile Lys Arg Cys Leu Leu
167                 172                 177                 182

atc gac tac aac ccc gac tcc cag gag ctg gac ttc cgc cac tat agc      690
Ile Asp Tyr Asn Pro Asp Ser Gln Glu Leu Asp Phe Arg His Tyr Ser
183                 188                 193                 198

atc aaa gtt gtt cct gtg ggc gcg agt cgc ggg atg aag aag ctg ctc      738
Ile Lys Val Val Pro Val Gly Ala Ser Arg Gly Met Lys Lys Leu Leu
199                 204                 209                 214

cag gag aag ttc ccc aac atg agc cgc ctg cag gac atc agc gag ctg      786
Gln Glu Lys Phe Pro Asn Met Ser Arg Leu Gln Asp Ile Ser Glu Leu
215                 220                 225                 230

ctg gcc acg ggc gcg ggg ctg tcg gag agc gag gca gag cct gac ggc      834
Leu Ala Thr Gly Ala Gly Leu Ser Glu Ser Glu Ala Glu Pro Asp Gly
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US 2005/0266000 A1

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231                 236                 241                 246

gac cac aac atc aca gag ctg cct cag gct gtc gct ggc cgt ggc aac      882
Asp His Asn Ile Thr Glu Leu Pro Gln Ala Val Ala Gly Arg Gly Asn
247                 252                 257                 262

atg cgg gcc cag cag agt gca gtg cgg ctc acc gag atc ggc ccg cgg      930
Met Arg Ala Gln Gln Ser Ala Val Arg Leu Thr Glu Ile Gly Pro Arg
263                 268                 273                 278

atg aca ctg cag ctc atc aag gtc cag gag ggc gtc ggg gag ggc aaa      978
Met Thr Leu Gln Leu Ile Lys Val Gln Glu Gly Val Gly Glu Gly Lys
279                 284                 289                 294

gtg atg ttc cac agt ttt gtg agc aag acg gag gag gag ctg cag gcc     1026
Val Met Phe His Ser Phe Val Ser Lys Thr Glu Glu Glu Leu Gln Ala
295                 300                 305                 310

atc ctg gaa gcc aag gag aag aag ctg cgg ctg aag gcg cag agg cag     1074
Ile Leu Glu Ala Lys Glu Lys Lys Leu Arg Leu Lys Ala Gln Arg Gln
311                 316                 321                 326

gcc cag cag gcc cag aat gtg cag cgc aag cag gag cag cgg gag gcc     1122
Ala Gln Gln Ala Gln Asn Val Gln Arg Lys Gln Glu Gln Arg Glu Ala
327                 332                 337                 342

cac aga aag aag agc ctg gag ggc atg aag aag gca cgg gtc ggg ggt     1170
His Arg Lys Lys Ser Leu Glu Gly Met Lys Lys Ala Arg Val Gly Gly
343                 348                 353                 358

agt gat gaa gag gcc gac gat gat atc gag tat ttc tgc cag gcg gtg     1218
Ser Asp Glu Glu Ala Asp Asp Asp Ile Glu Tyr Phe Cys Gln Ala Val
359                 364                 369                 374

ggc gag gcg ccc agt gag gac ctg ttc ccc gag gcc aag cag aaa cgg     1266
Gly Glu Ala Pro Ser Glu Asp Leu Phe Pro Glu Ala Lys Gln Lys Arg
375                 380                 385                 390

ctt gcc aag tct cca ggg cgg aag cgg aag cgg tgg gaa atg gat cga     1314
Leu Ala Lys Ser Pro Gly Arg Lys Arg Lys Arg Trp Glu Met Asp Arg
391                 396                 401                 406

ggc agg ggt cgc ctt tgt gac cag aag ttt ccc aag acc aag gac aag     1362
Gly Arg Gly Arg Leu Cys Asp Gln Lys Phe Pro Lys Thr Lys Asp Lys
407                 412                 417                 422

tcc cag gga gcc cag gcc agg cgg ggg ccc aga ggg gct tcc cgg gat     1410
Ser Gln Gly Ala Gln Ala Arg Arg Gly Pro Arg Gly Ala Ser Arg Asp
423                 428                 433                 438

ggt ggg cga ggc cgg ggc cgg ggc cgc cca ggg aag aga gtg gcc tga     1458
Gly Gly Arg Gly Arg Gly Arg Gly Arg Pro Gly Lys Arg Val Ala  *
439                 444                 449                 454

gcccaagccg caccggagca gcggctggat tgaacgcccc agattggggc ccgagatgtg   1518

gccctcggtt tcctttcata aaggagttgt gtccccagcc cttccactcc agtaaagaac   1578
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tgaattggcc aggggtccac gtcagcnttt gggatggggg attctggagc catacaaagc   1638

aacccagaga gtcctgggcc ggccacaccc gagagtccct cccacctggt ttcttcctgg   1698

aagctgggtc tntcccctac cctgcacggg gttggtttca ttggtggcag cagcagccat   1758

gagtggcccc tnccccccagt cccaccaaag agccgtgcaa gcagacaggt cacactttca   1818

gcaaatgagc ttgaacctca ggagggttgt ggcacaatga ggaaggaaac gtgggtggaa   1878

aggcacgctg gcctgctctg ctggctgggc cagtaactgg ggatggggct ggggcagggc   1938

ccactaagcc actggtgact gggggagggg ctgnggaact gggtagcaga cacaggctga   1998

ggatcggcac gggagcatgg cagccaacgt ctcgggtaag gaaaaggcat gttggctgtc   2058

tctgggggtc tgcagattgt caggaggtgg gggtagtggg tattggtaaa acacctaggt   2118

ctggggctgg gcacggtggc tcacgcctgt aatcccagca ctttgggagg tcgaggggggg   2178

tggaacacga ggtcaggggt tcgagaccac cctgaccaac aaggagaaac cccgtctcta   2238

ct                                                                  2240
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<210> 192
<211> 2389
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (52)..(2154)

<400> 192

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gaccagaccg gccccccga gactatagcc ttcactttcc ctcggtccac c atg gag      57
                                                        Met Glu
                                                          1

ccc ttg tgt cca ctc ctg ctg gtg ggt ttt agc ttg ccg ctc gcc agg      105
Pro Leu Cys Pro Leu Leu Leu Val Gly Phe Ser Leu Pro Leu Ala Arg
  3                   8                  13                  18

gct ctc agg ggc aac gag acc act gcc gac agc aac gag aca acc acg      153
Ala Leu Arg Gly Asn Glu Thr Thr Ala Asp Ser Asn Glu Thr Thr Thr
 19                  24                  29                  34

acc tca ggc cct ccg gac ccg ggc gcc tcc cag ccg ctg ctg gcc tgg      201
Thr Ser Gly Pro Pro Asp Pro Gly Ala Ser Gln Pro Leu Leu Ala Trp
 35                  40                  45                  50

ctg cta ctg ccg ctg ctg ctc ctc ctc ctc gtg ctc ctt ctc gcc gcc      249
Leu Leu Leu Pro Leu Leu Leu Leu Leu Leu Val Leu Leu Leu Ala Ala
 51                  56                  61                  66
```

```
tac ttc ttc agg ttc agg aag cag agg aaa gct gtg gtc agc acc agc      297
Tyr Phe Phe Arg Phe Arg Lys Gln Arg Lys Ala Val Val Ser Thr Ser
 67                  72                  77                  82

gac aag aag atg ccc aac gga atc ttg gag gag caa gag cag caa agg      345
Asp Lys Lys Met Pro Asn Gly Ile Leu Glu Glu Gln Glu Gln Gln Arg
 83                  88                  93                  98

gtg atg ctg ctc agc agg tca ccc tca ggg ccc aag aag tat ttt ccc      393
Val Met Leu Leu Ser Arg Ser Pro Ser Gly Pro Lys Lys Tyr Phe Pro
 99                 104                 109                 114

atc ccc gtg gag cac ctg gag gag gag atc cgt atc aga tcc gcc gac      441
Ile Pro Val Glu His Leu Glu Glu Glu Ile Arg Ile Arg Ser Ala Asp
115                 120                 125                 130

gac tgc aag cag ttt cgg gag gag ttc aac tca ttg cca tct gga cac      489
Asp Cys Lys Gln Phe Arg Glu Glu Phe Asn Ser Leu Pro Ser Gly His
131                 136                 141                 146

ata caa gga act ttt gaa ctg gca aat aaa gaa gaa aac aga gaa aaa      537
Ile Gln Gly Thr Phe Glu Leu Ala Asn Lys Glu Glu Asn Arg Glu Lys
147                 152                 157                 162

aac aga tat ccc aac atc ctt ccc aat gac cat tct agg gtg att ctg      585
Asn Arg Tyr Pro Asn Ile Leu Pro Asn Asp His Ser Arg Val Ile Leu
163                 168                 173                 178

agc caa ctg gat gga att ccc tgt tca gac tac atc aat gct tcc tac      633
Ser Gln Leu Asp Gly Ile Pro Cys Ser Asp Tyr Ile Asn Ala Ser Tyr
179                 184                 189                 194

ata gat ggt tac aaa gag aag aat aaa ttc ata gca gct caa ggt ccc      681
Ile Asp Gly Tyr Lys Glu Lys Asn Lys Phe Ile Ala Ala Gln Gly Pro
195                 200                 205                 210

aaa cag gaa acg gtt aac gac ttc tgg aga atg gtc tgg gag caa aag      729
Lys Gln Glu Thr Val Asn Asp Phe Trp Arg Met Val Trp Glu Gln Lys
211                 216                 221                 226

tct gcg acc atc gtc atg tta aca aac ttg aaa gaa agg aaa gag gaa      777
Ser Ala Thr Ile Val Met Leu Thr Asn Leu Lys Glu Arg Lys Glu Glu
227                 232                 237                 242

aag tgc cat cag tac tgg ccc gac caa ggc tgc tgg acc tat gga aac      825
Lys Cys His Gln Tyr Trp Pro Asp Gln Gly Cys Trp Thr Tyr Gly Asn
243                 248                 253                 258

atc cgg gtg tgc gtg gag gac tgc gtg gtt ttg gtc gac tac acc atc      873
Ile Arg Val Cys Val Glu Asp Cys Val Val Leu Val Asp Tyr Thr Ile
259                 264                 269                 274

cgg aag ttc tgc ata cag cca cag ctc ccc gac ggc tgc aaa gcc ccc      921
Arg Lys Phe Cys Ile Gln Pro Gln Leu Pro Asp Gly Cys Lys Ala Pro
275                 280                 285                 290
```

```
agg ctg gtc tca cag ctg cac ttc acc agc tgg ccc gac ttc gga gtg      969
Arg Leu Val Ser Gln Leu His Phe Thr Ser Trp Pro Asp Phe Gly Val
291                 296                 301                 306

cct ttt acc ccc att ggg atg ctg aag ttc ctc aag aaa gta aag acg     1017
Pro Phe Thr Pro Ile Gly Met Leu Lys Phe Leu Lys Lys Val Lys Thr
307                 312                 317                 322

ctc aac ccc gtg cac gct ggg ccc atc gtg gtc cac tgt agc gcg ggc     1065
Leu Asn Pro Val His Ala Gly Pro Ile Val Val His Cys Ser Ala Gly
323                 328                 333                 338

gtg ggc cgg acg ggc acc ttc att gtg atc gat gcc atg atg gcc atg     1113
Val Gly Arg Thr Gly Thr Phe Ile Val Ile Asp Ala Met Met Ala Met
339                 344                 349                 354

atg cac gcg gag cag aag gtg gat gtg ttt gaa ttt gtg tct cga atc     1161
Met His Ala Glu Gln Lys Val Asp Val Phe Glu Phe Val Ser Arg Ile
355                 360                 365                 370

cgt aat cag cgc cct cag atg gtt caa acg gat atg cag tac acg ttc     1209
Arg Asn Gln Arg Pro Gln Met Val Gln Thr Asp Met Gln Tyr Thr Phe
371                 376                 381                 386

atc tac caa gcc tta ctc gag tac tac ctc tac ggg gac aca gag ctg     1257
Ile Tyr Gln Ala Leu Leu Glu Tyr Tyr Leu Tyr Gly Asp Thr Glu Leu
387                 392                 397                 402

gac gtg tcc tcc ctg gag aag cac ctg cag acc atg cac ggc acc acc     1305
Asp Val Ser Ser Leu Glu Lys His Leu Gln Thr Met His Gly Thr Thr
403                 408                 413                 418

acc cac ttc gac aag atc ggg ctg gag gag gag ttc agg aaa ttg aca     1353
Thr His Phe Asp Lys Ile Gly Leu Glu Glu Glu Phe Arg Lys Leu Thr
419                 424                 429                 434

aat gtc cgg atc atg aag gag aac atg agg acg ggc aac ttg ccg gca     1401
Asn Val Arg Ile Met Lys Glu Asn Met Arg Thr Gly Asn Leu Pro Ala
435                 440                 445                 450

aac atg aag aag gcc agg gtc atc cag atc atc ccg tat gac ttc aac     1449
Asn Met Lys Lys Ala Arg Val Ile Gln Ile Ile Pro Tyr Asp Phe Asn
451                 456                 461                 466

cga gtg atc ctt tcc atg aaa agg ggt caa gaa tac aca gac tac atc     1497
Arg Val Ile Leu Ser Met Lys Arg Gly Gln Glu Tyr Thr Asp Tyr Ile
467                 472                 477                 482

aac gca tcc ttc ata gac ggc tac cga cag aag gac tat ttc atc gcc     1545
Asn Ala Ser Phe Ile Asp Gly Tyr Arg Gln Lys Asp Tyr Phe Ile Ala
483                 488                 493                 498

acc cag ggg cca ctg gca cac acg gtt gag gac ttc tgg agg atg atc     1593
Thr Gln Gly Pro Leu Ala His Thr Val Glu Asp Phe Trp Arg Met Ile
499                 504                 509                 514

tgg gaa tgg aaa tcc cac act atc gtg atg ctg acg gag gtg cag gag     1641
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Trp Glu Trp Lys Ser His Thr Ile Val Met Leu Thr Glu Val Gln Glu
515                 520                 525                 530

aga gag cag gat aaa tgc tac cag tat tgg cca acc gag ggc tca gtt     1689
Arg Glu Gln Asp Lys Cys Tyr Gln Tyr Trp Pro Thr Glu Gly Ser Val
531                 536                 541                 546

act cat gga gaa ata acg att gag ata aag aat gat acc ctt tca gaa     1737
Thr His Gly Glu Ile Thr Ile Glu Ile Lys Asn Asp Thr Leu Ser Glu
547                 552                 557                 562

gcc atc agt ata cga gac ttt ctg gtc act ctc aat cag ccc cag gcc     1785
Ala Ile Ser Ile Arg Asp Phe Leu Val Thr Leu Asn Gln Pro Gln Ala
563                 568                 573                 578

cgc cag gag gag cag gtc cga gta gtg cgc cag ttt cac ttc cac ggc     1833
Arg Gln Glu Glu Gln Val Arg Val Val Arg Gln Phe His Phe His Gly
579                 584                 589                 594

tgg cct gag atc ggg att ccc gcc gag ggc aaa ggc atg att gac ctc     1881
Trp Pro Glu Ile Gly Ile Pro Ala Glu Gly Lys Gly Met Ile Asp Leu
595                 600                 605                 610

atc gca gcc gtg cag aag cag cag cag cag aca ggc aac cac ccc atc     1929
Ile Ala Ala Val Gln Lys Gln Gln Gln Gln Thr Gly Asn His Pro Ile
611                 616                 621                 626

acc gtg cac tgc agt gcc gga gct ggg cga aca ggt aca ttc ata gcc     1977
Thr Val His Cys Ser Ala Gly Ala Gly Arg Thr Gly Thr Phe Ile Ala
627                 632                 637                 642

ctc agc aac att ttg gag cga gta aaa gcc gag gga ctt tta gat gta     2025
Leu Ser Asn Ile Leu Glu Arg Val Lys Ala Glu Gly Leu Leu Asp Val
643                 648                 653                 658

ttt caa gct gtg aag agt tta cga ctt cag aga cca cat atg gtg caa     2073
Phe Gln Ala Val Lys Ser Leu Arg Leu Gln Arg Pro His Met Val Gln
659                 664                 669                 674

acc ctg gaa cag tat gaa ttc tgc tac aaa gtg gta caa gat ttt att     2121
Thr Leu Glu Gln Tyr Glu Phe Cys Tyr Lys Val Val Gln Asp Phe Ile
675                 680                 685                 690

gat ata ttt tct gat tat gct aat ttc aaa tga agattcct gccttaaaat     2172
Asp Ile Phe Ser Asp Tyr Ala Asn Phe Lys  *
691                 696                 701

attttttaat ttaatggtca gtatattttg taaaaatcat gttaatttat ttcatagttg   2232

acattaatat cttccctaat ttctttgtat atattttgtt atgccttaaa ggccacctgc   2292

tatacagttg ttaaatctta aatatgcttt ttaaaaattg gaataatgta ttaaggtcaa   2352

ataatatccc ataaaatata tatttctgct aatatta                           2389
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tttaag atg gca ggg aca gcg cgc cat gac cga gag atg gcg atc cag 108
Met Ala Gly Thr Ala Arg His Asp Arg Glu Met Ala Ile Gln
1 5 10

gcc aag aaa aag ctc acc acg gcc acc gac ccc att gaa aga ctc cga 156
Ala Lys Lys Lys Leu Thr Thr Ala Thr Asp Pro Ile Glu Arg Leu Arg
15 20 25 30

ctg cag tgc ctg gcc agg ggc tct gct ggg atc aaa gga ctt ggc aga 204
Leu Gln Cys Leu Ala Arg Gly Ser Ala Gly Ile Lys Gly Leu Gly Arg
31 36 41 46

gtg ttt aga att atg gat gac gat aat aat cga acc ctt gat ttt aaa 252
Val Phe Arg Ile Met Asp Asp Asp Asn Asn Arg Thr Leu Asp Phe Lys
47 52 57 62

gaa ttt atg aaa ggg tta aat gat tat gct gtg gtc atg gaa aaa gaa 300
Glu Phe Met Lys Gly Leu Asn Asp Tyr Ala Val Val Met Glu Lys Glu
63 68 73 78

gag gtg gaa gaa ctt ttc cag agg ttt gat aaa gat gga aat gga aca 348
Glu Val Glu Glu Leu Phe Gln Arg Phe Asp Lys Asp Gly Asn Gly Thr
79 84 89 94

ata gac ttc aat gaa ttt ctt ctc aca tta aga cct cca atg tcc aga 396
Ile Asp Phe Asn Glu Phe Leu Leu Thr Leu Arg Pro Pro Met Ser Arg
95 100 105 110

gcc aga aaa gag gta atc atg caa gct ttt aga aag tta gac aag act 444
Ala Arg Lys Glu Val Ile Met Gln Ala Phe Arg Lys Leu Asp Lys Thr
111 116 121 126

gga gat ggt gtt ata aca atc gaa gac ctt cgt gaa gta tat aat gca 492
Gly Asp Gly Val Ile Thr Ile Glu Asp Leu Arg Glu Val Tyr Asn Ala
127 132 137 142

aaa cac cac cca aag tac cag aat ggg gaa tgg agt gag gaa caa gta 540
Lys His His Pro Lys Tyr Gln Asn Gly Glu Trp Ser Glu Glu Gln Val
143 148 153 158

ttt agg aaa ttt ctg gat aac ttt gat tca ccc tat gac aaa gat gga 588
Phe Arg Lys Phe Leu Asp Asn Phe Asp Ser Pro Tyr Asp Lys Asp Gly
159 164 169 174

```
ttg gtg acc cct gag gag ttc atg aac tac tat gca ggt gtg agc gca      636
Leu Val Thr Pro Glu Glu Phe Met Asn Tyr Tyr Ala Gly Val Ser Ala
175                 180                 185                 190

tcc att gac act gat gtg tac ttc atc atc atg atg aga acc gcc tgg      684
Ser Ile Asp Thr Asp Val Tyr Phe Ile Ile Met Met Arg Thr Ala Trp
191                 196                 201                 206

aag ctt taa gcacatg acctggggac caggccctgg gacagacatg tggctccaaa      740
Lys Leu  *
207

tgactaaatg tcagctcaaa aaccagaatc gtatttgatt tcacactcat cctaatgttt    800

ttttctgtgt caaaatattg cattttctgg ggccaaaaaa caggcagaaa taaaagacat    860

tgagtagcca actgtgagtt tgccttgcct aagactgttt cctttgttct aaaataggac    920

ttaaataaaa tgagctctgt aaaaa                                         945
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tgaaggaaga ggaaggtttt cctgaag    atg agg cga ctg aat cgg aaa aaa      111
                                 Met Arg Arg Leu Asn Arg Lys Lys
                                   1               5

act tta agt ttg gta aaa gag ttg gat gcc ttt ccg aag gtt cct gag      159
Thr Leu Ser Leu Val Lys Glu Leu Asp Ala Phe Pro Lys Val Pro Glu
  9                  14                  19                  24

agc tat gta gag act tca gcc agt gga ggt aca gtt tct cta ata gca      207
Ser Tyr Val Glu Thr Ser Ala Ser Gly Gly Thr Val Ser Leu Ile Ala
 25                  30                  35                  40

ttt aca act atg gct tta tta acc ata atg gaa ttc tca gta tat caa      255
Phe Thr Thr Met Ala Leu Leu Thr Ile Met Glu Phe Ser Val Tyr Gln
 41                  46                  51                  56

gat aca tgg atg aag tat gaa tac gaa gta gac aag gat ttt tct agc      303
Asp Thr Trp Met Lys Tyr Glu Tyr Glu Val Asp Lys Asp Phe Ser Ser
 57                  62                  67                  72

aaa tta aga att aat ata gat att act gtt gcc atg aag tgt caa tat      351
Lys Leu Arg Ile Asn Ile Asp Ile Thr Val Ala Met Lys Cys Gln Tyr
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 73                  78                  83                  88

gtt gga gcg gat gta ttg gat tta gca gaa aca atg gtt gca tct gca      399
Val Gly Ala Asp Val Leu Asp Leu Ala Glu Thr Met Val Ala Ser Ala
 89                  94                  99                 104

gat ggt tta gtt tat gaa cca aca gta ttt gat ctt tca cca cag cag      447
Asp Gly Leu Val Tyr Glu Pro Thr Val Phe Asp Leu Ser Pro Gln Gln
105                 110                 115                 120

aaa gag tgg cag agg atg ctg cag ctg att cag agt agg cta caa gaa      495
Lys Glu Trp Gln Arg Met Leu Gln Leu Ile Gln Ser Arg Leu Gln Glu
121                 126                 131                 136

gag cat tca ctt caa gat gtg ata ttt aaa agt gct ttt aaa agt aca      543
Glu His Ser Leu Gln Asp Val Ile Phe Lys Ser Ala Phe Lys Ser Thr
137                 142                 147                 152

tca aca gct ctt cca cca aga gaa gat gat tca tca cag tct cca aat      591
Ser Thr Ala Leu Pro Pro Arg Glu Asp Asp Ser Ser Gln Ser Pro Asn
153                 158                 163                 168

gca tgc aga att cat ggc cat cta tat gtc aat aaa gta gca ggg aat      639
Ala Cys Arg Ile His Gly His Leu Tyr Val Asn Lys Val Ala Gly Asn
169                 174                 179                 184

ttt cac ata aca gtg ggc aag gca att cca cat cct cgt ggg cat gca      687
Phe His Ile Thr Val Gly Lys Ala Ile Pro His Pro Arg Gly His Ala
185                 190                 195                 200

cat ttg gca gca ctt gtc aac cat gaa tct tac aat ttt tct cat aga      735
His Leu Ala Ala Leu Val Asn His Glu Ser Tyr Asn Phe Ser His Arg
201                 206                 211                 216

ata gat cat ttg tct ttt gga gag ctt gtt cca gca att att aat cct      783
Ile Asp His Leu Ser Phe Gly Glu Leu Val Pro Ala Ile Ile Asn Pro
217                 222                 227                 232

tta gat gga act gaa aaa att gct ata gat cac aac cag atg ttc caa      831
Leu Asp Gly Thr Glu Lys Ile Ala Ile Asp His Asn Gln Met Phe Gln
233                 238                 243                 248

tat ttt att aca gtt gtg cca aca aaa cta cat aca tat aaa ata tca      879
Tyr Phe Ile Thr Val Val Pro Thr Lys Leu His Thr Tyr Lys Ile Ser
249                 254                 259                 264

gca gac acc cat cag ttt tct gtg aca gaa agg gaa cgt atc att aac      927
Ala Asp Thr His Gln Phe Ser Val Thr Glu Arg Glu Arg Ile Ile Asn
265                 270                 275                 280

cat gct gca ggc agc cat gga gtc tct ggg ata ttt atg aaa tat gat      975
His Ala Ala Gly Ser His Gly Val Ser Gly Ile Phe Met Lys Tyr Asp
281                 286                 291                 296

ctc agt tct ctt atg gtg aca gtt act gag gag cac atg cca ttc tgg     1023
Leu Ser Ser Leu Met Val Thr Val Thr Glu Glu His Met Pro Phe Trp
297                 302                 307                 312
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cag ttt ttt gta aga ctc tgt ggt att gtt gga gga atc ttt tca aca     1071
Gln Phe Phe Val Arg Leu Cys Gly Ile Val Gly Gly Ile Phe Ser Thr
313                 318                 323                 328

aca ggc atg tta cat gga att gga aaa ttt ata gtt gaa ata att tgc     1119
Thr Gly Met Leu His Gly Ile Gly Lys Phe Ile Val Glu Ile Ile Cys
329                 334                 339                 344

tgt cgt ttc aga ctt gga tcc tat aaa cct gtc aat tct gtt cct ttt     1167
Cys Arg Phe Arg Leu Gly Ser Tyr Lys Pro Val Asn Ser Val Pro Phe
345                 350                 355                 360

gag gat ggc cac aca gac aac cac tta cct ctt tta gaa aat aat aca     1215
Glu Asp Gly His Thr Asp Asn His Leu Pro Leu Leu Glu Asn Asn Thr
361                 366                 371                 376

cat taa cacctcccga ttgaaggaga aaaacttttt gcctgagaca taaaaccttt      1271
His  *
377

ttttaataat aaaatattgt gcaatatatt caaagaaaag aaaacacaaa taagcagaaa   1331

acatacttat tttaaaaaaa aaaaa                                        1356
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ggcgcatgtc ccggccgagt gtggcgcagc agtggcggcg cttcccattc gccatgcgcc    120

gggggtgggt gcccgaaggt tgcatgatgg aatttgaaca ttacttcaag aggttttgta    180

ttttggatta gttaattggg tttgtcctct gctgactgtt tcttcggatg catttttggg    240

tgtgctcttg agggattaa atg caa aga gat cac acc atg gac tac aag gaa     292
                    Met Gln Arg Asp His Thr Met Asp Tyr Lys Glu
                      1               5

agc tgc cca agt gta agc att ccc agc tcc gat gaa cac aga gag aaa      340
Ser Cys Pro Ser Val Ser Ile Pro Ser Ser Asp Glu His Arg Glu Lys
 12                  17                  22                  27

aag aag agg ttt act gtt tat aaa gtt ctg gtt tca gtg gga aga agt      388
Lys Lys Arg Phe Thr Val Tyr Lys Val Leu Val Ser Val Gly Arg Ser
 28                  33                  38                  43
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gaa tgg ttt gtc ttc agg aga tat gca gag ttt gat aaa ctt tat aac      436
Glu Trp Phe Val Phe Arg Arg Tyr Ala Glu Phe Asp Lys Leu Tyr Asn
 44                  49                  54                  59

act tta aaa aaa cag ttt cct gct atg gcc ctg aag att cct gcc aag      484
Thr Leu Lys Lys Gln Phe Pro Ala Met Ala Leu Lys Ile Pro Ala Lys
 60                  65                  70                  75

aga ata ttt ggt gat aat ttt gat cca gat ttt att aaa caa aga cga      532
Arg Ile Phe Gly Asp Asn Phe Asp Pro Asp Phe Ile Lys Gln Arg Arg
 76                  81                  86                  91

gca gga cta aac gaa ttc att cag aac cta gtt agg tat cca gaa ctt      580
Ala Gly Leu Asn Glu Phe Ile Gln Asn Leu Val Arg Tyr Pro Glu Leu
 92                  97                 102                 107

tat aac cat cca gat gtc aga gca ttc ctt caa atg gac agt cca aaa      628
Tyr Asn His Pro Asp Val Arg Ala Phe Leu Gln Met Asp Ser Pro Lys
108                 113                 118                 123

cac cag tca gat cca tct gaa gat gag gat gaa aga agt tct cag aag      676
His Gln Ser Asp Pro Ser Glu Asp Glu Asp Glu Arg Ser Ser Gln Lys
124                 129                 134                 139

cta cac tct acc tca cag aac atc aac ctg gga ccg tct gga aat cct      724
Leu His Ser Thr Ser Gln Asn Ile Asn Leu Gly Pro Ser Gly Asn Pro
140                 145                 150                 155

cat gcc aaa cca act gac ttt gat ttc tta aaa gtt att gga aaa ggc      772
His Ala Lys Pro Thr Asp Phe Asp Phe Leu Lys Val Ile Gly Lys Gly
156                 161                 166                 171

agc ttt ggc aag gtt ctt ctt gca aaa cgg aaa ctg gat gga aaa ttt      820
Ser Phe Gly Lys Val Leu Leu Ala Lys Arg Lys Leu Asp Gly Lys Phe
172                 177                 182                 187

tat gct gtc aaa gtg tta cag aaa aaa ata gtt ctc aac aga aaa gag      868
Tyr Ala Val Lys Val Leu Gln Lys Lys Ile Val Leu Asn Arg Lys Glu
188                 193                 198                 203

caa aaa cat att atg gct gaa cgt aat gtg ctc ttg aaa aat gtg aaa      916
Gln Lys His Ile Met Ala Glu Arg Asn Val Leu Leu Lys Asn Val Lys
204                 209                 214                 219

cat ccg ttt ttg gtt gga ttg cat tat tcc ttc caa aca act gaa aag      964
His Pro Phe Leu Val Gly Leu His Tyr Ser Phe Gln Thr Thr Glu Lys
220                 225                 230                 235

ctt tat ttt gtt ctg gat ttt ggt tat gga ggg gag ctt ttt ttc cac     1012
Leu Tyr Phe Val Leu Asp Phe Gly Tyr Gly Gly Glu Leu Phe Phe His
236                 241                 246                 251

tta caa aga gaa cgg tcc ttt cct gag cac aga gct agg ttt tac gct     1060
Leu Gln Arg Glu Arg Ser Phe Pro Glu His Arg Ala Arg Phe Tyr Ala
252                 257                 262                 267
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gct gaa att gct agt gca ttg ggt tac tta cat tcc atc aaa ata gta     1108
Ala Glu Ile Ala Ser Ala Leu Gly Tyr Leu His Ser Ile Lys Ile Val
268                 273                 278                 283

tac aga gac ttg aaa cca gaa aat att ctt ttg gat tca gta gga cat     1156
Tyr Arg Asp Leu Lys Pro Glu Asn Ile Leu Leu Asp Ser Val Gly His
284                 289                 294                 299

gtt gtc tta aca gat ttt ggg ctt tgt aaa gaa gga att gct att tct     1204
Val Val Leu Thr Asp Phe Gly Leu Cys Lys Glu Gly Ile Ala Ile Ser
300                 305                 310                 315

gac acc act acc aca ttt tgt ggg aca cca gag tat ctt gca cct gaa     1252
Asp Thr Thr Thr Thr Phe Cys Gly Thr Pro Glu Tyr Leu Ala Pro Glu
316                 321                 326                 331

gta att aga aaa cag ccc tat gac aat act gta gat tgg tgg tgc ctt     1300
Val Ile Arg Lys Gln Pro Tyr Asp Asn Thr Val Asp Trp Trp Cys Leu
332                 337                 342                 347

ggg gct gtt ctg tat gaa atg ctg tat gga ttg cct cct ttt tat tgc     1348
Gly Ala Val Leu Tyr Glu Met Leu Tyr Gly Leu Pro Pro Phe Tyr Cys
348                 353                 358                 363

cga gat gtt gct gaa atg tat gac aat atc ctt cac aaa ccc cta agt     1396
Arg Asp Val Ala Glu Met Tyr Asp Asn Ile Leu His Lys Pro Leu Ser
364                 369                 374                 379

ttg agg cca gga gtg agt ctt aca gcc tgg tcc att ctg gaa gaa ctc     1444
Leu Arg Pro Gly Val Ser Leu Thr Ala Trp Ser Ile Leu Glu Glu Leu
380                 385                 390                 395

cta gaa aaa gac agg caa aat cga ctt ggt gcc aag gaa gac ttt ctt     1492
Leu Glu Lys Asp Arg Gln Asn Arg Leu Gly Ala Lys Glu Asp Phe Leu
396                 401                 406                 411

gaa att cag aat cat cct ttt ttt gaa tca ctc agc tgg gct gac ctt     1540
Glu Ile Gln Asn His Pro Phe Phe Glu Ser Leu Ser Trp Ala Asp Leu
412                 417                 422                 427

gta caa aag aag att cca cca cca ttt aat cct aat gtg gct gga cca     1588
Val Gln Lys Lys Ile Pro Pro Pro Phe Asn Pro Asn Val Ala Gly Pro
428                 433                 438                 443

gat gat atc aga aac ttt gac aca gca ttt aca gaa gaa aca gtt cca     1636
Asp Asp Ile Arg Asn Phe Asp Thr Ala Phe Thr Glu Glu Thr Val Pro
444                 449                 454                 459

tat tct gtg tgt gta tct tct gac tat tct ata gtg aat gcc agt gta     1684
Tyr Ser Val Cys Val Ser Ser Asp Tyr Ser Ile Val Asn Ala Ser Val
460                 465                 470                 475

ttg gag gca gat gat gca ttc gtt ggt ttc tct tat gca cct cct tca     1732
Leu Glu Ala Asp Asp Ala Phe Val Gly Phe Ser Tyr Ala Pro Pro Ser
476                 481                 486                 491

gaa gac tta ttt ttg tga gcaggg ggccattcag aaaccattga gcaaaataag     1786
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Glu Asp Leu Phe Leu *
492 497

tctatagatg ggactgaaac ttctatttgt gtgaatatat tcaaatatgt ataactagcg 1846

cctcattttt atatgtaatg atgaaaacta tgaaaaaatg tattttcttc tatgtgcaag 1906

aaaaataggg catttcaaag agctgttttg attaaaattt atattcttgt ttaataagct 1966

tatttttaaa caatttaaaa gctattattc ttagcattaa cctattttta aagaaacctt 2026

ttttgctatt gactgttttt tccctctaag tttacactaa catctaccca agatagactg 2086

ttttttaaca gtcaatttca gttcagctaa catatattaa tacctttgta actctttgct 2146

atggcttttg ttatcacacc aaaactatgc aattggtaca tggttgttta agaagaaacc 2206

gtatttttcc atgataaatc actgtttgaa atatttggtt catggtatga tcgaaatgta 2266

aaagcataat taacacattg gctgctagtt aacaattgga ataactttat tctgcagatc 2326

atttaagaag taacaggccg ggcgcggtgg ctcacgcctg taatcccagc actttgggag 2386

gctgaggcgg gcagatcacc tgaggtcagg agttggagac cagcctgacc aacatggaca 2446

aaccccgtct ctactaaaaa tacaaaattg gcagggtgtg gtggcacatg cctataatcc 2506

cagctacttg ggaggctaag gcaggagaat cgcttgaacc cgggaggcgg aggttgcagt 2566

gagccgagat cgcaccattg cactcctgcc tgggcaacaa gagtgaaact ccatctccaa 2626

aaaaaaaaag aaaaagtacc aaagggaaat tatttgtttt tgaaatacca gttcaacttt 2686

ggggattatt tttcctttga aggaaaaaaa aaggcttaag ggttaggatt tttaagtatt 2746

cccaaagatc tgaa 2760

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tgccctcggc cgatcgaaag ggagtcgggt tcagatcccc ggcgccgcc atg ggc 115
Met Gly
1

aag aag cac aag aag cac aag gcc gag tgg cgc tcg tcc tac gag gat 163

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Lys Lys His Lys Lys His Lys Ala Glu Trp Arg Ser Ser Tyr Glu Asp
  3                   8                  13                  18

tat gcc gac aag ccc ctg gag aag cct cta aag cta gtc ctg aag gtc      211
Tyr Ala Asp Lys Pro Leu Glu Lys Pro Leu Lys Leu Val Leu Lys Val
 19                  24                  29                  34

gga gga agt gaa gtg act gaa ctc tca gga tcc ggc cac gac tcc agt      259
Gly Gly Ser Glu Val Thr Glu Leu Ser Gly Ser Gly His Asp Ser Ser
 35                  40                  45                  50

tac tat gat gac agg tca gac cat gag cga gag agg cac aaa gaa aag      307
Tyr Tyr Asp Asp Arg Ser Asp His Glu Arg Glu Arg His Lys Glu Lys
 51                  56                  61                  66

aaa aag aag aag aag aag aag tcc gag aag gag aag cat ctg gac gat      355
Lys Lys Lys Lys Lys Lys Lys Ser Glu Lys Glu Lys His Leu Asp Asp
 67                  72                  77                  82

gag gaa aga agg aag cga aag gaa gag aag aag cgg aag cga gag agg      403
Glu Glu Arg Arg Lys Arg Lys Glu Glu Lys Lys Arg Lys Arg Glu Arg
 83                  88                  93                  98

gag cac tgt gac acg gag gga gag gct gac gac ttt gat cct ggg aag      451
Glu His Cys Asp Thr Glu Gly Glu Ala Asp Asp Phe Asp Pro Gly Lys
 99                 104                 109                 114

aag gtg gag gtg gag ccg ccc cca gat cgg cca gtc cga gcg tgc cgg      499
Lys Val Glu Val Glu Pro Pro Pro Asp Arg Pro Val Arg Ala Cys Arg
115                 120                 125                 130

aca cag cca gcc gaa aat gag agc aca cct att cag caa ctc ctg gaa      547
Thr Gln Pro Ala Glu Asn Glu Ser Thr Pro Ile Gln Gln Leu Leu Glu
131                 136                 141                 146

cac ttc ctc cgc cag ctt cag aga aaa gat ccc cat gga ttt ttt gct      595
His Phe Leu Arg Gln Leu Gln Arg Lys Asp Pro His Gly Phe Phe Ala
147                 152                 157                 162

ttt cct gtc acg gat gca att gct cct gga tat tca atg ata ata aaa      643
Phe Pro Val Thr Asp Ala Ile Ala Pro Gly Tyr Ser Met Ile Ile Lys
163                 168                 173                 178

cat ccc atg gat ttt ggc acc atg aaa gac aaa att gta gct aat gaa      691
His Pro Met Asp Phe Gly Thr Met Lys Asp Lys Ile Val Ala Asn Glu
179                 184                 189                 194

tac aag tca gtt acg gaa ttt aag gca gat ttc aag ctg atg tgt gat      739
Tyr Lys Ser Val Thr Glu Phe Lys Ala Asp Phe Lys Leu Met Cys Asp
195                 200                 205                 210

aat gca atg aca tac aat agg cca gat acc gtg tac tac aag ttg gcg      787
Asn Ala Met Thr Tyr Asn Arg Pro Asp Thr Val Tyr Tyr Lys Leu Ala
211                 216                 221                 226

aag aag atc ctt cac gca ggc ttt aag atg atg agc aaa cag gca gct      835
Lys Lys Ile Leu His Ala Gly Phe Lys Met Met Ser Lys Gln Ala Ala
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227                 232                 237                 242

ctt ttg ggc aat gaa gat aca gct gtt gag gaa cct gtc cct gaa gtt      883
Leu Leu Gly Asn Glu Asp Thr Ala Val Glu Glu Pro Val Pro Glu Val
243                 248                 253                 258

gta cca gta caa gta gaa act gcc aag aaa tcc aaa aag ccg agt aga      931
Val Pro Val Gln Val Glu Thr Ala Lys Lys Ser Lys Lys Pro Ser Arg
259                 264                 269                 274

gaa gtt atc agc tgc atg ttt gag cct gaa ggg aat gcc tgc agc ttg      979
Glu Val Ile Ser Cys Met Phe Glu Pro Glu Gly Asn Ala Cys Ser Leu
275                 280                 285                 290

acg gac agt acc gca aag gag cac gtg ctg gcg ctg gtg gag cac gca     1027
Thr Asp Ser Thr Ala Lys Glu His Val Leu Ala Leu Val Glu His Ala
291                 296                 301                 306

gct gac gaa gct cgg gac agg atc aac cgg ttc ctc cca ggc ggc aag     1075
Ala Asp Glu Ala Arg Asp Arg Ile Asn Arg Phe Leu Pro Gly Gly Lys
307                 312                 317                 322

atg ggc tat ctg aag agg aac ggg gac ggg agc ctg ctc tac agc gtg     1123
Met Gly Tyr Leu Lys Arg Asn Gly Asp Gly Ser Leu Leu Tyr Ser Val
323                 328                 333                 338

gtc aac acg gcc gag ccg gac gct gat gag gag gag acc cac ccg gtg     1171
Val Asn Thr Ala Glu Pro Asp Ala Asp Glu Glu Glu Thr His Pro Val
339                 344                 349                 354

gac ttg agc tcg ctc tcc agt aag cta ctc cca ggc ttc acc acg ctg     1219
Asp Leu Ser Ser Leu Ser Ser Lys Leu Leu Pro Gly Phe Thr Thr Leu
355                 360                 365                 370

ggc ttc aaa gac gag aga aga aac aaa gtc acc ttt ctc tcc agt gcc     1267
Gly Phe Lys Asp Glu Arg Arg Asn Lys Val Thr Phe Leu Ser Ser Ala
371                 376                 381                 386

act act gcg ctt tcg atg cag aat aat tca gta ttt ggc gac ttg aag     1315
Thr Thr Ala Leu Ser Met Gln Asn Asn Ser Val Phe Gly Asp Leu Lys
387                 392                 397                 402

tcg gac gag atg gag ctg ctc tac tca gcc tac gga gat gag aca ggc     1363
Ser Asp Glu Met Glu Leu Leu Tyr Ser Ala Tyr Gly Asp Glu Thr Gly
403                 408                 413                 418

gtg cag tgt gcg ctg agc ctg cag gag ttt gtg aag gat gct ggg agc     1411
Val Gln Cys Ala Leu Ser Leu Gln Glu Phe Val Lys Asp Ala Gly Ser
419                 424                 429                 434

tac agc aag aaa gtg gtg gac gac ctc ctg gac cag atc aca ggc gga     1459
Tyr Ser Lys Lys Val Val Asp Asp Leu Leu Asp Gln Ile Thr Gly Gly
435                 440                 445                 450

gac cac tct agg acg ctc ttc cag ctg aag cag aga aga aat gtt ccc     1507
Asp His Ser Arg Thr Leu Phe Gln Leu Lys Gln Arg Arg Asn Val Pro
451                 456                 461                 466
```

```
atg aag cct cca gat gaa gcc aag gtt ggg gac acc cta gga gac agc     1555
Met Lys Pro Pro Asp Glu Ala Lys Val Gly Asp Thr Leu Gly Asp Ser
467                 472                 477                 482

agc agc tct gtt ctg gag ttc atg tcg atg aag tcc tat ccc gac gtt     1603
Ser Ser Ser Val Leu Glu Phe Met Ser Met Lys Ser Tyr Pro Asp Val
483                 488                 493                 498

tct gtg gat atc tcc atg ctc agc tct ctg ggg aag gtg aag aag gag     1651
Ser Val Asp Ile Ser Met Leu Ser Ser Leu Gly Lys Val Lys Lys Glu
499                 504                 509                 514

ctg gac cct gac gac agc cat ttg aac ttg gat gag acg acg aag ctc     1699
Leu Asp Pro Asp Asp Ser His Leu Asn Leu Asp Glu Thr Thr Lys Leu
515                 520                 525                 530

ctg cag gac ctg cac gaa gca cag gcg gag cgc ggc ggc tct cgg ccg     1747
Leu Gln Asp Leu His Glu Ala Gln Ala Glu Arg Gly Gly Ser Arg Pro
531                 536                 541                 546

tcg tcc aac ctc agc tcc ctg tcc aac gcc tcc gag agg gac cag cac     1795
Ser Ser Asn Leu Ser Ser Leu Ser Asn Ala Ser Glu Arg Asp Gln His
547                 552                 557                 562

cac ctg gga agc cct tct cgc ctg agt gtc ggg gag cag cca gac gtc     1843
His Leu Gly Ser Pro Ser Arg Leu Ser Val Gly Glu Gln Pro Asp Val
563                 568                 573                 578

acc cac gac ccc tat gag ttt ctt cag tct cca gag cct gcg gcc tct     1891
Thr His Asp Pro Tyr Glu Phe Leu Gln Ser Pro Glu Pro Ala Ala Ser
579                 584                 589                 594

gcc aag acc taa ctc tagaccacct tcagctcttt tattttattt ttttagtttt     1946
Ala Lys Thr  *
595

attttgcacg tgtagagttt ttgtcatcag acaaggactt tgatcctgtc ccctttggca   2006

tgcgggaagc agccgcggcg gaggtaatga attgtctgtg gtatcatgtc agcagagtct   2066

ccaagcccca cgaaccctga ggagtggagt catacgcgaa ggccatatgg ccatcgtgtc   2126

agcagagaga gtctctgtac acagccccgt gaaccctgag gagtggagtc atacacgaag   2186

ggcgtgtggc catcgtgtca gcagagagag tctctgtaca cagccccgtg aaccctgagg   2246

agtggagtca tacgcgaagg gtgtgtggcc aggctgcaga gctgcgtgcc gtttgtgtcc   2306

gagcatcacg tgtggctcca gcccttgttt ctgccagtgt agacacctct gtctgcccca   2366

ctgtcctggg gtcgctcttg ggaggcacag gcatgggtgt gtctggcctc attctgtatc   2426

agtccagtgt gttcctgtca tagtttgtgt ctcccaggca ggccatggta ggggcctcgc   2486

aggggccatt ggggagcaca gggccaggct ggggtgagga gagctcccct gttttctgtt   2546
```

```
taattgatga gcctgggaaa ggagtgtgtt ctgcctgccc gttacagtgg agcgttccgt   2606

gtccataaaa cgttttctaa ctgggtgttt actgagtgcc catttatgtt agtatttgca   2666

aaataccata aacacagctt ccagtcacaa gacacagagc gccaaagtgc acccaactgc   2726

tcccagcacg cgagggtgct gtgtcctacc agctggtggt ggtcctctgg cccagctgtc   2786

gtgcccacag tgacatcagg tgcacctgtg cgcccaccag cacc                    2830
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<210> 197
<211> 1379
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (182)..(1171)

<400> 197

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ccacgcgtcc gcagagccgg ttcctggaaa gagctggttc cctggcaggc tggagggcag    120

gagctggggc cacgctggtc tgggatagtt gggcagggag gctgtctacc tggtctccag    180

a    atg gac ggc cct gtg gca gag cat gcc aag cag gag ccc ttt cac      226
     Met Asp Gly Pro Val Ala Glu His Ala Lys Gln Glu Pro Phe His
       1               5                  10

gtg gtc aca cct ctg ttg gag agc tgg gcg ctg tcc cag gtg gcg ggc      274
Val Val Thr Pro Leu Leu Glu Ser Trp Ala Leu Ser Gln Val Ala Gly
 16                  21                  26                  31

atg cct gtc ttc ctc aag tgt gag aat gtg cag ccc agc ggc tcc ttc      322
Met Pro Val Phe Leu Lys Cys Glu Asn Val Gln Pro Ser Gly Ser Phe
 32                  37                  42                  47

aag att cgg ggc att ggg cat ttc tgc cag gag atg gcc aag aag gga      370
Lys Ile Arg Gly Ile Gly His Phe Cys Gln Glu Met Ala Lys Lys Gly
 48                  53                  58                  63

tgc aga cac ctg gtg tgc tcc tca ggg ggt aat gcg ggc atc gct gct      418
Cys Arg His Leu Val Cys Ser Ser Gly Gly Asn Ala Gly Ile Ala Ala
 64                  69                  74                  79

gcc tat gct gct agg aag ctg ggc att cct gcc acc atc gtg ctc ccc      466
Ala Tyr Ala Ala Arg Lys Leu Gly Ile Pro Ala Thr Ile Val Leu Pro
 80                  85                  90                  95

gag agc acc tcc ctg cag gtg gtg cag agg ctg cag ggg gag ggg gcc      514
Glu Ser Thr Ser Leu Gln Val Val Gln Arg Leu Gln Gly Glu Gly Ala
 96                 101                 106                 111
```

```
gag gtt cag ctg act gga aag gtc tgg gac gag gcc aat ctg agg gcg      562
Glu Val Gln Leu Thr Gly Lys Val Trp Asp Glu Ala Asn Leu Arg Ala
112                 117                 122                 127

caa gag ttg gcc aag agg gac ggc tgg gag aat gtc ccc ccg ttt gac      610
Gln Glu Leu Ala Lys Arg Asp Gly Trp Glu Asn Val Pro Pro Phe Asp
128                 133                 138                 143

cac ccc cta ata tgg aaa ggc cac gcc agc ctg gtg cag gag ctg aaa      658
His Pro Leu Ile Trp Lys Gly His Ala Ser Leu Val Gln Glu Leu Lys
144                 149                 154                 159

gca gtg ctg agg acc cca cca ggt gcc ctg gtg ctg gca gtt ggg ggt      706
Ala Val Leu Arg Thr Pro Pro Gly Ala Leu Val Leu Ala Val Gly Gly
160                 165                 170                 175

ggg ggt ctc ctg gcc ggg gtg gtg gct ggc ctg ctg gag gtg ggc tgg      754
Gly Gly Leu Leu Ala Gly Val Val Ala Gly Leu Leu Glu Val Gly Trp
176                 181                 186                 191

cag cat gta ccc atc att gcc atg gag acc cat ggg gca cac tgc ttc      802
Gln His Val Pro Ile Ile Ala Met Glu Thr His Gly Ala His Cys Phe
192                 197                 202                 207

aat gcg gcc atc aca gcc ggc aag ctg gtc aca ctt cca gac atc acc      850
Asn Ala Ala Ile Thr Ala Gly Lys Leu Val Thr Leu Pro Asp Ile Thr
208                 213                 218                 223

agt gtg gcc aag agc ctg ggt gcc aag acg gtg gcc gct cgg gcc ctg      898
Ser Val Ala Lys Ser Leu Gly Ala Lys Thr Val Ala Ala Arg Ala Leu
224                 229                 234                 239

gag tgc atg cag gtg tgc aag att cac tct gaa gtg gtg gag gac acc      946
Glu Cys Met Gln Val Cys Lys Ile His Ser Glu Val Val Glu Asp Thr
240                 245                 250                 255

gag gct gtg agc gct gtg cag cag ctc ctg gat gat gag cgt atg ctg      994
Glu Ala Val Ser Ala Val Gln Gln Leu Leu Asp Asp Glu Arg Met Leu
256                 261                 266                 271

gtg gag cct gcc tgt ggg gca gcc tta gca gcc atc tac tca ggc ctc     1042
Val Glu Pro Ala Cys Gly Ala Ala Leu Ala Ala Ile Tyr Ser Gly Leu
272                 277                 282                 287

ctg cgg agg ctc cag gcc gag ggc tgc ctg ccc cct tcc ctg act tca     1090
Leu Arg Arg Leu Gln Ala Glu Gly Cys Leu Pro Pro Ser Leu Thr Ser
288                 293                 298                 303

gtt gtg gta atc gtg tgt gga ggc aac aac atc aac agc cga gag ctg     1138
Val Val Val Ile Val Cys Gly Gly Asn Asn Ile Asn Ser Arg Glu Leu
304                 309                 314                 319

cag gct ttg aaa acc cac ctg ggc cag gtc tga ggggtccc atcctggccc     1189
Gln Ala Leu Lys Thr His Leu Gly Gln Val  *
320                 325                 330

caaagacccc tgagaggccc atggacagtc ctgtgtctgg atgaggagga ctcagtgctg   1249
```

```
gcagatggca gtggaagctg ccctgtgcaa ctgtgctggc tgcctcctga aggaagccct   1309

cctggactgc ttcttttggc tctccgacaa ctccggccaa taaacacttt ctgaattgag   1369

aaaaaaaaaa                                                          1379
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<210> 198
<211> 3128
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (286)..(2319)

<400> 198

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gcggccgctc cctcccggac tcccggcctc ccggcctccc tggtcccgcc tgggaaggga     60

tgcaaggaag ccctccggcg ctgcgctccg aggcgggaga cagcgtcccc ctccgccgct    120

cgggtcctgg cgcctcagag cccggcccag gccgcggaac ggtgatgctc gggccggacg    180

ggcgggcgcg gatccctgcg tcccgctgaa aatgtgtgtc tgacatgcaa gctcagtggg    240

gcagagaccc gtggattgct gtgccctgcc ctccggacct ggatc    atg aag gtg     294
                                                     Met Lys Val
                                                       1

ttg gga aga agc ttc ttc tgg gtg ctg ttt ccc gtc ctt ccc tgg gcg      342
Leu Gly Arg Ser Phe Phe Trp Val Leu Phe Pro Val Leu Pro Trp Ala
  4                   9                  14                  19

gtg cag gct gtg gag cac gag gag gtg gcg cag cgt gtg atc aaa ctg      390
Val Gln Ala Val Glu His Glu Glu Val Ala Gln Arg Val Ile Lys Leu
 20                  25                  30                  35

cac cgc ggg cga ggg gtg gct gcc atg cag agc cgg cag tgg gtc cgg      438
His Arg Gly Arg Gly Val Ala Ala Met Gln Ser Arg Gln Trp Val Arg
 36                  41                  46                  51

gac agc tgc agg aag ctc tca ggg ctt ctc cgc cag aag aat gca gtt      486
Asp Ser Cys Arg Lys Leu Ser Gly Leu Leu Arg Gln Lys Asn Ala Val
 52                  57                  62                  67

ctg aac aaa ctg aaa act gca att gga gca gtg gag aaa gac gtg ggc      534
Leu Asn Lys Leu Lys Thr Ala Ile Gly Ala Val Glu Lys Asp Val Gly
 68                  73                  78                  83

ctg tcg gat gaa gag aaa ctg ttt cag gtg cac acg ttt gaa att ttc      582
Leu Ser Asp Glu Glu Lys Leu Phe Gln Val His Thr Phe Glu Ile Phe
 84                  89                  94                  99

cag aaa gag ctg aat gaa agt gaa aat tcc gtt ttc caa gct gtc tac      630
```

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Gln Lys Glu Leu Asn Glu Ser Glu Asn Ser Val Phe Gln Ala Val Tyr
100                 105                 110                 115

gga ctg cag aga gcc ctg cag ggg gat tac aaa gat gtc gtg aac atg      678
Gly Leu Gln Arg Ala Leu Gln Gly Asp Tyr Lys Asp Val Val Asn Met
116                 121                 126                 131

aag gag agc agc cgg cag cgc ctg gag gcc ctg aga gag gct gca ata      726
Lys Glu Ser Ser Arg Gln Arg Leu Glu Ala Leu Arg Glu Ala Ala Ile
132                 137                 142                 147

aag gaa gaa aca gaa tat atg gaa ctt ctg gca gca gaa aaa cat caa      774
Lys Glu Glu Thr Glu Tyr Met Glu Leu Leu Ala Ala Glu Lys His Gln
148                 153                 158                 163

gtt gaa gcc ctt aaa aat atg caa cat caa aac caa agt tta tcc atg      822
Val Glu Ala Leu Lys Asn Met Gln His Gln Asn Gln Ser Leu Ser Met
164                 169                 174                 179

ctt gac gag att ctt gaa gat gta aga aag gca gcg gat cgt ctg gag      870
Leu Asp Glu Ile Leu Glu Asp Val Arg Lys Ala Ala Asp Arg Leu Glu
180                 185                 190                 195

gaa gag ata gag gaa cat gct ttt gac gac aat aaa tca gtc aag ggg      918
Glu Glu Ile Glu Glu His Ala Phe Asp Asp Asn Lys Ser Val Lys Gly
196                 201                 206                 211

gtc aat ttt gag gca gtt ctg agg gtg gag gaa gaa gag gcc aat tct      966
Val Asn Phe Glu Ala Val Leu Arg Val Glu Glu Glu Glu Ala Asn Ser
212                 217                 222                 227

aag caa aat ata aca aaa cga gaa gtg gag gat gac ttg ggt ctt agc     1014
Lys Gln Asn Ile Thr Lys Arg Glu Val Glu Asp Asp Leu Gly Leu Ser
228                 233                 238                 243

atg ctg att gac tcc cag aac aac cag tat att ttg acc aag ccc aga     1062
Met Leu Ile Asp Ser Gln Asn Asn Gln Tyr Ile Leu Thr Lys Pro Arg
244                 249                 254                 259

gat tca acc atc cca cgt gca gat cac cac ttt ata aag gac att gtt     1110
Asp Ser Thr Ile Pro Arg Ala Asp His His Phe Ile Lys Asp Ile Val
260                 265                 270                 275

acc ata gga atg ctg tcc ttg cct tgt ggc tgg cta tgt aca gcc ata     1158
Thr Ile Gly Met Leu Ser Leu Pro Cys Gly Trp Leu Cys Thr Ala Ile
276                 281                 286                 291

gga ttg cct aca atg ttt ggt tat att att tgt ggt gta ctt ctg gga     1206
Gly Leu Pro Thr Met Phe Gly Tyr Ile Ile Cys Gly Val Leu Leu Gly
292                 297                 302                 307

cct tca gga cta aat agt att aag tct att gtg caa gtg gag aca tta     1254
Pro Ser Gly Leu Asn Ser Ile Lys Ser Ile Val Gln Val Glu Thr Leu
308                 313                 318                 323

gga gaa ttt ggg gtg ttt ttt act ctt ttt ctt gtt ggc tta gaa ttt     1302
Gly Glu Phe Gly Val Phe Phe Thr Leu Phe Leu Val Gly Leu Glu Phe
```

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324                 329                 334                 339

tct cca gaa aag cta aga aag gtg tgg aag att tcc tta caa ggg ccg     1350
Ser Pro Glu Lys Leu Arg Lys Val Trp Lys Ile Ser Leu Gln Gly Pro
340                 345                 350                 355

tgt tac atg aca ctg tta atg att gca ttt ggc ttg ctg tgg ggg cat     1398
Cys Tyr Met Thr Leu Leu Met Ile Ala Phe Gly Leu Leu Trp Gly His
356                 361                 366                 371

ctc ttg cgg atc aaa ccc acg cag agc gtc ttc att tcc acg tgt ctg     1446
Leu Leu Arg Ile Lys Pro Thr Gln Ser Val Phe Ile Ser Thr Cys Leu
372                 377                 382                 387

tcc ttg tca agc aca ccc ctc gtg tcc agg ttc ctc atg ggc agt gct     1494
Ser Leu Ser Ser Thr Pro Leu Val Ser Arg Phe Leu Met Gly Ser Ala
388                 393                 398                 403

cgg ggt gac aaa gaa ggc gac att gac tac agc acc gtg ctc ctc ggc     1542
Arg Gly Asp Lys Glu Gly Asp Ile Asp Tyr Ser Thr Val Leu Leu Gly
404                 409                 414                 419

atg ctg gtg acg cag gac gtg cag ctc ggg ctc ttc atg gcc gtc atg     1590
Met Leu Val Thr Gln Asp Val Gln Leu Gly Leu Phe Met Ala Val Met
420                 425                 430                 435

ccg act ctc ata cag gcg ggc gcc agt gca tct tct agc att gtc gtg     1638
Pro Thr Leu Ile Gln Ala Gly Ala Ser Ala Ser Ser Ser Ile Val Val
436                 441                 446                 451

gaa gtt ctc cga atc ctg gtt ttg att ggt cag att ctt ttt tca cta     1686
Glu Val Leu Arg Ile Leu Val Leu Ile Gly Gln Ile Leu Phe Ser Leu
452                 457                 462                 467

gcg gcg gtt ttt ctt tta tgt ctt gtt ata aag aag tat ctc att gga     1734
Ala Ala Val Phe Leu Leu Cys Leu Val Ile Lys Lys Tyr Leu Ile Gly
468                 473                 478                 483

ccc tat tat cgg aag ctg cac atg gaa agc aag ggg aac aaa gaa atc     1782
Pro Tyr Tyr Arg Lys Leu His Met Glu Ser Lys Gly Asn Lys Glu Ile
484                 489                 494                 499

ctg atc ttg gga ata tct gcc ttt atc ttc tta atg tta acg gtc acg     1830
Leu Ile Leu Gly Ile Ser Ala Phe Ile Phe Leu Met Leu Thr Val Thr
500                 505                 510                 515

gag ctg ctg gac gtc tcc atg gag ctg ggc tgt ttc ctg gct gga gcg     1878
Glu Leu Leu Asp Val Ser Met Glu Leu Gly Cys Phe Leu Ala Gly Ala
516                 521                 526                 531

ctc gtc tcc tct cag ggc ccc gtg gtc acc gag gag atc gcc acc tcc     1926
Leu Val Ser Ser Gln Gly Pro Val Val Thr Glu Glu Ile Ala Thr Ser
532                 537                 542                 547

atc gaa ccc atc cgc gac ttc ctg gcc atc gtt ttc ttc gcc tcc ata     1974
Ile Glu Pro Ile Arg Asp Phe Leu Ala Ile Val Phe Phe Ala Ser Ile
548                 553                 558                 563
```

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ggg ctc cac gtg ttc ccc acg ttt gtg gcg tac gag ctc acg gtg ctg     2022
Gly Leu His Val Phe Pro Thr Phe Val Ala Tyr Glu Leu Thr Val Leu
564                 569                 574                 579

gtg ttc ctc acc ttg tca gtg gtg gtg atg aag ttt ctc ctg gcg gcg     2070
Val Phe Leu Thr Leu Ser Val Val Val Met Lys Phe Leu Leu Ala Ala
580                 585                 590                 595

ctg gtc ctg tct ctc att ctg ccg agg agc agc cag tac atc aag tgg     2118
Leu Val Leu Ser Leu Ile Leu Pro Arg Ser Ser Gln Tyr Ile Lys Trp
596                 601                 606                 611

atc gtc tct gcg ggg ctt gcc cag gtc agc gag ttt tcc ttt gtc ctg     2166
Ile Val Ser Ala Gly Leu Ala Gln Val Ser Glu Phe Ser Phe Val Leu
612                 617                 622                 627

ggg agc cgg gcg cga aga gcg ggc gtc atc tct cgg gag gtg tac ctc     2214
Gly Ser Arg Ala Arg Arg Ala Gly Val Ile Ser Arg Glu Val Tyr Leu
628                 633                 638                 643

ctt ata ctg agt gtg acc acg ctc agc ctc ttg ctc gcc ccg gtg ctg     2262
Leu Ile Leu Ser Val Thr Thr Leu Ser Leu Leu Leu Ala Pro Val Leu
644                 649                 654                 659

tgg aga gct gca atc acg agg tgt gtg ccc aga ccg gag aga cgg tcc     2310
Trp Arg Ala Ala Ile Thr Arg Cys Val Pro Arg Pro Glu Arg Arg Ser
660                 665                 670                 675

agc ctc tga tggctcg gagatgatgg accgtggaag ggaagcgtct gtggggagtg     2366
Ser Leu  *
676

agcgcttaga tggccagcag ctgctccttc tgggaagctc gcaccttggc aacagaacag   2426

ccctctagca gagcgtcagt gcagtcgtgt tatcccggct tttacagaat attcttgtcc   2486

tattttagaa ttttccggag tagtttattt gcagtctgtt gattatgtgc agtagacccg   2546

ggacactgcg ttttaccgat caccttgaat gtggtgcctg gatgtgcctt ttttttttc    2606

cctgaaatta ttattaattt tctattgtga gttcatcagt tcatagtttt tttagtaaag   2666

aagcaaaatt aaaaggcttt taaaaatgta caacttcaga attataatct gttagtcaaa   2726

tatttgttat taaacatttc tgtaatatga agttgtaatc ctggccgtga gcttggaagc   2786

ttacttttga ttcttaaagc ctatgttttc taaaatgaga caaatacgga tgtctatttg   2846

ccttttattg taacttttaa atgaaataat ttcatgtcaa tttctattag atatatcact   2906

taaaatattt ggttttaaat cacaagaata tgtattcttt aataaagata atttatgatc   2966

atggtataat taattgaaat ttattaaaat ctgtttttat taatttttt gacttgagct   3026

tatctttata caaaattcca gccaattttt ttttttact aagatgattt ctatattaac   3086
```

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atgctattct ccaagacacc aaattaatgc agggttaatt gg                          3128
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<210> 199
<211> 1804
<212> DNA
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<220>
<221> CDS
<222> (344)..(1420)

<220>
<221> misc_feature
<222> (1)...(1804)
<223> n = a,t,c or g

<400> 199

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ggtggaattc agctgcgact gcagttctga agcctaactg gttgcccgtg ccgcctcgga      60

ggtgaagtgt actgcgctga ttggcttcca ggcgccggcc gcgtgtgatg tcccgggcaa     120

cgattggctc tcgcctaccg ggggcttctc tcaccgggac tcgggactcc cgggaagtgg     180

accggcagaa gaggggggcta gctagctgtc tctgcggacc agggagaccc ccgcgccccc    240

ccggtgtgag gcggcctcac agggccgggt gggctggcga gccgacgcgg cggcggagga    300

ggctgtgagg agtgtgtgga acaggacccg ggacagagga acc  atg gct ccg cag      355
                                                 Met Ala Pro Gln
                                                   1

aac ctg agc acc ttt tgc ctg ttg ctg cta tac ctc atc ggg gcg gtg      403
Asn Leu Ser Thr Phe Cys Leu Leu Leu Leu Tyr Leu Ile Gly Ala Val
  5                  10                  15                  20

att gcc gga cga gat ttc tat aag atc ttg ggg gtg cct cga agt gcc      451
Ile Ala Gly Arg Asp Phe Tyr Lys Ile Leu Gly Val Pro Arg Ser Ala
 21                  26                  31                  36

tct ata aag gat att aaa aag gcc tat agg aaa cta gcc ctg cag ctt      499
Ser Ile Lys Asp Ile Lys Lys Ala Tyr Arg Lys Leu Ala Leu Gln Leu
 37                  42                  47                  52

cat ccc gac cgg aac cct gat gat cca caa gcc cag gag aaa ttc cag      547
His Pro Asp Arg Asn Pro Asp Asp Pro Gln Ala Gln Glu Lys Phe Gln
 53                  58                  63                  68

gat ctg ggt gct gct tat gag gtt ctg tca gat agt gag aaa cgg aaa      595
Asp Leu Gly Ala Ala Tyr Glu Val Leu Ser Asp Ser Glu Lys Arg Lys
 69                  74                  79                  84

cag tac gat act tat ggt gaa gaa gga tta aaa gat ggt cat cag agc      643
Gln Tyr Asp Thr Tyr Gly Glu Glu Gly Leu Lys Asp Gly His Gln Ser
 85                  90                  95                 100
```

```
tcc cat gga gac att ttt tca cac ttc ttt ggg gat ttt ggt ttc atg      691
Ser His Gly Asp Ile Phe Ser His Phe Phe Gly Asp Phe Gly Phe Met
101                 106                 111                 116

ttt gga gga acc cct cgt cag caa gac aga aat att cca aga gga agt      739
Phe Gly Gly Thr Pro Arg Gln Gln Asp Arg Asn Ile Pro Arg Gly Ser
117                 122                 127                 132

gat att att gta gat cta gaa gtc act ttg gaa gaa gta tat gca gga      787
Asp Ile Ile Val Asp Leu Glu Val Thr Leu Glu Glu Val Tyr Ala Gly
133                 138                 143                 148

aat ttt gtg gaa gta gtt aga aac aaa cct gtg gca agg cag gct cct      835
Asn Phe Val Glu Val Val Arg Asn Lys Pro Val Ala Arg Gln Ala Pro
149                 154                 159                 164

ggc aaa cgg aag tgc aat tgt cgg caa gag atg cgg acc acc cag ctg      883
Gly Lys Arg Lys Cys Asn Cys Arg Gln Glu Met Arg Thr Thr Gln Leu
165                 170                 175                 180

ggc cct ggg cgc ttc caa atg acc cag gag gtg gtc tgc gac gaa tgc      931
Gly Pro Gly Arg Phe Gln Met Thr Gln Glu Val Val Cys Asp Glu Cys
181                 186                 191                 196

cct aat gtc aaa cta gtg aat gaa gaa cga acg ctg gaa gta gaa ata      979
Pro Asn Val Lys Leu Val Asn Glu Glu Arg Thr Leu Glu Val Glu Ile
197                 202                 207                 212

gag cct ggg gtg aga gac ggc atg gag tac ccc ttt att gga gaa ggt     1027
Glu Pro Gly Val Arg Asp Gly Met Glu Tyr Pro Phe Ile Gly Glu Gly
213                 218                 223                 228

gag cct cac gtg gat ggg gag cct gga gat tta cgg ttc cga atc aaa     1075
Glu Pro His Val Asp Gly Glu Pro Gly Asp Leu Arg Phe Arg Ile Lys
229                 234                 239                 244

gtt gtc aag cac cca ata ttt gaa agg aga gga gat gat ttg tac aca     1123
Val Val Lys His Pro Ile Phe Glu Arg Arg Gly Asp Asp Leu Tyr Thr
245                 250                 255                 260

aat gtg aca atc tca tta gtt gag tca ctg gtt ggc ttt gag atg gat     1171
Asn Val Thr Ile Ser Leu Val Glu Ser Leu Val Gly Phe Glu Met Asp
261                 266                 271                 276

att act cac ttg gat ggt cac aag gta cat att tcc cgg gat aag atc     1219
Ile Thr His Leu Asp Gly His Lys Val His Ile Ser Arg Asp Lys Ile
277                 282                 287                 292

acc agg cca gga gcg aag cta tgg aag aaa ggg gaa ggg ctc ccc aac     1267
Thr Arg Pro Gly Ala Lys Leu Trp Lys Lys Gly Glu Gly Leu Pro Asn
293                 298                 303                 308

ttt gac aac aac aat atc aag ggc tct ttg ata atc act ttt gat gtg     1315
Phe Asp Asn Asn Asn Ile Lys Gly Ser Leu Ile Ile Thr Phe Asp Val
309                 314                 319                 324
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gat ttt cca aaa gaa cag tta aca gag gaa gcg aga gaa ggt atc aaa     1363
Asp Phe Pro Lys Glu Gln Leu Thr Glu Glu Ala Arg Glu Gly Ile Lys
325                 330                 335                 340

cag cta ctg aaa caa ggg tca gtg cag aag gta tac aat gga ctg caa     1411
Gln Leu Leu Lys Gln Gly Ser Val Gln Lys Val Tyr Asn Gly Leu Gln
341                 346                 351                 356

gga tat tga gagtgaa taaaattgga ctttgtttaa aataagtgaa taagcgatat     1467
Gly Tyr  *
357

ttattatctg caaggttttt ttgtgtgtgt ttttgttttt attttcaata tgcaagttag   1527

gcttaatttt ttatctaatg atcatccatg aaatgaaata agagggctta agaatttgtc   1587

catttgcatt cggaaaagaa tgaccagcaa aaggtttact aatacctctc cctttgggga   1647

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caaaagaaac acaatataga gggttggagt tgttagcaat ttcattcaaa atgccaactg   1767

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                 Met Ser Lys Asn Cys Val Pro Met Glu Phe Glu Glu
                   1               5                  10

tat tta ctg cgt atg ttc cag ggg act ttc tac ctc ctg cag aaa atc     157
Tyr Leu Leu Arg Met Phe Gln Gly Thr Phe Tyr Leu Leu Gln Lys Ile
 13                  18                  23                  28

acc aag gat aac aat gcc cac aca gtg aag agc agg cta gaa gag ctc     205
Thr Lys Asp Asn Asn Ala His Thr Val Lys Ser Arg Leu Glu Glu Leu
 29                  34                  39                  44

gat gag agc tat atc gag aag ttt act gac ttt ctt cgg ctc ttt gtg     253
Asp Glu Ser Tyr Ile Glu Lys Phe Thr Asp Phe Leu Arg Leu Phe Val
 45                  50                  55                  60

agt gtt cac cta aga aga atc gag tct tac tcc cag ttc cct gtg gtg     301
Ser Val His Leu Arg Arg Ile Glu Ser Tyr Ser Gln Phe Pro Val Val
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 61                  66                  71                  76

gag ttt ttg aca ctt ttg ttc aag tac aca ttt cat cag cct act cat      349
Glu Phe Leu Thr Leu Leu Phe Lys Tyr Thr Phe His Gln Pro Thr His
 77                  82                  87                  92

gaa ggt tac ttc tct tgt ttg gat atc tgg acg ctg ttt ttg gac tat      397
Glu Gly Tyr Phe Ser Cys Leu Asp Ile Trp Thr Leu Phe Leu Asp Tyr
 93                  98                 103                 108

ctg aca agt aaa att aaa agt cgt ctt gga gac aag gaa gca gtt ctc      445
Leu Thr Ser Lys Ile Lys Ser Arg Leu Gly Asp Lys Glu Ala Val Leu
109                 114                 119                 124

aac agg tac gaa gat gcc ctg gtg ctc ctg ctc aca gag gtg ttg aat      493
Asn Arg Tyr Glu Asp Ala Leu Val Leu Leu Leu Thr Glu Val Leu Asn
125                 130                 135                 140

cga atc cag ttc aga tac aac caa gcc cag ctg gag gag ttg gat gat      541
Arg Ile Gln Phe Arg Tyr Asn Gln Ala Gln Leu Glu Glu Leu Asp Asp
141                 146                 151                 156

gag act ctg gat gac gat cag cag acg gag tgg cag cgg tac tta cgg      589
Glu Thr Leu Asp Asp Asp Gln Gln Thr Glu Trp Gln Arg Tyr Leu Arg
157                 162                 167                 172

cag agc ttg gag gtg gtg gcc aaa gtg atg gag ctc ctg ccc acg cac      637
Gln Ser Leu Glu Val Val Ala Lys Val Met Glu Leu Leu Pro Thr His
173                 178                 183                 188

gcc ttc tcc aca ctg ttc cct gtt ctt cag gac aat tta gaa gtt tat      685
Ala Phe Ser Thr Leu Phe Pro Val Leu Gln Asp Asn Leu Glu Val Tyr
189                 194                 199                 204

ttg gga tta caa cag ttt ata gtc act tca ggg tca gga cac agg ttg      733
Leu Gly Leu Gln Gln Phe Ile Val Thr Ser Gly Ser Gly His Arg Leu
205                 210                 215                 220

aac atc acg gcg gag aac gac tgc cgg cgg ctg cac tgc tcc ctg aga      781
Asn Ile Thr Ala Glu Asn Asp Cys Arg Arg Leu His Cys Ser Leu Arg
221                 226                 231                 236

gac ttg agc tcc ctg ctg cag gcc gtg ggc cgc ctg gcc gag tac ttt      829
Asp Leu Ser Ser Leu Leu Gln Ala Val Gly Arg Leu Ala Glu Tyr Phe
237                 242                 247                 252

atc ggg gat gtg ttt gct gca cgg ttc aat gat gcc ctc aca gtc gtg      877
Ile Gly Asp Val Phe Ala Ala Arg Phe Asn Asp Ala Leu Thr Val Val
253                 258                 263                 268

gaa agg ttg gtc aaa gtc act ctg tac gga tct cag ata aaa ttg tac      925
Glu Arg Leu Val Lys Val Thr Leu Tyr Gly Ser Gln Ile Lys Leu Tyr
269                 274                 279                 284

aac att gaa act gct gtg cca tca gta ttg aaa cct gac ctc att gat      973
Asn Ile Glu Thr Ala Val Pro Ser Val Leu Lys Pro Asp Leu Ile Asp
285                 290                 295                 300
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gtg cat gct cag tcc ctg gct gcg ctg cag gct tac tct cac tgg tta     1021
Val His Ala Gln Ser Leu Ala Ala Leu Gln Ala Tyr Ser His Trp Leu
301                 306                 311                 316

gca cag tat tgc agt gaa gtt cac cgg cag aac acg cag cag ttc gtg     1069
Ala Gln Tyr Cys Ser Glu Val His Arg Gln Asn Thr Gln Gln Phe Val
317                 322                 327                 332

aca ctc atc tct act acc atg gat gca atc aca cct cta atc agc acc     1117
Thr Leu Ile Ser Thr Thr Met Asp Ala Ile Thr Pro Leu Ile Ser Thr
333                 338                 343                 348

aag gtc caa gac aag ctg ctg cta tct gcg tgc cac tta ctg gtc tca     1165
Lys Val Gln Asp Lys Leu Leu Leu Ser Ala Cys His Leu Leu Val Ser
349                 354                 359                 364

ctg gcc acc acc gtg cgg ccc gtc ttt ctg atc agc atc cct gca gtg     1213
Leu Ala Thr Thr Val Arg Pro Val Phe Leu Ile Ser Ile Pro Ala Val
365                 370                 375                 380

cag aaa gta ttc aac aga atc act gat gcc tct gcc ctg cga ctt gtc     1261
Gln Lys Val Phe Asn Arg Ile Thr Asp Ala Ser Ala Leu Arg Leu Val
381                 386                 391                 396

gat aag gcc cag gtg ttg gtg tgc cga gcc ctc tct aac atc ttg ctg     1309
Asp Lys Ala Gln Val Leu Val Cys Arg Ala Leu Ser Asn Ile Leu Leu
397                 402                 407                 412

ctt ccg tgg cca aac ctt cca gag aat gag cag cag tgg ccc gtg cgc     1357
Leu Pro Trp Pro Asn Leu Pro Glu Asn Glu Gln Gln Trp Pro Val Arg
413                 418                 423                 428

tcc atc aac cac gcc agc ctc atc tct gca ctc tcc cgg gac tat cgc     1405
Ser Ile Asn His Ala Ser Leu Ile Ser Ala Leu Ser Arg Asp Tyr Arg
429                 434                 439                 444

aac ctg aag ccc agt gct gtt gcc cca cag aga aag atg cca ctg gat     1453
Asn Leu Lys Pro Ser Ala Val Ala Pro Gln Arg Lys Met Pro Leu Asp
445                 450                 455                 460

gac acc aaa ctg att atc cac cag aca ctc agc gtc tta gaa gat att     1501
Asp Thr Lys Leu Ile Ile His Gln Thr Leu Ser Val Leu Glu Asp Ile
461                 466                 471                 476

gtg gag aat atc tcg ggg gag tcc acc aag tct cga cag att tgc tac     1549
Val Glu Asn Ile Ser Gly Glu Ser Thr Lys Ser Arg Gln Ile Cys Tyr
477                 482                 487                 492

cag tcg ctg cag gaa tct gtt cag gtc tcc ctg gcc ctc ttt cca gct     1597
Gln Ser Leu Gln Glu Ser Val Gln Val Ser Leu Ala Leu Phe Pro Ala
493                 498                 503                 508

ttt atc cat cag tca gat gtg act gat gag atg ctg agc ttc ttc ctc     1645
Phe Ile His Gln Ser Asp Val Thr Asp Glu Met Leu Ser Phe Phe Leu
509                 514                 519                 524
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act ctg ttt cga ggc ctt aga gta cag atg ggt gtg cct ttc act gag     1693
Thr Leu Phe Arg Gly Leu Arg Val Gln Met Gly Val Pro Phe Thr Glu
525                 530                 535                 540

caa atc ata cag act ttc ctc aac atg ttt acc aga gag cag tta gcc     1741
Gln Ile Ile Gln Thr Phe Leu Asn Met Phe Thr Arg Glu Gln Leu Ala
541                 546                 551                 556

gag agc atc ctc cac gag ggc agc aca ggc tgc cgg gtg gtg gag aag     1789
Glu Ser Ile Leu His Glu Gly Ser Thr Gly Cys Arg Val Val Glu Lys
557                 562                 567                 572

ttt ctg aag atc ctg cag gtg gtg gtc cag gag cca ggc cag gtg ttc     1837
Phe Leu Lys Ile Leu Gln Val Val Val Gln Glu Pro Gly Gln Val Phe
573                 578                 583                 588

aag ccc ttc ctc ccc agc atc atc gcc ctg tgc atg gag caa gtg tat     1885
Lys Pro Phe Leu Pro Ser Ile Ile Ala Leu Cys Met Glu Gln Val Tyr
589                 594                 599                 604

ccc atc att gcc gag cgt ccc tcc cct gat gtg aag gcc gag ctg ttt     1933
Pro Ile Ile Ala Glu Arg Pro Ser Pro Asp Val Lys Ala Glu Leu Phe
605                 610                 615                 620

gag ctc ctt ttc cgg acg ctc cat cac aac tgg agg tac ttc ttc aag     1981
Glu Leu Leu Phe Arg Thr Leu His His Asn Trp Arg Tyr Phe Phe Lys
621                 626                 631                 636

tcc acc gtg ctg gcc agt gtc cag agg ggg atc gct gag gag cag atg     2029
Ser Thr Val Leu Ala Ser Val Gln Arg Gly Ile Ala Glu Glu Gln Met
637                 642                 647                 652

gag aat gag ccc cag ttc agt gcc atc atg cag gct ttc gga cag tcc     2077
Glu Asn Glu Pro Gln Phe Ser Ala Ile Met Gln Ala Phe Gly Gln Ser
653                 658                 663                 668

ttt ctc cag ccc gac atc cac ctt ttt aaa caa aat ctc ttc tac ttg     2125
Phe Leu Gln Pro Asp Ile His Leu Phe Lys Gln Asn Leu Phe Tyr Leu
669                 674                 679                 684

gag act ctc aac acc aag cag aag ctg tac cac aag aag atc ttc cgg     2173
Glu Thr Leu Asn Thr Lys Gln Lys Leu Tyr His Lys Lys Ile Phe Arg
685                 690                 695                 700

act gcc atg ctg ttc cag ttt gtg aac gtg ctg ctc cag gtc ctg gtc     2221
Thr Ala Met Leu Phe Gln Phe Val Asn Val Leu Leu Gln Val Leu Val
701                 706                 711                 716

cac aag tcc cat gat ctt ctg cag gag gag att ggc atc gcc atc tac     2269
His Lys Ser His Asp Leu Leu Gln Glu Glu Ile Gly Ile Ala Ile Tyr
717                 722                 727                 732

aac atg gcc tca gtc gac ttt gat ggc ttc ttt gcc gcc ttc ctc cca     2317
Asn Met Ala Ser Val Asp Phe Asp Gly Phe Phe Ala Ala Phe Leu Pro
733                 738                 743                 748

gag ttc ctg acc agc tgt gat ggt gtg gat gcc aac cag aaa agt gtg     2365
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Leu Gly Arg Asn Phe Lys Met Asp Arg Val Arg Arg Glu Arg Gly Arg
765                 770                 775                 780

gct aag agg agg gca gag tgg gca cgc aag cct ggc acc tgt gca gca     2461
Ala Lys Arg Arg Ala Glu Trp Ala Arg Lys Pro Gly Thr Cys Ala Ala
781                 786                 791                 796

agg agg ggg cac att gag gcc tct ggg cgt ggt ctg tgc cca ccc tgc     2509
Arg Arg Gly His Ile Glu Ala Ser Gly Arg Gly Leu Cys Pro Pro Cys
797                 802                 807                 812

agc ttg gcg gca gct cac gag atg cct gct gac ctg gtg ctg tag cct     2557
Ser Leu Ala Ala Ala His Glu Met Pro Ala Asp Leu Val Leu  *
813                 818                 823

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Gly Arg Phe Cys Ile Leu Gly Ser Glu Ala Ala Thr Arg Lys His Leu
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Pro Ala Arg Asn His Cys Gly Leu Ser Asp Ser Ser Pro Gln Leu Trp
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Leu Asp Phe Lys Arg Tyr Val Thr Asp Arg Arg Leu Ala Glu Thr Leu
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gcg caa atc tat ttg gga aaa cca agt aga cct cca cac cta ctg ctg      464
Ala Gln Ile Tyr Leu Gly Lys Pro Ser Arg Pro Pro His Leu Leu Leu
 85                  90                  95                 100

gag tgc aat cca ggt cct gga atc ctg act cag gca tta ctt gaa gct      512
Glu Cys Asn Pro Gly Pro Gly Ile Leu Thr Gln Ala Leu Leu Glu Ala
101                 106                 111                 116

ggt gcc aaa gtg gtt gcg ctc gaa agt gac aaa act ttt att cca cat      560
Gly Ala Lys Val Val Ala Leu Glu Ser Asp Lys Thr Phe Ile Pro His
117                 122                 127                 132

ttg gag tcc tta gga aaa aat ctg gat gga aaa cta cga gtg att cac      608
Leu Glu Ser Leu Gly Lys Asn Leu Asp Gly Lys Leu Arg Val Ile His
133                 138                 143                 148

tgt gac ttc ttt aaa cta gat cct aga agt ggt gga gta ata aaa cca      656
Cys Asp Phe Phe Lys Leu Asp Pro Arg Ser Gly Gly Val Ile Lys Pro
149                 154                 159                 164

cct gct atg tct tct cga ggg ctc ttt aag aat ttg gga ata gaa gca      704
Pro Ala Met Ser Ser Arg Gly Leu Phe Lys Asn Leu Gly Ile Glu Ala
165                 170                 175                 180

gtt cct tgg aca gca gac atc cct tta aaa gta gtt gga atg ttc cca      752
Val Pro Trp Thr Ala Asp Ile Pro Leu Lys Val Val Gly Met Phe Pro
181                 186                 191                 196

agt aga ggt gag aaa agg gca ctt tgg aaa ctc gca tat gac ttg tat      800
Ser Arg Gly Glu Lys Arg Ala Leu Trp Lys Leu Ala Tyr Asp Leu Tyr
197                 202                 207                 212

tcc tgt act tct ata tat aaa ttt gga cga ata gaa gta aat atg ttt      848
Ser Cys Thr Ser Ile Tyr Lys Phe Gly Arg Ile Glu Val Asn Met Phe
213                 218                 223                 228

att ggt gaa aaa gaa ttc cag aaa cta atg gca gat ccc gga aat cca      896
Ile Gly Glu Lys Glu Phe Gln Lys Leu Met Ala Asp Pro Gly Asn Pro
229                 234                 239                 244

gac ttg tat cat gta tta agt gtt atc tgg caa tta gct tgt gag att      944
Asp Leu Tyr His Val Leu Ser Val Ile Trp Gln Leu Ala Cys Glu Ile
245                 250                 255                 260

aag gtt ctg cac atg gag cct tgg tca tca ttt gat ata tac acc cgg      992
Lys Val Leu His Met Glu Pro Trp Ser Ser Phe Asp Ile Tyr Thr Arg
261                 266                 271                 276

aaa ggg ccg ctg gaa aac cca aag cgt agg gaa tta tta gac caa tta     1040
Lys Gly Pro Leu Glu Asn Pro Lys Arg Arg Glu Leu Leu Asp Gln Leu
277                 282                 287                 292
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caa caa aag ctg tat ctt att caa atg att cct cgt caa aat tta ttt     1088
Gln Gln Lys Leu Tyr Leu Ile Gln Met Ile Pro Arg Gln Asn Leu Phe
293                 298                 303                 308

acc aag aac tta aca cct atg aac tat aat ata ttt ttt cac ttg tta     1136
Thr Lys Asn Leu Thr Pro Met Asn Tyr Asn Ile Phe Phe His Leu Leu
309                 314                 319                 324

aag cac tgt ttt ggg agg cgc agc gcc act gta ata gac cac tta cgt     1184
Lys His Cys Phe Gly Arg Arg Ser Ala Thr Val Ile Asp His Leu Arg
325                 330                 335                 340

tca ttg act cca ctt gat gcg aga gat ata ttg atg caa ata gga aaa     1232
Ser Leu Thr Pro Leu Asp Ala Arg Asp Ile Leu Met Gln Ile Gly Lys
341                 346                 351                 356

cag gag gat gag aaa gta gtt aac atg cac cct caa gac ttc aaa aca     1280
Gln Glu Asp Glu Lys Val Val Asn Met His Pro Gln Asp Phe Lys Thr
357                 362                 367                 372

ctt ttt gaa act ata gag cgt tcc aaa gat tgt gct tat aaa tgg ctg     1328
Leu Phe Glu Thr Ile Glu Arg Ser Lys Asp Cys Ala Tyr Lys Trp Leu
373                 378                 383                 388

tat gat gaa acc ctg gaa gat agg tag caact agactgtcgt ttttggtgga     1380
Tyr Asp Glu Thr Leu Glu Asp Arg  *
389                 394

gcggttcatt tatttggaaa ctatgacatg aaaaccaaat ttgaaaactc acatcctttc   1440

agcagaaggt aactgttctt gtcttgcaca agccaggcag atcatttctc ctaagctgat   1500

atcattggct tattggatga aacagtgtct gctattttat tcacaattaa ataaaatgaa   1560

aacttcaatt aattgtggat ttgatcagat tgaattcgtt ttgtttcaga ttcctattta   1620

aatatttcac ttgtactgtt gctgattttt gcatcttctt gaagagcaag agtctgtaca   1680

ttattaagct tagaaagtaa gcaaaactga tttactggtt tgcctttcag tttgttgaaa   1740

tgtattgtca agtactgtac aatgaaattg tttaaatttt aatatgattt aagcttttta   1800

gaaattaaaa tattttaaat aagaagaaaa aaaaaa                              1836
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<213> Homo sapiens

<220>
<221> CDS
<222> (366)..(1652)

<220>
<221> misc_feature
<222> (1)...(1721)
<223> n = a,t,c or g

<400> 202
ttcgagtaca ctacnccagn gcggnggaat ncgccaactt ggnntcccna tgaatgttcc 60

tcgtcgggca aaagataagg atccgatctc ccccggcccg gtgtgcagca ggagcgacca 120

accccgaccc gggttaaaac tcccagggac tcttcgctgc tgccacctct tgttctctcc 180

cccgttccca ctcggggtct ccctcagggc cgggaggcac agcggtccct gcttgctgaa 240

gggctggatg tacgcatccg caggttcccg cggacttggg ggcgcccgct gagccccggc 300

gcccgcagaa gacttgtgtt tgcctcctgc agcctcaacc cggagggcag cgagggccta 360

ccacc atg atc act ggt gtg ttc agc atg cgc ttg tgg acc cca gtg 407
Met Ile Thr Gly Val Phe Ser Met Arg Leu Trp Thr Pro Val
1 5 10

ggc gtc ctg acc tcg ctg gcg tac tgc ctg cac cag cgg cgg gtg gcc 455
Gly Val Leu Thr Ser Leu Ala Tyr Cys Leu His Gln Arg Arg Val Ala
15 20 25 30

ctg gcc gag ctg cag gag gcc gat ggc cag tgt ccg gtc gac cgc agc 503
Leu Ala Glu Leu Gln Glu Ala Asp Gly Gln Cys Pro Val Asp Arg Ser
31 36 41 46

ctg ctg aag ttg aaa atg gtg cag gtc gtg ttt cga cac ggg gct cgg 551
Leu Leu Lys Leu Lys Met Val Gln Val Val Phe Arg His Gly Ala Arg
47 52 57 62

agt cct ctc aag ccg ctc ccg ctg gag gag cag gta gag tgg aac ccc 599
Ser Pro Leu Lys Pro Leu Pro Leu Glu Glu Gln Val Glu Trp Asn Pro
63 68 73 78

cag cta tta gag gtc cca ccc caa act cag ttt gat tac aca gtc acc 647
Gln Leu Leu Glu Val Pro Pro Gln Thr Gln Phe Asp Tyr Thr Val Thr
79 84 89 94

aat cta gct ggt ggt ccg aaa cca tat tct cct tac gac tct caa tac 695
Asn Leu Ala Gly Gly Pro Lys Pro Tyr Ser Pro Tyr Asp Ser Gln Tyr
95 100 105 110

cat gag acc acc ctg aag ggg ggc atg ttt gct ggg cag ctg acc aag 743
His Glu Thr Thr Leu Lys Gly Gly Met Phe Ala Gly Gln Leu Thr Lys
111 116 121 126

gtg ggc atg cag caa atg ttt gcc ttg gga gag aga ctg agg aag aac 791
Val Gly Met Gln Gln Met Phe Ala Leu Gly Glu Arg Leu Arg Lys Asn
127 132 137 142

tat gtg gaa gac att ccc ttt ctt tca cca acc ttc aac cca cag gag 839
Tyr Val Glu Asp Ile Pro Phe Leu Ser Pro Thr Phe Asn Pro Gln Glu
143 148 153 158

Document: 2006/0063250 A1

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gtc ttt att cgt tcc act aac att ttt cgg aat ctg gag tcc acc cgt      887
Val Phe Ile Arg Ser Thr Asn Ile Phe Arg Asn Leu Glu Ser Thr Arg
159                 164                 169                 174

tgt ttg ctg gct ggg ctt ttc cag tgt cag aaa gaa gga ccc atc atc      935
Cys Leu Leu Ala Gly Leu Phe Gln Cys Gln Lys Glu Gly Pro Ile Ile
175                 180                 185                 190

atc cac act gat gaa gca gat tca gaa gtc ttg tat ccc aac tac caa      983
Ile His Thr Asp Glu Ala Asp Ser Glu Val Leu Tyr Pro Asn Tyr Gln
191                 196                 201                 206

agc tgc tgg agc ctg agg cag aga acc aga ggc cgg agg cag act gcc     1031
Ser Cys Trp Ser Leu Arg Gln Arg Thr Arg Gly Arg Arg Gln Thr Ala
207                 212                 217                 222

tct tta cag cca gga atc tca gag gat ttg aaa aag gtg aag gac agg     1079
Ser Leu Gln Pro Gly Ile Ser Glu Asp Leu Lys Lys Val Lys Asp Arg
223                 228                 233                 238

atg ggc att gac agt agt gat aaa gtg gac ttc ttc atc ctc ctg gac     1127
Met Gly Ile Asp Ser Ser Asp Lys Val Asp Phe Phe Ile Leu Leu Asp
239                 244                 249                 254

aac gtg gct gcc gag cag gca cac aac ctc cca agc tgc ccc atg ctg     1175
Asn Val Ala Ala Glu Gln Ala His Asn Leu Pro Ser Cys Pro Met Leu
255                 260                 265                 270

aag aga ttt gca cgg atg atc gaa cag aga gct gtg gac aca tcc ttg     1223
Lys Arg Phe Ala Arg Met Ile Glu Gln Arg Ala Val Asp Thr Ser Leu
271                 276                 281                 286

tac ata ctg ccc aag gaa gac agg gaa agt ctt cag atg gca gta ggc     1271
Tyr Ile Leu Pro Lys Glu Asp Arg Glu Ser Leu Gln Met Ala Val Gly
287                 292                 297                 302

cca ttc ctc cac atc cta gag agc aac ctg ctg aaa gcc atg gac tct     1319
Pro Phe Leu His Ile Leu Glu Ser Asn Leu Leu Lys Ala Met Asp Ser
303                 308                 313                 318

gcc act gcc ccc gac aag atc aga aag ctg tat ctc tat gcg gct cat     1367
Ala Thr Ala Pro Asp Lys Ile Arg Lys Leu Tyr Leu Tyr Ala Ala His
319                 324                 329                 334

gat gtg acc ttc ata ccg ctc tta atg acc ctg ggg att ttt gac cac     1415
Asp Val Thr Phe Ile Pro Leu Leu Met Thr Leu Gly Ile Phe Asp His
335                 340                 345                 350

aaa tgg cca ccg ttt gct gtt gac ctg acc atg gaa ctt tac cag cac     1463
Lys Trp Pro Pro Phe Ala Val Asp Leu Thr Met Glu Leu Tyr Gln His
351                 356                 361                 366

ctg gaa tct aag gag tgg ttt gtg cag ctc tat tac cac ggg aag gag     1511
Leu Glu Ser Lys Glu Trp Phe Val Gln Leu Tyr Tyr His Gly Lys Glu
367                 372                 377                 382
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cag gtg ccg aga ggt tgc cct gat ggg ctc tgc ccg ctg gac atg ttc     1559
Gln Val Pro Arg Gly Cys Pro Asp Gly Leu Cys Pro Leu Asp Met Phe
383                 388                 393                 398

ttg aat gcc atg tca gtt tat acc tta agc cca gaa aaa tac cat gca     1607
Leu Asn Ala Met Ser Val Tyr Thr Leu Ser Pro Glu Lys Tyr His Ala
399                 404                 409                 414

ctc tgc tct caa act cag gtg atg gaa gtt gga aat gaa gag taa ctg     1655
Leu Cys Ser Gln Thr Gln Val Met Glu Val Gly Asn Glu Glu  *
415                 420                 425

atttataaaa gcaggatgtg ttgattttaa aataaagtgc ctttatacaa aaaaaaaaaa   1715

aaaaaa                                                             1721
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<210> 203
<211> 4071
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (267)..(2069)

<400> 203

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ccttgtatag cgatgaccca gctggctagc gtttaaactt aagcttggta ccgagctcgg     60

atccactagt ccagtgtggt ggaattcgct gcgtccagtg aacacttcag cacctgcagc    120

acagaagggc caaggagctg cagtcctcga ccagcaggag gtttgctcct cagcccactc    180

gctgcatcca gatcagctca cccctctccc ttccctgccc accaggactc tgatagcccc    240

tggcagccac agcccatttt gccaag atg tct aga gta gcc aaa tat cgc cgg     293
                              Met Ser Arg Val Ala Lys Tyr Arg Arg
                                1               5

cag gtg agt gaa gac ccc gac atc gac agc ctg ctg gag acc ctg tct      341
Gln Val Ser Glu Asp Pro Asp Ile Asp Ser Leu Leu Glu Thr Leu Ser
 10                  15                  20                  25

ccc gag gag atg gag gag ctg gag aag gag ctg gac gtg gtg gac cca      389
Pro Glu Glu Met Glu Glu Leu Glu Lys Glu Leu Asp Val Val Asp Pro
 26                  31                  36                  41

gac ggg agt gtt ccc gtg ggg ctg cgg cag aga aac cag acg gag aaa      437
Asp Gly Ser Val Pro Val Gly Leu Arg Gln Arg Asn Gln Thr Glu Lys
 42                  47                  52                  57

cag tcc acg ggt gtg tac aac cgg gag gcc atg ctc aac ttc tgt gaa      485
Gln Ser Thr Gly Val Tyr Asn Arg Glu Ala Met Leu Asn Phe Cys Glu
 58                  63                  68                  73
```

```
aag gag acc aag aaa ctt atg cag agg gag atg tcc atg gat gaa agc      533
Lys Glu Thr Lys Lys Leu Met Gln Arg Glu Met Ser Met Asp Glu Ser
 74                  79                  84                  89

aag caa gtg gag acc aag aca gat gcc aag aat gga cag gaa agg ggc      581
Lys Gln Val Glu Thr Lys Thr Asp Ala Lys Asn Gly Gln Glu Arg Gly
 90                  95                 100                 105

aga gat gcc agc aaa aaa gcc ctg ggc ccc aga cgg aac tca gat ctg      629
Arg Asp Ala Ser Lys Lys Ala Leu Gly Pro Arg Arg Asn Ser Asp Leu
106                 111                 116                 121

ggg aag gag cca aag agg ggt ggt tta aag aaa agc ttc tct aga gac      677
Gly Lys Glu Pro Lys Arg Gly Gly Leu Lys Lys Ser Phe Ser Arg Asp
122                 127                 132                 137

aga gat gaa gct ggt ggc aag agt ggc gag aag ccc aag gag gag aag      725
Arg Asp Glu Ala Gly Gly Lys Ser Gly Glu Lys Pro Lys Glu Glu Lys
138                 143                 148                 153

atc atc cgg ggc att gac aag ggc cgg gtc agg gct gca gtg gat aag      773
Ile Ile Arg Gly Ile Asp Lys Gly Arg Val Arg Ala Ala Val Asp Lys
154                 159                 164                 169

aag gag gca ggg aag gat ggg aga gga gag gag agg gca gtg gcc acc      821
Lys Glu Ala Gly Lys Asp Gly Arg Gly Glu Glu Arg Ala Val Ala Thr
170                 175                 180                 185

aag aag gaa gag gag aag aaa ggg agt gac agg aac aca ggc ttg agc      869
Lys Lys Glu Glu Glu Lys Lys Gly Ser Asp Arg Asn Thr Gly Leu Ser
186                 191                 196                 201

agg gac aag gat aaa aag aga gag gag atg aag gag gtg gcc aag aaa      917
Arg Asp Lys Asp Lys Lys Arg Glu Glu Met Lys Glu Val Ala Lys Lys
202                 207                 212                 217

gag gat gat gag aag gta aaa ggg gag cgt agg aac aca gac acc aga      965
Glu Asp Asp Glu Lys Val Lys Gly Glu Arg Arg Asn Thr Asp Thr Arg
218                 223                 228                 233

aaa gag ggt gag aag atg aaa aga gca ggt ggg aac aca gac atg aaa     1013
Lys Glu Gly Glu Lys Met Lys Arg Ala Gly Gly Asn Thr Asp Met Lys
234                 239                 244                 249

aag gag gat gag aag gta aaa aga gga act ggg aac aca gac acc aaa     1061
Lys Glu Asp Glu Lys Val Lys Arg Gly Thr Gly Asn Thr Asp Thr Lys
250                 255                 260                 265

aag gac gat gaa aaa gtc aag aag aat gaa ccc tta cat gaa aag gaa     1109
Lys Asp Asp Glu Lys Val Lys Lys Asn Glu Pro Leu His Glu Lys Glu
266                 271                 276                 281

gcc aag gat gac agc aag acc aaa aca ccc gag aaa cag acg ccc agt     1157
Ala Lys Asp Asp Ser Lys Thr Lys Thr Pro Glu Lys Gln Thr Pro Ser
282                 287                 292                 297

ggc ccc acc aag ccc tct gaa gga ccg gcc aag gtg gag gag gag gca     1205
```

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Gly Pro Thr Lys Pro Ser Glu Gly Pro Ala Lys Val Glu Glu Glu Ala
298                 303                 308                 313

gct ccc agc ata ttt gat gag cct ctg gag aga gtg aag aac aat gac     1253
Ala Pro Ser Ile Phe Asp Glu Pro Leu Glu Arg Val Lys Asn Asn Asp
314                 319                 324                 329

ccc gag atg act gag gtg aac gtc aac aac tca gac tgc atc aca aat     1301
Pro Glu Met Thr Glu Val Asn Val Asn Asn Ser Asp Cys Ile Thr Asn
330                 335                 340                 345

gag atc ttg gtc cgg ttt act gag gct ctg gag ttc aac act gtg gtt     1349
Glu Ile Leu Val Arg Phe Thr Glu Ala Leu Glu Phe Asn Thr Val Val
346                 351                 356                 361

aag ctg ttc gcc ttg gcc aac acg cga gcc gat gac cac gtg gcc ttt     1397
Lys Leu Phe Ala Leu Ala Asn Thr Arg Ala Asp Asp His Val Ala Phe
362                 367                 372                 377

gcc att gcc atc atg ctc aag gcc aac aag acc atc acc agc ctc aac     1445
Ala Ile Ala Ile Met Leu Lys Ala Asn Lys Thr Ile Thr Ser Leu Asn
378                 383                 388                 393

ctg gac tcc aac cac atc aca ggc aaa ggc atc ctg gcc atc ttc cgg     1493
Leu Asp Ser Asn His Ile Thr Gly Lys Gly Ile Leu Ala Ile Phe Arg
394                 399                 404                 409

gcc ctc ctc cag aac aac acg ctg acc gag ctc cgc ttc cac aac cag     1541
Ala Leu Leu Gln Asn Asn Thr Leu Thr Glu Leu Arg Phe His Asn Gln
410                 415                 420                 425

cga cac atc tgt gga ggc aag acg gag atg gag atc gcc aag ctg ctg     1589
Arg His Ile Cys Gly Gly Lys Thr Glu Met Glu Ile Ala Lys Leu Leu
426                 431                 436                 441

aag gag aat act acc ctg ctc aag ctg ggc tac cat ttt gag ctg gcc     1637
Lys Glu Asn Thr Thr Leu Leu Lys Leu Gly Tyr His Phe Glu Leu Ala
442                 447                 452                 457

ggg ccc cga atg act gtc acc aat ctg ctc agc cgc aac atg gac aag     1685
Gly Pro Arg Met Thr Val Thr Asn Leu Leu Ser Arg Asn Met Asp Lys
458                 463                 468                 473

cag aga caa aag cgg ctg cag gag caa agg cag gca cag gaa gcc aag     1733
Gln Arg Gln Lys Arg Leu Gln Glu Gln Arg Gln Ala Gln Glu Ala Lys
474                 479                 484                 489

gga gag aag aag gat ctg ctg gag gta ccc aag gcc ggg gcc gtg gct     1781
Gly Glu Lys Lys Asp Leu Leu Glu Val Pro Lys Ala Gly Ala Val Ala
490                 495                 500                 505

aag ggc tcc cca aaa cct tca cct caa cca tct cca aag ccc tct cca     1829
Lys Gly Ser Pro Lys Pro Ser Pro Gln Pro Ser Pro Lys Pro Ser Pro
506                 511                 516                 521

aag aac tca ccc aaa aaa ggg ggt gct cca gct gcc cca cca ccc cct     1877
Lys Asn Ser Pro Lys Lys Gly Gly Ala Pro Ala Ala Pro Pro Pro Pro
```

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522                 527                 532                 537

ccc cct ccc ttg gct cca ccc ctt atc atg gag aac ctg aag aat tca     1925
Pro Pro Pro Leu Ala Pro Pro Leu Ile Met Glu Asn Leu Lys Asn Ser
538                 543                 548                 553

ctc tca cca gct acc cag agg aag atg gga gac aaa gtc ctc cct gcc     1973
Leu Ser Pro Ala Thr Gln Arg Lys Met Gly Asp Lys Val Leu Pro Ala
554                 559                 564                 569

cag gag aag aac tcc cgt gac cag cta ttg gct gcc atc cgc tcc agc     2021
Gln Glu Lys Asn Ser Arg Asp Gln Leu Leu Ala Ala Ile Arg Ser Ser
570                 575                 580                 585

aac ctc aag cag ctc aag aag gtg gaa gtg ccc aaa ctg ctt cag tag     2069
Asn Leu Lys Gln Leu Lys Lys Val Glu Val Pro Lys Leu Leu Gln  *
586                 591                 596                 601

gaccaggctg ccaggcacca tctgccaatg ccatgactgc tcaggcctca cctcccaggg   2129

ctacacagac cctgcccacc ccatccctgg ctgacctgct gtggatgtcc ctattctgcc   2189

atgggagagt ccaggcctgg gtcacgctca aggaaggatg ccttatctct tctcactttc   2249

cttttcttgt ctctgaggct ctccaaattt tgctttagta catggagctc aggtttctgg   2309

acaagaagag tccttttagc acatcactga gaagatggca ctgtccaggg cccatgtagc   2369

tggcaagctg caaaaggcct gtgatccagg aaagatgtcc cacagggacc acatccaccc   2429

cagccccact gccctccagg gccaggattc aggcctctga ggagcccacg gggcaaagct   2489

gctgggccag tggcactctg tgtgggaaaa tggcagaaag atggagaggc atgggggccc   2549

aaaggggagc gtggggaggg gctgaggata ccccaaagtc caggctaatt agaggatgtg   2609

gcaggggcag tggcctggat gcacagtgcc tgatgggagt aggctccaga caggaggagt   2669

gggacagaca gcagctggac ttgaaggttt gatgccaaag cagacatttt cctcacaccc   2729

acctgctgct gtatgaatag ctgtgtatct gtttttccat aagattttga taatatatac   2789

aaacctttag ctgtgaatgg ctgtgcccca cctgttgtcc tgaactgtga gtcctgatcc   2849

taaccctggg ctccctggag gactctagaa gctcaggttc cctgccacac tatttgagtt   2909

ggccaagaaa taaattcaca tcctcagaaa gtgcagcatg gaggaaaatc tgaactctaa   2969

gcagaagact ctccactgac ctggttgtcc aggtctagaa ggccaggcct ctactaggtc   3029

tgctcctgaa ccagtcctgc tgcctggagt cagtagccag agttgttctc aggggtgctg   3089

gggcagagtg gagcccaggg tgctgggatg gctatattag gcatgttcag ggatgctcat   3149

tccatgactc tgcctaacca tgggctcagg gccaggtcct cacagcagtc acaggcccag   3209

gaaggcggca ggcagagaag tggagtgact atttggagaa tagcacccat atctgtgtgc   3269
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cctagggctc agcaggggcc tcatcttccc cagccctccc cacctgctca ccaattccac   3329

ttcctgcccc aactgcagga atgctgacaa tgctgccatg cccaccatcg ggtgtaggtg   3389

aaaggcatct ttctgaattt cattctcttg aaggtgctgc cacccccttgg cactgtggaa   3449

ctgccacctt gggtctgtgt cacttgtagg tttctctgcc tccaggttgc ctcaacagca   3509

ggaggcacag cagtttcacc atctttgagg tgagggtggg gtgccccagc taggaagcaa   3569

gatcgctgtg ctaggtctga ccaaaaccag agggcagtct agtcctgggg gtaaagccct   3629

cagatcccag ggtacactct tctccattcc ctccacccac ttgcctgtca ccccagtcac   3689

ctaagcaatc actgggccca gaggagagga gacagacaca cactggctcc tggacctaaa   3749

gggtatgagc tggagctaag gccagctaga gcttccactg tcagccctca ctgtcagccc   3809

cactgcaccc ccctgtgcct gctgggcact gggcactagc tagatgcttt aggttgcttc   3869

agctgatcct tcaactctgt gaggtggata ccaatattct attttgcaga tagaatttgg   3929

cccagagagg ttaactaata tatccatgat cacacagcta ataaaagtca ggtcgacgcg   3989

gccgcgaatt ccagatctat gaatcgtaga tactgaaaaa ccccgcaagt tcacttcaac   4049

tgtgcatcgt gcaccatctc aa                                            4071
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<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (99)..(974)

<400> 204

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ctatagggag acccaagctg gctagcgttt aaacttaagc ttggtaccga gctcggatcc     60

actagtccag tgtggtggaa ttcgccctga gcgtctcc    atg gcc tgc ctg agc      113
                                             Met Ala Cys Leu Ser
                                               1

ccc tcg cag ctc cag aag ttc caa cag gat gga ttc ctg gtg ctg gaa      161
Pro Ser Gln Leu Gln Lys Phe Gln Gln Asp Gly Phe Leu Val Leu Glu
  6                  11                  16                  21

gga ttc ttg tct gcg gaa gag tgt gtg gcc atg caa caa agg att ggc      209
Gly Phe Leu Ser Ala Glu Glu Cys Val Ala Met Gln Gln Arg Ile Gly
 22                  27                  32                  37

gag ata gtg gct gaa atg gat gtt cct ctc cac tgc cgc aca gaa ttc      257
```

```
Glu Ile Val Ala Glu Met Asp Val Pro Leu His Cys Arg Thr Glu Phe
 38                  43                  48                  53

tcc acc cag gaa gag gag cag ctt cga gcc cag ggc agc aca gac tat      305
Ser Thr Gln Glu Glu Glu Gln Leu Arg Ala Gln Gly Ser Thr Asp Tyr
 54                  59                  64                  69

ttc ttg agc agt ggt gac aag att cga ttc ttc ttt gag aaa ggc gtt      353
Phe Leu Ser Ser Gly Asp Lys Ile Arg Phe Phe Phe Glu Lys Gly Val
 70                  75                  80                  85

ttt gat gag aaa gga aat ttc ctg gtc cct ccg gag aaa tcc atc aac      401
Phe Asp Glu Lys Gly Asn Phe Leu Val Pro Pro Glu Lys Ser Ile Asn
 86                  91                  96                 101

aaa att ggc cac gct ctg cac gcc cac gac ccc gtc ttc aag agc atc      449
Lys Ile Gly His Ala Leu His Ala His Asp Pro Val Phe Lys Ser Ile
102                 107                 112                 117

aca cac tcc ttc aag gtg cag acc ttg gcc aga agt ctg ggc ctc cag      497
Thr His Ser Phe Lys Val Gln Thr Leu Ala Arg Ser Leu Gly Leu Gln
118                 123                 128                 133

atg ccc gtg gtg gtg cag agc atg tac atc ttt aag caa cct cac ttt      545
Met Pro Val Val Val Gln Ser Met Tyr Ile Phe Lys Gln Pro His Phe
134                 139                 144                 149

ggc ggt gaa gtc tcc cct cat cag gac gcc tcc ttc ctg tac acg gag      593
Gly Gly Glu Val Ser Pro His Gln Asp Ala Ser Phe Leu Tyr Thr Glu
150                 155                 160                 165

ccc ctg ggc cgg gtg ctg ggc gtg tgg atc gca gtg gag gat gcc acg      641
Pro Leu Gly Arg Val Leu Gly Val Trp Ile Ala Val Glu Asp Ala Thr
166                 171                 176                 181

ctg gag aac ggc tgt ctc tgg ttc atc cct ggc tcc cac acc agt ggt      689
Leu Glu Asn Gly Cys Leu Trp Phe Ile Pro Gly Ser His Thr Ser Gly
182                 187                 192                 197

gtg tca aga agg atg gtc cgg gcc cct gtt ggc tca gcg cct ggt acc      737
Val Ser Arg Arg Met Val Arg Ala Pro Val Gly Ser Ala Pro Gly Thr
198                 203                 208                 213

agc ttc ctt ggg tca gag cca gcc cgg gat aac agc ctc ttt gtg ccc      785
Ser Phe Leu Gly Ser Glu Pro Ala Arg Asp Asn Ser Leu Phe Val Pro
214                 219                 224                 229

acc cca gtg cag aga ggg gcc ctg gtc ctc atc cat gga gaa gtg gta      833
Thr Pro Val Gln Arg Gly Ala Leu Val Leu Ile His Gly Glu Val Val
230                 235                 240                 245

cac aag agc aag cag aac ctc tct gac cgc tcg cgc cag gcc tac act      881
His Lys Ser Lys Gln Asn Leu Ser Asp Arg Ser Arg Gln Ala Tyr Thr
246                 251                 256                 261

ttc cac ctc atg gag gcc tct ggc acc acc tgg agc ccg gag aac tgg      929
Phe His Leu Met Glu Ala Ser Gly Thr Thr Trp Ser Pro Glu Asn Trp
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Case No. 77630-20

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262                 267                 272                 277

ctc cag cca aca gct gaa ctg ccc ttt ccc caa ctg tac acc taa agg      977
Leu Gln Pro Thr Ala Glu Leu Pro Phe Pro Gln Leu Tyr Thr  *
278                 283                 288

ctctcgcagg gcaggagccc tcgcccctcc cgggtgaagc tgtgggctgt aaacaccagt   1037

gccttgctca gcctcctggt tgcaacaggg aggtcttgtc tcccctcctg ggctttcctc   1097

ctgccctgtg ggcagcagcc taggctgggt caggggcttc cctaagatct tcacctctct   1157

gcctccctac tgccccaaca tagccttgag gaggcttctc agccaccaaa gggttctggc   1217

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Date Recue/Date Received 2020-06-26

<210> 205
<211> 4253
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1996)..(2481)

<220>
<221> misc_feature
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<223> n = a,t,c or g

<400> 205

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tgcgacgggc gcggtgcgta ngtacctcgc cggtggtggc cgttctccgt aagatggcgg    240

accggcggcg gcagcgcgct tcgcaagaca ccgaggacga ggaatctggt gcttcgggct    300

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ttaattcttc aacaaaagaa gagaagggag aagaaaagcc tgacaccaaa agcactgtga    660
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ctcggaaagg gctcttcttt gagcatgatc ttcgagggca aactcaggag gaggaagtca 840

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cctattcccg ggcaagaaga actcgaacca aagttggaga tgcagtcaag cttgcagagg 1500

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agcaagatgt ggcacaacta aatatagcag aacagaattg gagtccgggg cagccttctt 1680

tcctgcaacc acgggaactt cgaggtatgc ccaaccatat acacatggga gcaggacctc 1740

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catgtaccaa gtgtttttca acacctaaag gaaggtagga cttgatatga gagccctcta 1860

gaattcttat tgtttaggcc tctttctttg tctcagggtg tccagggtgt ccagggtggt 1920

cgagccaaac gctattcatc ccagcggcaa agacctgtgc cagagccccc cgcccctcca 1980

gtgcatatca gtatc atg gag gga cat tac tat gat cca ctg cag ttc cag 2031
Met Glu Gly His Tyr Tyr Asp Pro Leu Gln Phe Gln
1 5 10

gga cca atc tat acc cat ggt gac agc cct gcc ccg ctg cct cca cag 2079
Gly Pro Ile Tyr Thr His Gly Asp Ser Pro Ala Pro Leu Pro Pro Gln
13 18 23 28

ggc atg ctt gtg cag cca gga atg aac ctt ccc cac cca ggt tta cat 2127
Gly Met Leu Val Gln Pro Gly Met Asn Leu Pro His Pro Gly Leu His
29 34 39 44

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ccc cat cag aca cca gct cct ctg ccc aat cca ggc ctc tat ccc cca     2175
Pro His Gln Thr Pro Ala Pro Leu Pro Asn Pro Gly Leu Tyr Pro Pro
 45                  50                  55                  60

cca gtg tcc atg tct cca gga cag cca cca cct cag cag ttg ctt gct     2223
Pro Val Ser Met Ser Pro Gly Gln Pro Pro Pro Gln Gln Leu Leu Ala
 61                  66                  71                  76

cct act tac ttt tct gct cca ggc gtc atg aac ttt ggt aat ccc agt     2271
Pro Thr Tyr Phe Ser Ala Pro Gly Val Met Asn Phe Gly Asn Pro Ser
 77                  82                  87                  92

tac cct tat gct cca ggg gca ctg cct ccc cca cca ccg cct cat ctg     2319
Tyr Pro Tyr Ala Pro Gly Ala Leu Pro Pro Pro Pro Pro Pro His Leu
 93                  98                 103                 108

tat cct aat aca cag gcc cca tca cag gta tat gga gga gtg acc tac     2367
Tyr Pro Asn Thr Gln Ala Pro Ser Gln Val Tyr Gly Gly Val Thr Tyr
109                 114                 119                 124

tat aac ccc gcc cag cag cag gtg cag cca aag ccc tcc cca ccc cgg     2415
Tyr Asn Pro Ala Gln Gln Gln Val Gln Pro Lys Pro Ser Pro Pro Arg
125                 130                 135                 140

agg act ccc cag cca gtc acc atc aag ccc cct cca cct gag gtt gta     2463
Arg Thr Pro Gln Pro Val Thr Ile Lys Pro Pro Pro Pro Glu Val Val
141                 146                 151                 156

agc agg ggt tcc agt taa tacaag tttctgaata ttttaaatct taacatcata     2517
Ser Arg Gly Ser Ser  *
157                 162

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gggcttcaaa gatatagggt gtggctccta ccagcaaaca gctgaaagag gaggacccct   2637

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tgtcttctgt tcccaaggaa gctccttcct gtttgttttg ttttctaaga tgttcatttt   2877

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gattcccttt tgactcttcc gtgcatccca gataatggag aatgtatcag ccagccttcc   3057

ccaccaagtc taaaaagacc tggcctttca cttttagttg gcatttgtta tcctcttgta   3117

tacttgtatt cccttaactc taaccctgtg gaagcatggc tgtctgcaca gagggtccca   3177

ttgtgcagaa aagctcagag taggtgggta ggagcccttc tctttgactt aggtttttag   3237

gagtctgagc atccatcaat acctgtacta tgatgggctt ctgttctctg ctgagggcca   3297
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US 10,000,000 B2

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gtaagtggaa ttagagggcc ttgcttctct tctttccatt cttcttgcta caccccttt 3477

ccagttgctg tggaccaatg catctcttta aaggcaaata ttatccagca agcagtctac 3537

cctgtccttt gcaattgctc ttctccacgt ctttcctgct acaagtgttt tagatgttac 3597

taccttattt tccccgaatt ctatttttgt ccttgcagac agaatataaa aactcctggg 3657

cttaaggcct aaggaagcca gtcaccttct gggcaagggc tcctatcttt cctccctatc 3717

catggcacta aaccacttct ctgctgcctc tgtggaagag attcctatta ctgcagtaca 3777

tacgtctgcc aggggtaacc tggccactgt ccctgtcctt ctacagaacc tgagggcaaa 3837

gatggtggct gtgtctctcc ccggtaatgt cactgttttt attccttcca tctagcagct 3897

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ttgcaaggat ttttccatgt gtggtggtgt tttttgttac tgttttaaag ggtgcccatt 4197

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<213> Homo sapiens

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Met Ser Phe Phe
1

ccg gag ctt tac ttt aac gtg gac aat ggc tac ttg gag gga ctg gtg 164
Pro Glu Leu Tyr Phe Asn Val Asp Asn Gly Tyr Leu Glu Gly Leu Val
5 10 15 20

cgc ggc ctg aag gcc ggg gtg ctc agc cag gcc gac tac ctc aac ctg 212

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Arg Gly Leu Lys Ala Gly Val Leu Ser Gln Ala Asp Tyr Leu Asn Leu
 21                  26                  31                  36

gtg cag tgc gag acg cta gag gac ttg aaa ctg cat ctg cag agc act      260
Val Gln Cys Glu Thr Leu Glu Asp Leu Lys Leu His Leu Gln Ser Thr
 37                  42                  47                  52

gat tat ggt aac ttc ctg gcc aac gag gca tca cct ctg acg gtg tca      308
Asp Tyr Gly Asn Phe Leu Ala Asn Glu Ala Ser Pro Leu Thr Val Ser
 53                  58                  63                  68

gtc atc gat gac cgg ctc aag gag aag atg gtg gtg gag ttc cgc cac      356
Val Ile Asp Asp Arg Leu Lys Glu Lys Met Val Val Glu Phe Arg His
 69                  74                  79                  84

atg agg aac cat gcc tat gag cca ctc gcc agc ttc cta gac ttc att      404
Met Arg Asn His Ala Tyr Glu Pro Leu Ala Ser Phe Leu Asp Phe Ile
 85                  90                  95                 100

act tac agt tac atg atc gac aac gtg atc ctg ctc atc aca ggc acg      452
Thr Tyr Ser Tyr Met Ile Asp Asn Val Ile Leu Leu Ile Thr Gly Thr
101                 106                 111                 116

ctg cac cag cgc tcc atc gct gag ctc gtg ccc aag tgc cac cca cta      500
Leu His Gln Arg Ser Ile Ala Glu Leu Val Pro Lys Cys His Pro Leu
117                 122                 127                 132

ggc agc ttc gag cag atg gag gcc gtg aac att gct cag aca cct gct      548
Gly Ser Phe Glu Gln Met Glu Ala Val Asn Ile Ala Gln Thr Pro Ala
133                 138                 143                 148

gag ctc tac aat gcc att ctg gtg gac acg cct ctt gcg gct ttt ttc      596
Glu Leu Tyr Asn Ala Ile Leu Val Asp Thr Pro Leu Ala Ala Phe Phe
149                 154                 159                 164

cag gac tgc att tca gag cag gac ctt gac gag atg aac atc gag atc      644
Gln Asp Cys Ile Ser Glu Gln Asp Leu Asp Glu Met Asn Ile Glu Ile
165                 170                 175                 180

atc cgc aac acc ctc tac aag gcc tac ctg gag tcc ttc tac aag ttc      692
Ile Arg Asn Thr Leu Tyr Lys Ala Tyr Leu Glu Ser Phe Tyr Lys Phe
181                 186                 191                 196

tgc acc cta ctg ggc ggg act acg gct gat gcc atg tgc ccc atc ctg      740
Cys Thr Leu Leu Gly Gly Thr Thr Ala Asp Ala Met Cys Pro Ile Leu
197                 202                 207                 212

gag ttt gaa gca gac cgc cgc gcc ttc atc atc acc atc aat tct ttc      788
Glu Phe Glu Ala Asp Arg Arg Ala Phe Ile Ile Thr Ile Asn Ser Phe
213                 218                 223                 228

ggc aca gag ctg tcc aaa gag gac cgt gcc aag ctc ttt cca cac tgt      836
Gly Thr Glu Leu Ser Lys Glu Asp Arg Ala Lys Leu Phe Pro His Cys
229                 234                 239                 244

ggg cgg ctc tac cct gag ggc ctg gcg cag ctg gct cgg gct gac gac      884
Gly Arg Leu Tyr Pro Glu Gly Leu Ala Gln Leu Ala Arg Ala Asp Asp
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Application Serial No. 09/760,854

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245                 250                 255                 260

tat gaa cag gtc aag aac gtg gcc gat tac tac ccg gag tac aag ctg      932
Tyr Glu Gln Val Lys Asn Val Ala Asp Tyr Tyr Pro Glu Tyr Lys Leu
261                 266                 271                 276

ctc ttc gag ggt gca ggt agc aac cct gga gac aag acg ctg gag gac      980
Leu Phe Glu Gly Ala Gly Ser Asn Pro Gly Asp Lys Thr Leu Glu Asp
277                 282                 287                 292

cga ttc ttt gag cac gag gta aag ctg aac aag ttg gcc ttc ctg aac     1028
Arg Phe Phe Glu His Glu Val Lys Leu Asn Lys Leu Ala Phe Leu Asn
293                 298                 303                 308

cag ttc cac ttt ggt gtc ttc tat gcc ttc gtg aag ctc aag gag cag     1076
Gln Phe His Phe Gly Val Phe Tyr Ala Phe Val Lys Leu Lys Glu Gln
309                 314                 319                 324

gag tgt cgc aac atc gtg tgg atc gct gaa tgt atc gcc cag cgc cac     1124
Glu Cys Arg Asn Ile Val Trp Ile Ala Glu Cys Ile Ala Gln Arg His
325                 330                 335                 340

cgc gcc aaa atc gac aac tac atc cct atc ttc tag cgtc ctggcccaag     1174
Arg Ala Lys Ile Asp Asn Tyr Ile Pro Ile Phe  *
341                 346                 351

gctctcaatt gcactctttg tgtgtgtgtg tgtgtgtgtg cgcgtgtgtg tgcgtgtgtg   1234

tgtatgtggt ctgtgacaag cctgtggctc acctgcctgt ccggggtgta gtacgctgtc   1294

ctagcggctg cccagttctc ctgaccctct tagagactgt tcttaggcct gaaaaggggc   1354

tgggcacccc cccccaccaa ggatggacga agacccccctc cagagcaagg aggcccccctc  1414

agccctgtgg ttacagccgc tgatgtatct aagaagcatg tcactttcat gttcctccct   1474

aactccctga cctgagaacc ctggggcctg ggggcagttt gagcctcctc tccctttgt    1534

gggtcgctcc caaagccatg gcccatggga aggacaaagt gtgtgtgtcc ttggggcctg   1594

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<213> Homo sapiens

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<400> 207

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                                                  Met Ser Phe Phe
                                                    1

ccg gag ctt tac ttt aac gtg gac aat ggc tac ttg gag gga ctg gtg      164
Pro Glu Leu Tyr Phe Asn Val Asp Asn Gly Tyr Leu Glu Gly Leu Val
  5                  10                  15                  20

cgc ggc ctg aag gcc ggg gtg ctc agc cag gcc gac tac ctc aac ctg      212
Arg Gly Leu Lys Ala Gly Val Leu Ser Gln Ala Asp Tyr Leu Asn Leu
 21                  26                  31                  36

gtg cag tgc gag acg cta gag gac ttg aaa ctg cat ctg cag agc act      260
Val Gln Cys Glu Thr Leu Glu Asp Leu Lys Leu His Leu Gln Ser Thr
 37                  42                  47                  52

gat tat ggt aac ttc ctg gcc aac gag gca tca cct ctg acg gtg tca      308
Asp Tyr Gly Asn Phe Leu Ala Asn Glu Ala Ser Pro Leu Thr Val Ser
 53                  58                  63                  68

gtc atc gat gac cgg ctc aag gag aag atg gtg gtg gag ttc cgc cac      356
Val Ile Asp Asp Arg Leu Lys Glu Lys Met Val Val Glu Phe Arg His
 69                  74                  79                  84

atg agg aac cat gcc tat gag cca ctc gcc agc ttc cta gac ttc att      404
Met Arg Asn His Ala Tyr Glu Pro Leu Ala Ser Phe Leu Asp Phe Ile
 85                  90                  95                 100

act tac agt tac atg atc gac aac gtg atc ctg ctc atc aca ggc acg      452
Thr Tyr Ser Tyr Met Ile Asp Asn Val Ile Leu Leu Ile Thr Gly Thr
101                 106                 111                 116

ctg cac cag cgc tcc atc gct gag ctc gtg ccc aag tgc cac cca cta      500
Leu His Gln Arg Ser Ile Ala Glu Leu Val Pro Lys Cys His Pro Leu
117                 122                 127                 132

ggc agc ttc gag cag atg gag gcc gtg aac att gct cag aca cct gct      548
Gly Ser Phe Glu Gln Met Glu Ala Val Asn Ile Ala Gln Thr Pro Ala
133                 138                 143                 148

gag ctc tac aat gcc att ctg gtg gac acg cct ctt gcg gct ttt ttc      596
Glu Leu Tyr Asn Ala Ile Leu Val Asp Thr Pro Leu Ala Ala Phe Phe
149                 154                 159                 164

cag gac tgc att tca gag cag gac ctt gac gag atg aac atc gag atc      644
Gln Asp Cys Ile Ser Glu Gln Asp Leu Asp Glu Met Asn Ile Glu Ile
165                 170                 175                 180

atc cgc aac acc ctc tac aag gcc tac ctg gag tcc ttc tac aag ttc      692
Ile Arg Asn Thr Leu Tyr Lys Ala Tyr Leu Glu Ser Phe Tyr Lys Phe
181                 186                 191                 196

tgc acc cta ctg ggc ggg act acg gct gat gcc atg tgc ccc atc ctg      740
Cys Thr Leu Leu Gly Gly Thr Thr Ala Asp Ala Met Cys Pro Ile Leu
197                 202                 207                 212
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gag gag ctg tcc aaa gag gac cgt gcc aag ctc ttt cca cac tgt ggg      788
Glu Glu Leu Ser Lys Glu Asp Arg Ala Lys Leu Phe Pro His Cys Gly
213                 218                 223                 228

cgg ctc tac cct gag ggc ctg gcg cag ctg gct cgg gct gac gac tat      836
Arg Leu Tyr Pro Glu Gly Leu Ala Gln Leu Ala Arg Ala Asp Asp Tyr
229                 234                 239                 244

gaa cag gtc aag aac gtg gcc gat tac tac ccg gag tac aag ctg ctc      884
Glu Gln Val Lys Asn Val Ala Asp Tyr Tyr Pro Glu Tyr Lys Leu Leu
245                 250                 255                 260

ttc gag ggt gca ggt agc aac cct gga gac aag acg ctg gag gac cga      932
Phe Glu Gly Ala Gly Ser Asn Pro Gly Asp Lys Thr Leu Glu Asp Arg
261                 266                 271                 276

ttc ttt gag cac gag gta aag ctg aac aag ttg gcc ttc ctg aac cag      980
Phe Phe Glu His Glu Val Lys Leu Asn Lys Leu Ala Phe Leu Asn Gln
277                 282                 287                 292

ttc cac ttt ggt gtc ttc tat gcc ttc gtg aag ctc aag gag cag gag     1028
Phe His Phe Gly Val Phe Tyr Ala Phe Val Lys Leu Lys Glu Gln Glu
293                 298                 303                 308

tgt cgc aac atc gtg tgg atc gct gaa tgt atc gcc cag cgc cac cgc     1076
Cys Arg Asn Ile Val Trp Ile Ala Glu Cys Ile Ala Gln Arg His Arg
309                 314                 319                 324

gcc aaa atc gac aac tac atc cct atc ttc tag cgtcctgg cccaaggctc     1127
Ala Lys Ile Asp Asn Tyr Ile Pro Ile Phe  *
325                 330                 335

tcaattgcac tctttgtgtg tgtgtgtgtg tgtgtgcgcg tgtgtgtgcg tgtgtgtgta   1187

tgtggtctgt gacaagcctg tggctcacct gcctgtccgg ggtgtagtac gctgtcctag   1247

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cgctcccaaa gccatggccc atgggaagga caaagtgtgt gtgtccttgg ggcctggggg   1547

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<213> Homo sapiens

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             Met Ser Gly Gly Trp Met Ala Gln Val Gly Ala Trp Arg
               1               5                  10

aca ggg gct ctg ggc ctg gcg ctg ctg ctg ctg ctc ggc ctc gga cta      156
Thr Gly Ala Leu Gly Leu Ala Leu Leu Leu Leu Leu Gly Leu Gly Leu
 14                  19                  24                  29

ggc ctg gag gcc gcc gcg agc ccg ctt tcc acc ccg acc tct gcc cag      204
Gly Leu Glu Ala Ala Ala Ser Pro Leu Ser Thr Pro Thr Ser Ala Gln
 30                  35                  40                  45

gcc gca ggc ccc agc tca ggc tcg tgc cca ccc acc aag ttc cag tgc      252
Ala Ala Gly Pro Ser Ser Gly Ser Cys Pro Pro Thr Lys Phe Gln Cys
 46                  51                  56                  61

cgc acc agt ggc tta tgc gtg ccc ctc acc tgg cgc tgc gac agg gac      300
Arg Thr Ser Gly Leu Cys Val Pro Leu Thr Trp Arg Cys Asp Arg Asp
 62                  67                  72                  77

ttg gac tgc agc gat ggc agc gat gag gag gag tgc agg att gag cca      348
Leu Asp Cys Ser Asp Gly Ser Asp Glu Glu Glu Cys Arg Ile Glu Pro
 78                  83                  88                  93

tgt acc cag aaa ggg caa tgc cca ccg ccc cct ggc ctc ccc tgc ccc      396
Cys Thr Gln Lys Gly Gln Cys Pro Pro Pro Pro Gly Leu Pro Cys Pro
 94                  99                 104                 109

tgc acc ggc gtc agt gac tgc tct ggg gga act gac aag aaa ctg cgc      444
Cys Thr Gly Val Ser Asp Cys Ser Gly Gly Thr Asp Lys Lys Leu Arg
110                 115                 120                 125

aac tgc agc cgc ctg gcc tgc cta gca ggc gag ctc cgt tgc acg ctg      492
Asn Cys Ser Arg Leu Ala Cys Leu Ala Gly Glu Leu Arg Cys Thr Leu
126                 131                 136                 141

agc gat gac tgc att cca ctc acg tgg cgc tgc gac ggc cac cca gac      540
Ser Asp Asp Cys Ile Pro Leu Thr Trp Arg Cys Asp Gly His Pro Asp
142                 147                 152                 157

tgt ccc gac tcc agc gac gag ctc ggc tgt gga acc aat gag atc ctc      588
Cys Pro Asp Ser Ser Asp Glu Leu Gly Cys Gly Thr Asn Glu Ile Leu
158                 163                 168                 173

ccg gaa ggg gat gcc aca acc atg ggg ccc cct gtg acc ctg gag agt      636
Pro Glu Gly Asp Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser
174                 179                 184                 189
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Val Thr Ser Leu Arg Asn Ala Thr Thr Met Gly Pro Pro Val Thr Leu
190                 195                 200                 205

gag agt gtc ccc tct gtc ggg aat gcc aca tcc tcc tct gcc gga gac      732
Glu Ser Val Pro Ser Val Gly Asn Ala Thr Ser Ser Ser Ala Gly Asp
206                 211                 216                 221

cag tct gga agc cca act gcc tat ggg gtt att gca gct gct gcg gtg      780
Gln Ser Gly Ser Pro Thr Ala Tyr Gly Val Ile Ala Ala Ala Ala Val
222                 227                 232                 237

ctc agt gca agc ctg gtc acc gcc acc ctc ctc ctt ttg tcc tgg ctc      828
Leu Ser Ala Ser Leu Val Thr Ala Thr Leu Leu Leu Leu Ser Trp Leu
238                 243                 248                 253

cga gcc cag gag cgc ctc cgc cca ctg ggg tta ctg gtg gcc atg aag      876
Arg Ala Gln Glu Arg Leu Arg Pro Leu Gly Leu Leu Val Ala Met Lys
254                 259                 264                 269

gag tcc ctg ctg ctg tca gaa cag aag acc tcg ctg ccc tga ggacaag      925
Glu Ser Leu Leu Leu Ser Glu Gln Lys Thr Ser Leu Pro  *
270                 275                 280

cacttgccac caccgtcact cagccctggg cgtagccgga caggaggaga gcagtgatgc    985

ggatgggtac ccgggcacac cagccctcag agacctgagc tcttctggcc acgtggaacc   1045

tcgaacccga gctcctgcag aagtggccct ggagattgag ggtccctgga cactccctat   1105

ggagatccgg ggagctagga tggggaacct gccacagcca gaactgaggg gctggcccca   1165

ggcagctccc agggggtaga acggccctgt gcttaagaca ctcctgctgc cccgtctgag   1225

ggtggcgatt aaagttgctt cacatcctca aaaaaaaaaa aaaaaaaggg ggggccgttt   1285

taaagaatcc ctgggggggc ccaagtttac gggggcaggc aaggctaaag ctttttccct   1345

taagggagcc gtttataagc ttactgggga attttgggga gggaccttta ttttatgggg   1405

gggaaataat tggaccaact actttccgaa atttaaaagc ttctaaggaa aattataaat   1465

ttttttaggg gggtaaaggg gaaaactagg tggaaaaggc tgcgccc                 1512
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<210> 209
<211> 1025
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (108)..(881)

<220>

<221> misc_feature
<222> (1)...(1025)
<223> n = a,t,c or g

<400> 209
tttgatcgca gatcactagt ccagngcggt ggaattcacc gaaccccgcc cgcgccggga 60

gcatctcgcg tccccaacgg gccccccgggt cggtttccgc ggtggcc atg act gcg 116
Met Thr Ala
1

gcc gtg ttc ttc ggc tgc gcc ttc att gcc ttc ggg cct gcg ctc gcc 164
Ala Val Phe Phe Gly Cys Ala Phe Ile Ala Phe Gly Pro Ala Leu Ala
4 9 14 19

ctt tat gtc ttc acc atc gcc acc gag ccg ttg cgt atc atc ttc ctc 212
Leu Tyr Val Phe Thr Ile Ala Thr Glu Pro Leu Arg Ile Ile Phe Leu
20 25 30 35

atc gcc gga gct ttc ttc tgg ttg gtg tct cta ctg att tcg tcc ctt 260
Ile Ala Gly Ala Phe Phe Trp Leu Val Ser Leu Leu Ile Ser Ser Leu
36 41 46 51

gtt tgg ttc atg gca aga gtc att att gac aac aaa gat gga cca aca 308
Val Trp Phe Met Ala Arg Val Ile Ile Asp Asn Lys Asp Gly Pro Thr
52 57 62 67

cag aaa tat ctg ctg atc ttt gga gcg ttt gtc tct gtc tat atc caa 356
Gln Lys Tyr Leu Leu Ile Phe Gly Ala Phe Val Ser Val Tyr Ile Gln
68 73 78 83

gaa atg ttc cga ttt gca tat tat aaa ctc tta aaa aaa gcc agt gaa 404
Glu Met Phe Arg Phe Ala Tyr Tyr Lys Leu Leu Lys Lys Ala Ser Glu
84 89 94 99

ggt ttg aag agt ata aac cca ggt gag aca gca ccc tct atg cga ctg 452
Gly Leu Lys Ser Ile Asn Pro Gly Glu Thr Ala Pro Ser Met Arg Leu
100 105 110 115

ctg gcc tat gtt tct ggc ttg ggc ttt gga atc atg agt gga gta ttt 500
Leu Ala Tyr Val Ser Gly Leu Gly Phe Gly Ile Met Ser Gly Val Phe
116 121 126 131

tcc ttt gtg aat acc cta tct gac tcc ttg ggg cca ggc aca gtg ggc 548
Ser Phe Val Asn Thr Leu Ser Asp Ser Leu Gly Pro Gly Thr Val Gly
132 137 142 147

att cat gga gat tct cct caa ttc ttc ctt tat tca gct ttc atg acg 596
Ile His Gly Asp Ser Pro Gln Phe Phe Leu Tyr Ser Ala Phe Met Thr
148 153 158 163

ctg gtc att atc ttg ctg cat gta ttc tgg ggc att gta ttt ttt gat 644
Leu Val Ile Ile Leu Leu His Val Phe Trp Gly Ile Val Phe Phe Asp
164 169 174 179

ggc tgt gag aag aaa aag tgg ggc atc ctc ctt atc gtt ctc ctg acc 692
Gly Cys Glu Lys Lys Lys Trp Gly Ile Leu Leu Ile Val Leu Leu Thr

```
180                 185                 190                 195

cac ctg ctg gtg tca gcc cag acc ttc ata agt tct tat tat gga ata      740
His Leu Leu Val Ser Ala Gln Thr Phe Ile Ser Ser Tyr Tyr Gly Ile
196                 201                 206                 211

aac ctg gcg tca gca ttt ata atc ctg gtg ctc atg ggc acc tgg gca      788
Asn Leu Ala Ser Ala Phe Ile Ile Leu Val Leu Met Gly Thr Trp Ala
212                 217                 222                 227

ttc tta gct gcg gga ggc agc tgc cga agc ctg aaa ctc tgc ctg ctc      836
Phe Leu Ala Ala Gly Gly Ser Cys Arg Ser Leu Lys Leu Cys Leu Leu
228                 233                 238                 243

tgc caa gac aag aac ttt ctt ctt tac aac cag cgc tcc aga taa cct      884
Cys Gln Asp Lys Asn Phe Leu Leu Tyr Asn Gln Arg Ser Arg  *
244                 249                 254

cagggaacca gcacttccca aaccgcagac tacatcttta gaggaagcac aactgtgcct    944

ttttctgaaa atccctttt ctggtggaat tgagaaagaa ataaaactat gcagatatgc   1004

gttccattca aaaaaaaaaa a                                           1025
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<210> 210
<211> 1232
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (353)..(1120)

<400> 210

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cagaagcctg gagctgggca tccaagaaga agcagcctca tttgttttct ggtgtcatcg    120

taggtggcca cctatggctt ttgggaatgt aaaaagggca gctctctggc atgttcctga    180

ctgaggatct cataacattt aacttgagga acttcctcct tttccagctt tgggagtcaa    240

gcttctcacc tggggcgggt gggttctgca ccaccctccc accctccttc ctccgtgtgg    300

acgatagagc cacatccagc accacggacg tggggcccaa gcccccgtga ag    atg     355
                                                            Met
                                                              1

gtg tcc tgg atg atc tcc aga gcc gtg gtg ctg gtg ttt gga atg ctt      403
Val Ser Trp Met Ile Ser Arg Ala Val Val Leu Val Phe Gly Met Leu
  2                   7                  12                  17

tat cct gca tat tat tca tac aaa gct gtg aaa aca aaa aac gtg aag      451
Tyr Pro Ala Tyr Tyr Ser Tyr Lys Ala Val Lys Thr Lys Asn Val Lys
```

```
 18                  23                  28                  33

gaa tat gtt cga tgg atg atg tac tgg att gtt ttt gct ctc tat act      499
Glu Tyr Val Arg Trp Met Met Tyr Trp Ile Val Phe Ala Leu Tyr Thr
 34                  39                  44                  49

gtg att gaa aca gta gcc gat caa aca gtt gct tgg ttt ccc ctg tac      547
Val Ile Glu Thr Val Ala Asp Gln Thr Val Ala Trp Phe Pro Leu Tyr
 50                  55                  60                  65

tat gag ctg aag att gct ttt gtc ata tgg ctg ctt tct ccc tat acc      595
Tyr Glu Leu Lys Ile Ala Phe Val Ile Trp Leu Leu Ser Pro Tyr Thr
 66                  71                  76                  81

aaa gga gca agt tta ata tat aga aaa ttc ctt cat cca ctt ctt tct      643
Lys Gly Ala Ser Leu Ile Tyr Arg Lys Phe Leu His Pro Leu Leu Ser
 82                  87                  92                  97

tca aag gaa agg gag att gat gat tat att gta caa gca aag gaa cga      691
Ser Lys Glu Arg Glu Ile Asp Asp Tyr Ile Val Gln Ala Lys Glu Arg
 98                 103                 108                 113

ggc tat gaa acc atg gta aac ttt gga cgg caa ggt tta aac ctt gca      739
Gly Tyr Glu Thr Met Val Asn Phe Gly Arg Gln Gly Leu Asn Leu Ala
114                 119                 124                 129

gct act gct gct gtt act gca gca gta aag agc caa gga gca ata act      787
Ala Thr Ala Ala Val Thr Ala Ala Val Lys Ser Gln Gly Ala Ile Thr
130                 135                 140                 145

gaa cgt tta aga agc ttc agt atg cat gat tta aca act atc caa ggt      835
Glu Arg Leu Arg Ser Phe Ser Met His Asp Leu Thr Thr Ile Gln Gly
146                 151                 156                 161

gat gag cct gtg gga caa aga cca tac caa cct cta cca gaa gca aaa      883
Asp Glu Pro Val Gly Gln Arg Pro Tyr Gln Pro Leu Pro Glu Ala Lys
162                 167                 172                 177

aag aaa agt aaa cca gcc ccc agt gaa tca gca ggt tat gga att cca      931
Lys Lys Ser Lys Pro Ala Pro Ser Glu Ser Ala Gly Tyr Gly Ile Pro
178                 183                 188                 193

ctg aaa gac gga gat gag aaa aca gat gaa gaa gca gag ggg cca tat      979
Leu Lys Asp Gly Asp Glu Lys Thr Asp Glu Glu Ala Glu Gly Pro Tyr
194                 199                 204                 209

tca gat aat gag atg tta aca cac aaa ggg ctt cga aga tcg caa agc     1027
Ser Asp Asn Glu Met Leu Thr His Lys Gly Leu Arg Arg Ser Gln Ser
210                 215                 220                 225

atg aaa tct gtg aaa acc acc aaa ggc cgc aaa gag gtg cgg tac ggg     1075
Met Lys Ser Val Lys Thr Thr Lys Gly Arg Lys Glu Val Arg Tyr Gly
226                 231                 236                 241

tcg cta aaa tac aaa gtg aag aaa cga cca caa gtg tat ttt tag tca     1123
Ser Leu Lys Tyr Lys Val Lys Lys Arg Pro Gln Val Tyr Phe  *
242                 247                 252
```

```
tctacacgtc aaatatccca agacagatta tgctaaatac atcgacttca tcttctaaca   1183

tgatatattc aggatttaca cattaaaatg attatttaaa aaaaaaaaa               1232
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<210> 211
<211> 1559
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (98)..(1330)

<400> 211

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gcacgaggag ttccttggga gtggggtcag ccctgacttg gccaacgagg acggcctgac     60

ggccctgcac cagtgctgca ttgatgattt ccgagag atg gtg cag cag ctc ctg     115
                                          Met Val Gln Gln Leu Leu
                                            1

gag gct ggg gcc aac atc aat gcc tgt gac agt gag tgc tgg acg cct      163
Glu Ala Gly Ala Asn Ile Asn Ala Cys Asp Ser Glu Cys Trp Thr Pro
  7                  12                  17                  22

ctg cat gct gcg gcc acc tgc ggc cac ctg cac ctg gtg gag ctg ctc      211
Leu His Ala Ala Ala Thr Cys Gly His Leu His Leu Val Glu Leu Leu
 23                  28                  33                  38

atc gcc agt ggc gcc aat ctc ctg gcg gtc aac acc gac ggg aac atg      259
Ile Ala Ser Gly Ala Asn Leu Leu Ala Val Asn Thr Asp Gly Asn Met
 39                  44                  49                  54

ccc tat gac ctg tgt gat gat gag cag acg ctg gac tgc ctg gag act      307
Pro Tyr Asp Leu Cys Asp Asp Glu Gln Thr Leu Asp Cys Leu Glu Thr
 55                  60                  65                  70

gcc atg gcc gac cgt ggc atc acc cag gac agc atc gag gcc gcc cgg      355
Ala Met Ala Asp Arg Gly Ile Thr Gln Asp Ser Ile Glu Ala Ala Arg
 71                  76                  81                  86

gcc gtg cca gaa ctg cgc atg ctg gac gac atc cgg agc cgg ctg cag      403
Ala Val Pro Glu Leu Arg Met Leu Asp Asp Ile Arg Ser Arg Leu Gln
 87                  92                  97                 102

gcc ggg gca gac ctc cat gcc ccc ctg gac cac ggg gcc acg ctg ctg      451
Ala Gly Ala Asp Leu His Ala Pro Leu Asp His Gly Ala Thr Leu Leu
103                 108                 113                 118

cac gtc gca gcc gcc aac ggg ttc agc gag gcg gct gcc ctg ctg ctg      499
His Val Ala Ala Ala Asn Gly Phe Ser Glu Ala Ala Ala Leu Leu Leu
119                 124                 129                 134

gaa cac cga gcc agc ctg agc gct aag gac caa gac ggc tgg gag ccg      547
```

```
Glu His Arg Ala Ser Leu Ser Ala Lys Asp Gln Asp Gly Trp Glu Pro
135                 140                 145                 150

ctg cac gcc gcg gcc tac tgg ggc cag gtg ccc ctg gtg gag ctg ctc      595
Leu His Ala Ala Ala Tyr Trp Gly Gln Val Pro Leu Val Glu Leu Leu
151                 156                 161                 166

gtg gcg cac ggg gcc gac ctg aac gca aag tcc ctg atg gac gag acg      643
Val Ala His Gly Ala Asp Leu Asn Ala Lys Ser Leu Met Asp Glu Thr
167                 172                 177                 182

ccc ctt gat gtg tgc ggg gac gag gag gtg cgg gcc aag ctg ctg gag      691
Pro Leu Asp Val Cys Gly Asp Glu Glu Val Arg Ala Lys Leu Leu Glu
183                 188                 193                 198

ctg aag cac aag cac gac gcc ctc ctg cgc gcc cag agc cgc cag cgc      739
Leu Lys His Lys His Asp Ala Leu Leu Arg Ala Gln Ser Arg Gln Arg
199                 204                 209                 214

tcc ttg ctg cgc cgc cgc acc tcc agc gcc ggc agc cgc ggg aag gtg      787
Ser Leu Leu Arg Arg Arg Thr Ser Ser Ala Gly Ser Arg Gly Lys Val
215                 220                 225                 230

gtg agg cgg gtg agc cta acc cag cgc acc gac ctg tac cgc aag cag      835
Val Arg Arg Val Ser Leu Thr Gln Arg Thr Asp Leu Tyr Arg Lys Gln
231                 236                 241                 246

cac gcc cag gag gcc atc gtg tgg caa cag ccg ccg ccc acc agc ccg      883
His Ala Gln Glu Ala Ile Val Trp Gln Gln Pro Pro Pro Thr Ser Pro
247                 252                 257                 262

gag ccg ccc gag gac aac gat gac cgc cag aca ggc gca gag ctc agg      931
Glu Pro Pro Glu Asp Asn Asp Asp Arg Gln Thr Gly Ala Glu Leu Arg
263                 268                 273                 278

ccg ccg ccc ccg gag gag gac aac ccc gaa gtg gtc agg ccg cac aat      979
Pro Pro Pro Pro Glu Glu Asp Asn Pro Glu Val Val Arg Pro His Asn
279                 284                 289                 294

ggc cga gta ggg ggc tcc cca gtg cgg cat cta tac tcc aag cga cta     1027
Gly Arg Val Gly Gly Ser Pro Val Arg His Leu Tyr Ser Lys Arg Leu
295                 300                 305                 310

gac cgg agt gtc tcc tac cag ctg agc ccc ctg gac agc acc acc ccc     1075
Asp Arg Ser Val Ser Tyr Gln Leu Ser Pro Leu Asp Ser Thr Thr Pro
311                 316                 321                 326

cac acc ctg gtc cac gac aag gcc cac cac acc ctg gct gac ctg aag     1123
His Thr Leu Val His Asp Lys Ala His His Thr Leu Ala Asp Leu Lys
327                 332                 337                 342

cgc cag cga gct gct gcc aag ctg cag cga ccc cca cct gag ggg ccc     1171
Arg Gln Arg Ala Ala Ala Lys Leu Gln Arg Pro Pro Pro Glu Gly Pro
343                 348                 353                 358

gag agc cct gag aca gct gag cct ggc ctg cct ggt gac acg gtg acc     1219
Glu Ser Pro Glu Thr Ala Glu Pro Gly Leu Pro Gly Asp Thr Val Thr
```

```
359                 364                 369                 374

ccc cag cct gac tgt ggc ttc agg gca ggc ggg gac cca ccc ctg ctc     1267
Pro Gln Pro Asp Cys Gly Phe Arg Ala Gly Gly Asp Pro Pro Leu Leu
375                 380                 385                 390

aag ctc aca gcc ccg gcg gtg gag gct ccc gtg gag agg agg ccg tgc     1315
Lys Leu Thr Ala Pro Ala Val Glu Ala Pro Val Glu Arg Arg Pro Cys
391                 396                 401                 406

tgc ctg ctc atg tga ggctgttgct cagcatgcag gggccctgtc gcgggcacag     1370
Cys Leu Leu Met  *
407

cccaaggctg cctccccacg gtgcgtgccc tggtgctgcg ggtgcagcac ggaaaccccg   1430

gcttctactg tacaggacac tggcccctct caggtcagaa gacatgcctg gagggatgtc   1490

tggctgcaaa gactattttt atcctgcaac tcttgataaa gggctgtttt gccatggaaa   1550

aaaaaaaaa                                                           1559
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US 6,686,179 B2

<210> 212
<211> 1783
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (106)..(1200)

<400> 212

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attgaacgcc tgcagtaccg gtccggaatt cccgggtcga cccacgcgtc cggagcagag     60

gaccggcagc cggcgtcgag gcggggcgcg ggaacgacgg cggcc    atg gcg gcc     114
                                                     Met Ala Ala
                                                       1

tcg ggg ccc ggg tgt cgc agc tgg tgc ttg tgt ccc gag gtg cca tcc     162
Ser Gly Pro Gly Cys Arg Ser Trp Cys Leu Cys Pro Glu Val Pro Ser
  4                   9                  14                  19

gcc acc ttc ttc act gcg ctg ctc tcg ctg ctg gtt tcc ggg cct cgc     210
Ala Thr Phe Phe Thr Ala Leu Leu Ser Leu Leu Val Ser Gly Pro Arg
 20                  25                  30                  35

ctg ttc ctg ctg cag cag ccc ctg gcg ccc tcg ggc ctc acg ctg aag     258
Leu Phe Leu Leu Gln Gln Pro Leu Ala Pro Ser Gly Leu Thr Leu Lys
 36                  41                  46                  51

tcc gag gcc ctt cgc aac tgg caa gtt tac agg ctg gta acc tac atc     306
Ser Glu Ala Leu Arg Asn Trp Gln Val Tyr Arg Leu Val Thr Tyr Ile
 52                  57                  62                  67
```

```
ttt gtc tac gag aat ccc atc tcc ctg ctc tgc ggc gct atc atc atc      354
Phe Val Tyr Glu Asn Pro Ile Ser Leu Leu Cys Gly Ala Ile Ile Ile
 68                  73                  78                  83

tgg cgc ttt gct ggc aat ttc gag aga acc gtg ggc acc gtc cgc cac      402
Trp Arg Phe Ala Gly Asn Phe Glu Arg Thr Val Gly Thr Val Arg His
 84                  89                  94                  99

tgc ttc ttc acc gtg atc ttc gcc atc ttc tcc gct atc atc ttc ctg      450
Cys Phe Phe Thr Val Ile Phe Ala Ile Phe Ser Ala Ile Ile Phe Leu
100                 105                 110                 115

tca ttc gag gct gtg tca tca ctg tca aag ctg ggg gaa gtg gag gat      498
Ser Phe Glu Ala Val Ser Ser Leu Ser Lys Leu Gly Glu Val Glu Asp
116                 121                 126                 131

gcc aga ggt ttc acc cca gtg gcc ttt gcc atg ctg gga gtc acc acc      546
Ala Arg Gly Phe Thr Pro Val Ala Phe Ala Met Leu Gly Val Thr Thr
132                 137                 142                 147

gtc cgt tct cgg atg agg cgg gcc ctg gtg ttt ggc atg gtt gtg ccc      594
Val Arg Ser Arg Met Arg Arg Ala Leu Val Phe Gly Met Val Val Pro
148                 153                 158                 163

tca gtc ctg gtt ccg tgg ctc ctg ctg ggt gcc tcg tgg ctc att ccc      642
Ser Val Leu Val Pro Trp Leu Leu Leu Gly Ala Ser Trp Leu Ile Pro
164                 169                 174                 179

cag acc tct ttc ctc agt aat gtc tgc ggg ctg tcc atc ggg ctg gcc      690
Gln Thr Ser Phe Leu Ser Asn Val Cys Gly Leu Ser Ile Gly Leu Ala
180                 185                 190                 195

tat ggc ctc acc tac tgc tat tcc atc gac ctc tca gag cga gtg gcg      738
Tyr Gly Leu Thr Tyr Cys Tyr Ser Ile Asp Leu Ser Glu Arg Val Ala
196                 201                 206                 211

ctg aag ctc gat cag acc ttc ccc ttc agc ctg atg agg agg ata tcc      786
Leu Lys Leu Asp Gln Thr Phe Pro Phe Ser Leu Met Arg Arg Ile Ser
212                 217                 222                 227

gtg ttc aag tac gtc tca ggg tct tca gcc gag agg agg gca gcc cag      834
Val Phe Lys Tyr Val Ser Gly Ser Ser Ala Glu Arg Arg Ala Ala Gln
228                 233                 238                 243

agc cgg aaa ctg aac ccg gtg cct ggc tcc tac ccc aca cag agc tgc      882
Ser Arg Lys Leu Asn Pro Val Pro Gly Ser Tyr Pro Thr Gln Ser Cys
244                 249                 254                 259

cac cct cac ctg tcc cca agc cac cct gtg tcc cag acg cag cac gcc      930
His Pro His Leu Ser Pro Ser His Pro Val Ser Gln Thr Gln His Ala
260                 265                 270                 275

agt ggt cag aag ctg gcc tcc tgg ccc tcc tgc acc ccc ggg cac atg      978
Ser Gly Gln Lys Leu Ala Ser Trp Pro Ser Cys Thr Pro Gly His Met
276                 281                 286                 291

ccc acc ttg cct ccg tac cag cct gcc tcc ggc ctg tgc tat gtg cag     1026
```

```
Pro Thr Leu Pro Pro Tyr Gln Pro Ala Ser Gly Leu Cys Tyr Val Gln
292                 297                 302                 307

aac cac ttt ggt cca aac ccc acc tcc tcc agt gtc tac cca gct tct     1074
Asn His Phe Gly Pro Asn Pro Thr Ser Ser Ser Val Tyr Pro Ala Ser
308                 313                 318                 323

gcg ggc acc tcc ctg ggc atc cag ccc ccc acg cct gtg aac agc cct     1122
Ala Gly Thr Ser Leu Gly Ile Gln Pro Pro Thr Pro Val Asn Ser Pro
324                 329                 334                 339

ggc acg gtg tat tct ggg gcc ttg ggc aca cca ggg gct gca ggc tcc     1170
Gly Thr Val Tyr Ser Gly Ala Leu Gly Thr Pro Gly Ala Ala Gly Ser
340                 345                 350                 355

aag gag tcc tcc agg gtc ccc atg ccc tga g agaatttcta gggaagtcat     1221
Lys Glu Ser Ser Arg Val Pro Met Pro  *
356                 361

ctcacttggc cttctgaagg tcctccctaa gagtctcctg acaaaagtta cttattgaac   1281

acctctatgt gccaggctct gtgttgggta ctttgatcaa tgcccctgtt tcagtctcat   1341

ctgtactcac ggcagccctg tggagtacgg tgtactggcc cagcttacag atgcagaaag   1401

cgagacgttc tgccatcaga taaagtcacg tggctcttta gtaacacgga caaggctcct   1461

cgccaaggaa ctcgtggcag aagagggcag cagttggcag tagctgccga tgtctgtccc   1521

cagctccacc attcctccct gtggctgtgc catgctcgtg gtttcagtgt ccgtgtgtcc   1581

atgtgtctgc ccttcaggag ctcgcagctg gtgtgcttgg cggtcccagg cctgtgtagt   1641

gtctctcccc tgctgcgggc gcccccaccc cgattcctct ccccagaagc ggtgggatgg   1701

gcccccatga actgcagcag catgctgagg tgtccatgtt gtctgccttt gtataaagaa   1761

acagcctctg aaaaaaaaaa aa                                            1783
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US 2006/0063160 A1

<210> 213
<211> 5201
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (847)..(3063)

<400> 213

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atttcagatt ttcagattag tgctgctcag cttgtattct gtcagtgttg cgtgtcaagg    120

ttttttttta acaaaatcaa tttatgtatc atttcatggt tctctgactc attgttaggg    180
```

```
acaaatatgc cttcccattt gagccgcaca ggattaaagc agctccgagc tgcttcccag    240

ctctgacatt ttgccattct aaaaaatgag tttactcacc acttccccat cttactcttt    300

gagtattatg tattttcaat tgaaaactgt agttttgtga tgatgaattg gaaagctcaa    360

tagaacatga tctgtattcc ttgaagaaat gcaggatcca ctggaaatga ggtggagaga    420

gacctttcc acccatcaga gtgaagcggt gtactctaca aggtgcattc ctgacgagga    480

aggccctgtg tgctgtgctg ccaattctgg cttttcctca gttcaggtgt atgcccatgc    540

tactacgttt gtccatcagc atttttgttt tggtttgttt tcagatgtaa atgagaggaa    600

gcaaagattt ttatggagac tatcaataat ctcaagaaaa tacatattca aaatgggatt    660

aaagccgtgc agtaagatgg gccaccaaac ataccttggt tctgatgcac tgcaagcaag    720

taaccagctt ctcactccag tttcaagtgg ctattatgta atataaattc aaagcacata    780

agtgagcctg agtgcagcag tgagcagcat cctgaggtta gcattacact tctcccagtg    840

gagccc   atg act tct gat cag gac gct aag gtt gtg gct gaa ccg cag      888
         Met Thr Ser Asp Gln Asp Ala Lys Val Val Ala Glu Pro Gln
           1               5                  10

acg cag aga gtc cag gag ggc aag gac agc gct cat ctg atg aat ggt      936
Thr Gln Arg Val Gln Glu Gly Lys Asp Ser Ala His Leu Met Asn Gly
 15                  20                  25                  30

cct ata tct caa acc act tct cag aca agt tcc atc cca cct ttg agt      984
Pro Ile Ser Gln Thr Thr Ser Gln Thr Ser Ser Ile Pro Pro Leu Ser
 31                  36                  41                  46

cag gta cca gca act aag gtt tca gag ctg aac cct aat gca gaa gtg     1032
Gln Val Pro Ala Thr Lys Val Ser Glu Leu Asn Pro Asn Ala Glu Val
 47                  52                  57                  62

tgg ggg gct cct gtg tta cat ctg gaa gca agc agt gct gct gac ggt     1080
Trp Gly Ala Pro Val Leu His Leu Glu Ala Ser Ser Ala Ala Asp Gly
 63                  68                  73                  78

gtg agt gct gca tgg gag gag gtg gct ggc cac cac gca gac cgt ggc     1128
Val Ser Ala Ala Trp Glu Glu Val Ala Gly His His Ala Asp Arg Gly
 79                  84                  89                  94

ccg cag gga tcg gat gcc aat ggt gat ggt gac cag ggc cat gag aat     1176
Pro Gln Gly Ser Asp Ala Asn Gly Asp Gly Asp Gln Gly His Glu Asn
 95                 100                 105                 110

gcc gca ttg cca gac ccg cag gag tcg gac cca gca gac atg aac gct     1224
Ala Ala Leu Pro Asp Pro Gln Glu Ser Asp Pro Ala Asp Met Asn Ala
111                 116                 121                 126

ctc gct ctg ggt ccc tca gaa tat gac tct ctg cct gaa aat agc gag     1272
Leu Ala Leu Gly Pro Ser Glu Tyr Asp Ser Leu Pro Glu Asn Ser Glu
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127                 132                 137                 142

aca gga gga aat gag tct caa cca gac agc cag gaa gac ccc cga gaa     1320
Thr Gly Gly Asn Glu Ser Gln Pro Asp Ser Gln Glu Asp Pro Arg Glu
143                 148                 153                 158

gta ctt aaa aaa aca ttg gaa ttc tgc tta tct agg gag aac ctt gct     1368
Val Leu Lys Lys Thr Leu Glu Phe Cys Leu Ser Arg Glu Asn Leu Ala
159                 164                 169                 174

agt gac atg tat ctt ata tca cag atg gat agt gac cag tat gtg cca     1416
Ser Asp Met Tyr Leu Ile Ser Gln Met Asp Ser Asp Gln Tyr Val Pro
175                 180                 185                 190

atc aca acg gtg gct aac ctc gac cac atc aag aag ctc agc act gat     1464
Ile Thr Thr Val Ala Asn Leu Asp His Ile Lys Lys Leu Ser Thr Asp
191                 196                 201                 206

gtg gac ttg att gtg gaa gtg cta aga tct tta cct tta gtc caa gtg     1512
Val Asp Leu Ile Val Glu Val Leu Arg Ser Leu Pro Leu Val Gln Val
207                 212                 217                 222

gat gaa aag gga gaa aaa gta agg cca aat caa aat cgc tgc ata gta     1560
Asp Glu Lys Gly Glu Lys Val Arg Pro Asn Gln Asn Arg Cys Ile Val
223                 228                 233                 238

ata ttg cgt gaa ata tct gaa tct acc ccc gtg gaa gaa gta gaa gca     1608
Ile Leu Arg Glu Ile Ser Glu Ser Thr Pro Val Glu Glu Val Glu Ala
239                 244                 249                 254

cta ttt aaa gga gat aat tta cca aaa ttt ata aac tgt gaa ttt gca     1656
Leu Phe Lys Gly Asp Asn Leu Pro Lys Phe Ile Asn Cys Glu Phe Ala
255                 260                 265                 270

tat aat gat aat tgg ttt att aca ttt gaa aca gaa gct gat gca caa     1704
Tyr Asn Asp Asn Trp Phe Ile Thr Phe Glu Thr Glu Ala Asp Ala Gln
271                 276                 281                 286

cag gct tac aaa tac ctt cga gaa gaa gtc aaa act ttt caa gga aaa     1752
Gln Ala Tyr Lys Tyr Leu Arg Glu Glu Val Lys Thr Phe Gln Gly Lys
287                 292                 297                 302

cca att aag gca cgg ata aaa gca aag gca ata gct ata aac aca ttt     1800
Pro Ile Lys Ala Arg Ile Lys Ala Lys Ala Ile Ala Ile Asn Thr Phe
303                 308                 313                 318

ttg cca aag aat gga ttt aga ccc ctg gac gtg agc ctg tat gcc cag     1848
Leu Pro Lys Asn Gly Phe Arg Pro Leu Asp Val Ser Leu Tyr Ala Gln
319                 324                 329                 334

cag cgc tac gcg acg tcg ttc tac ttc cct ccc atg tac agc ccc cag     1896
Gln Arg Tyr Ala Thr Ser Phe Tyr Phe Pro Pro Met Tyr Ser Pro Gln
335                 340                 345                 350

cag cag ttc ccc ctg tac agc ctg atc act ccc cag acg tgg tca gca     1944
Gln Gln Phe Pro Leu Tyr Ser Leu Ile Thr Pro Gln Thr Trp Ser Ala
351                 356                 361                 366
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acg cac agc tat ctt gac cca ccc ttg gta act cca ttt cca aat act     1992
Thr His Ser Tyr Leu Asp Pro Pro Leu Val Thr Pro Phe Pro Asn Thr
367                 372                 377                 382

gga ttt ata aat ggg ttt acg tct cca gcg ttc aag cct gcg gcg tct     2040
Gly Phe Ile Asn Gly Phe Thr Ser Pro Ala Phe Lys Pro Ala Ala Ser
383                 388                 393                 398

cct ctg act tct ctc aga cag tat cct cct cga agc agg aat cct agt     2088
Pro Leu Thr Ser Leu Arg Gln Tyr Pro Pro Arg Ser Arg Asn Pro Ser
399                 404                 409                 414

aaa tct cat ctg cgg cat gcg att cct agt gca gag agg gga cct ggg     2136
Lys Ser His Leu Arg His Ala Ile Pro Ser Ala Glu Arg Gly Pro Gly
415                 420                 425                 430

tta tta gaa agt cct tca ata ttt aac ttc act gca gat cga tta att     2184
Leu Leu Glu Ser Pro Ser Ile Phe Asn Phe Thr Ala Asp Arg Leu Ile
431                 436                 441                 446

aat ggt gtc cgg agt cca caa aca agg caa gca ggt caa act aga aca     2232
Asn Gly Val Arg Ser Pro Gln Thr Arg Gln Ala Gly Gln Thr Arg Thr
447                 452                 457                 462

cgg att caa aac cct tca gca tat gcc aag aga gag gct ggg cct ggg     2280
Arg Ile Gln Asn Pro Ser Ala Tyr Ala Lys Arg Glu Ala Gly Pro Gly
463                 468                 473                 478

cgt gtg gag cca ggc agt ctc gaa tcc tct cct ggt tta ggg agg gga     2328
Arg Val Glu Pro Gly Ser Leu Glu Ser Ser Pro Gly Leu Gly Arg Gly
479                 484                 489                 494

agg aag aat tcc ttt ggc tac cgg aag aaa agg gag gag aag ttt aca     2376
Arg Lys Asn Ser Phe Gly Tyr Arg Lys Lys Arg Glu Glu Lys Phe Thr
495                 500                 505                 510

agc agc cag aca cag tct cca acg cca cca aag cct ccg tcg cca agc     2424
Ser Ser Gln Thr Gln Ser Pro Thr Pro Pro Lys Pro Pro Ser Pro Ser
511                 516                 521                 526

ttc gag ctg ggg ctg tcc agc ttc cct cca tta cct gga gct gcc ggc     2472
Phe Glu Leu Gly Leu Ser Ser Phe Pro Pro Leu Pro Gly Ala Ala Gly
527                 532                 537                 542

aat ttg aag aca gag gac ttg ttt gaa aac agg cta tct agc ttg ata     2520
Asn Leu Lys Thr Glu Asp Leu Phe Glu Asn Arg Leu Ser Ser Leu Ile
543                 548                 553                 558

ata gga cca tcc aaa gaa agg acc ctc agt gca gac gca agc gtg aac     2568
Ile Gly Pro Ser Lys Glu Arg Thr Leu Ser Ala Asp Ala Ser Val Asn
559                 564                 569                 574

acc ctt cct gta gtg gtc tcc aga gag ccc tcg gtg ccg gct tct tgt     2616
Thr Leu Pro Val Val Val Ser Arg Glu Pro Ser Val Pro Ala Ser Cys
575                 580                 585                 590
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gct gta tca gca acg tac gag cga tcc ccc tcc cca gct cat tta ccc     2664
Ala Val Ser Ala Thr Tyr Glu Arg Ser Pro Ser Pro Ala His Leu Pro
591                 596                 601                 606

gat gat ccc aag gtg gcg gag aaa cag agg gaa acc cac agt gtg gac     2712
Asp Asp Pro Lys Val Ala Glu Lys Gln Arg Glu Thr His Ser Val Asp
607                 612                 617                 622

aga ctt cct tcc gcc ctc act gcg acc gcg tgt aaa tcg gtg cag gtg     2760
Arg Leu Pro Ser Ala Leu Thr Ala Thr Ala Cys Lys Ser Val Gln Val
623                 628                 633                 638

aac gga gcc gcc acg gaa ttg cga aag ccc agc tac gca gag att tgt     2808
Asn Gly Ala Ala Thr Glu Leu Arg Lys Pro Ser Tyr Ala Glu Ile Cys
639                 644                 649                 654

cag aga acg agt aaa gag cct cct tct tcc cca ttg caa ccc caa aaa     2856
Gln Arg Thr Ser Lys Glu Pro Pro Ser Ser Pro Leu Gln Pro Gln Lys
655                 660                 665                 670

gaa caa aag cca aac act gtt ggt tgt ggg aag gag gaa aag aag ctg     2904
Glu Gln Lys Pro Asn Thr Val Gly Cys Gly Lys Glu Glu Lys Lys Leu
671                 676                 681                 686

gca gag ccc gca gag aga tac cgg gag ccc cca gcc ctc aag tcc aca     2952
Ala Glu Pro Ala Glu Arg Tyr Arg Glu Pro Pro Ala Leu Lys Ser Thr
687                 692                 697                 702

cct gga gcc ccc aga gac cag agg cgg ccg gcg ggg ggc cgg ccc tcg     3000
Pro Gly Ala Pro Arg Asp Gln Arg Arg Pro Ala Gly Gly Arg Pro Ser
703                 708                 713                 718

ccc tcg gcc atg ggg aag cgt ctc agc cga gag cag agc act ccc ccc     3048
Pro Ser Ala Met Gly Lys Arg Leu Ser Arg Glu Gln Ser Thr Pro Pro
719                 724                 729                 734

aag tct cct cag tga aaaccgtacg tctgggaggg gtcgcagagc gctgtgttaa     3103
Lys Ser Pro Gln  *
735

ccacaaacga gacactctcc cactcagtgc gagggcgagc cgctggttag gagcttgcag   3163

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cttctccggg   atg gac gtg ggg ccc agc tcc ctg ccc cac ctt ggg ctg     169
             Met Asp Val Gly Pro Ser Ser Leu Pro His Leu Gly Leu
               1               5                  10

aag ctg ctg ctg ctc ctg ctg ctg ctg ccc ctc agg ggc caa gcc aac      217
Lys Leu Leu Leu Leu Leu Leu Leu Leu Pro Leu Arg Gly Gln Ala Asn
 14                  19                  24                  29

aca ggc tgc tac ggg atc cca ggg atg ccc ggc ctg ccc ggg gca cca      265
Thr Gly Cys Tyr Gly Ile Pro Gly Met Pro Gly Leu Pro Gly Ala Pro
 30                  35                  40                  45

ggg aag gat ggg tac gac gga ctg ccg ggg ccc aag ggg gag cca gga      313
Gly Lys Asp Gly Tyr Asp Gly Leu Pro Gly Pro Lys Gly Glu Pro Gly
 46                  51                  56                  61

atc cca gcc att ccc ggg atc cga gga ccc aaa ggg cag aag gga gaa      361
Ile Pro Ala Ile Pro Gly Ile Arg Gly Pro Lys Gly Gln Lys Gly Glu
 62                  67                  72                  77

ccc ggc tta ccc ggc cat cct ggg aaa aat ggc ccc atg gga ccc cct      409
Pro Gly Leu Pro Gly His Pro Gly Lys Asn Gly Pro Met Gly Pro Pro
 78                  83                  88                  93

ggg atg cca ggg gtg ccc ggc ccc atg ggc atc cct gga gag cca ggt      457
Gly Met Pro Gly Val Pro Gly Pro Met Gly Ile Pro Gly Glu Pro Gly
 94                  99                 104                 109

gag gag ggc aga tac aag cag aaa ttc cag tca gtg ttc acg gtc act      505
Glu Glu Gly Arg Tyr Lys Gln Lys Phe Gln Ser Val Phe Thr Val Thr
110                 115                 120                 125

cgg cag acc cac cag ccc cct gca ccc aac agc ctg atc aga ttc aac      553
Arg Gln Thr His Gln Pro Pro Ala Pro Asn Ser Leu Ile Arg Phe Asn
126                 131                 136                 141

gcg gtc ctc acc aac ccg cag gga gat tat gac acg agc act ggc aag      601
Ala Val Leu Thr Asn Pro Gln Gly Asp Tyr Asp Thr Ser Thr Gly Lys
142                 147                 152                 157

ttc acc tgc aaa gtc ccc ggc ctc tac tac ttt gtc tac cac gcg tcg      649
Phe Thr Cys Lys Val Pro Gly Leu Tyr Tyr Phe Val Tyr His Ala Ser
158                 163                 168                 173
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cat aca gcc aac ctg tgc gtg ctg ctg tac cgc agc ggc gtc aaa gtg      697
His Thr Ala Asn Leu Cys Val Leu Leu Tyr Arg Ser Gly Val Lys Val
174                 179                 184                 189

gtc acc ttc tgt ggc cac acg tcc aaa acc aat cag gtc aac tcg ggc      745
Val Thr Phe Cys Gly His Thr Ser Lys Thr Asn Gln Val Asn Ser Gly
190                 195                 200                 205

ggt gtg ctg ctg agg ttg cag gtg ggc gag gag gtg tgg ctg gct gtc      793
Gly Val Leu Leu Arg Leu Gln Val Gly Glu Glu Val Trp Leu Ala Val
206                 211                 216                 221

aat gac tac tac gac atg gtg ggc atc cag ggc tct gac agc gtc ttc      841
Asn Asp Tyr Tyr Asp Met Val Gly Ile Gln Gly Ser Asp Ser Val Phe
222                 227                 232                 237

tcc ggc ttc ctg ctc ttc ccc gac tag ggcgg gcagatgcgc tcgagcccca      893
Ser Gly Phe Leu Leu Phe Pro Asp  *
238                 243

cgggccttcc acctccctca gcttcctgca tggacccacc ttactggcca gtctgcatcc    953

ttgcctagac cattctcccc accagatgga cttctcctcc agggagccca ccctgaccca   1013

cccccactgc acccccctccc catgggttct ctccttcctc tgaacttctt taggagtcac   1073

tgcttgtgtg gttcctggga cacttaacca atgccttctg gtactgccat tctttttttt   1133

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ccgggcgccg cagggtcccc acccccaccc ggccggacag tgcccggtgt tcccccgtgc    240

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gccgaggaag ggagagaggc ggcggcgaca cc  atg tca tct ccc agt ccg ggc      413
                                     Met Ser Ser Pro Ser Pro Gly
                                       1               5

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Lys Arg Arg Met Asp Thr Asp Val Val Lys Leu Ile Glu Ser Lys His
  8                  13                  18                  23

gag gtt acg atc ctg gga gga ctt aat gaa ttt gta gtg aag ttt tat      509
Glu Val Thr Ile Leu Gly Gly Leu Asn Glu Phe Val Val Lys Phe Tyr
 24                  29                  34                  39

gga cca caa gga aca cca tat gaa ggc gga gta tgg aaa gtt aga gtg      557
Gly Pro Gln Gly Thr Pro Tyr Glu Gly Gly Val Trp Lys Val Arg Val
 40                  45                  50                  55

gac cta cct gat aaa tac cct ttc aaa tct cca tct ata gga ttc atg      605
Asp Leu Pro Asp Lys Tyr Pro Phe Lys Ser Pro Ser Ile Gly Phe Met
 56                  61                  66                  71

aat aaa att ttc cat ccc aac att gat gaa gcg tca gga act gtg tgt      653
Asn Lys Ile Phe His Pro Asn Ile Asp Glu Ala Ser Gly Thr Val Cys
 72                  77                  82                  87

cta gat gta att aat caa act tgg aca gct ctc tat gat ctt acc aat      701
Leu Asp Val Ile Asn Gln Thr Trp Thr Ala Leu Tyr Asp Leu Thr Asn
 88                  93                  98                 103

ata ttt gag tcc ttc ctg cct cag tta ttg gcc tat cct aac ccc ata      749
Ile Phe Glu Ser Phe Leu Pro Gln Leu Leu Ala Tyr Pro Asn Pro Ile
104                 109                 114                 119

gat cct ctc aat ggt gac gct gca gcc atg tac ctc cac cga cca gaa      797
Asp Pro Leu Asn Gly Asp Ala Ala Ala Met Tyr Leu His Arg Pro Glu
120                 125                 130                 135

gaa tac aag cag aaa att aaa gag tac atc cag aaa tac gcc acg gag      845
Glu Tyr Lys Gln Lys Ile Lys Glu Tyr Ile Gln Lys Tyr Ala Thr Glu
136                 141                 146                 151

gag gcg ctg aaa gaa cag gaa gag ggt acc ggg gac agc tca tcg gag      893
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152                 157                 162                 167

agc tct atg tct gac ttt tcc gaa gat gag gcc cag gat atg gag ttg      941
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184

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cgcagaggag cgccggggca gggccgcggc ggaaccacag ccggagaggg gcagcccgag 180

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Met Ser Ser Pro Ser Pro Gly
1 5

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40 45 50 55

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56 61 66 71

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72 77 82 87

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Leu Asp Val Ile Asn Gln Thr Trp Thr Ala Leu Tyr Asp Pro Leu Asn
88 93 98 103

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104 109 114 119

aaa att aaa gag tac atc cag aaa tac gcc acg gag gag gcg ctg aaa 797
Lys Ile Lys Glu Tyr Ile Gln Lys Tyr Ala Thr Glu Glu Ala Leu Lys

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120                 125                 130                 135

gaa cag gaa gag ggt acc ggg gac agc tca tcg gag agc tct atg tct      845
Glu Gln Glu Glu Gly Thr Gly Asp Ser Ser Ser Glu Ser Ser Met Ser
136                 141                 146                 151

gac ttt tcc gaa gat gag gcc cag gat atg gag ttg tag tagaaaaagc      894
Asp Phe Ser Glu Asp Glu Ala Gln Asp Met Glu Leu  *
152                 157                 162

acctgctttt cagaaagact attatttcct aaccatgaga agcagactat aatattcata    954

tttaaacaaa gcaatttttt ttattactaa acaaggtttt tatgaataat agcattgata   1014

tatatatatt atatatcacc ctttagatct tgatttcttg gtcatttctc aacctgaggt   1074

gcatagcata ttcccacatt ccatttggta gcaatatgcg gtctgaatgc atgcattcat   1134

gagtccatgt ggccaagtca gcctgtgtgc tactgaactg tcgaaggaaa tagccgctct   1194

gataggtaga tgtgagtaaa aagaacagga aaaaattgct tcttttattg gtttccaaag   1254

aaacaaacca aaccaaccag ctcttggatg tgaagataaa atagtgcttt tttgaaatgg   1314

agaggaaaaa cttggggagg aagaggcctg ctgtgggggc atcggagcca gccatgtaag   1374

aatcagagct gctccttcct gtgaatccta ggtggcccta tgtcttctgt ggagttacag   1434

tataaagcag ggagctaatt aagagtatta aaacttaaaa ccatttttg actctgattt   1494

taagtacatt tttatatgtc agttgctgcc cttcacacta ccaggccctg cagccacagt   1554

gttctgttgg agaaacttgg ggaagtgttt tctgaaccag ttctttttct tggggtagag   1614

cgtgaaatcc agacctgttt ttgaaaggac agcacaggag gagaaaagtg actgggacga   1674

tgcttcctct catccaaaac acatgcagag tcacatcctc atcctagtgt ttggcagttt   1734

gagaccgcta ccctgaactt aagagcttta aatatgaggg ttgtgtttct ggggggggtta   1794

ttttttggt gtgtgtgtgt gtgtattgtg cttagaaagg ttgcagattt catcttcacc   1854

taccaagagg cggccgcctc cttggacaag ccgctcatgg accattagac ttgagaagac   1914

gacccacgtg gtgactgcaa agccctgggt acttgccttc atgttctggt ttggttttcc   1974

ctttttctgc tgctcttggc agcagcctgg tcatcatctg cttgtgggag tgggaaatgg   2034

gtattttaga cccaacacag gttctaaatt taaaacaaat aataattgga acaaataaag   2094

gttcttgtac ccagagtgat tctacatggg aaaaacaaac cagcttttt cagagagtga   2154

ccgaatagga agaagggatt cagaaatatg atgtagtaga acatgccctg caggaagaaa   2214

atgttttctc tcctgcgtat gttaagagga aatcagttta aaatgcctgc taatcaaatg   2274

tcgactcagc taaccatatg tccaggttgc tgcagagttt ctttcaaatc tgagtgttgc   2334
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ctgctgaact cggaggggag tttggagaaa ttttagacag cagctctgtg ttctttttt   2394

gccgcagcca ataagataat agcagaatta gccaatccta aaaccttcta aagacgattt   2454

ttgagcatcc cactgggatt atttaatttt tctttttgac gtgtgttttt agtttagaag   2514

tgctgtattc cacaaggttt aagtcagtga ggttggaaga taccctatct tttttattca   2574

aaaagcacaa tcaatctttt gtttgaaaat ctatataaag tacaacttgc ttttagcatg   2634

attattttcc taaataaaaa gacaaagaat ttacttactt tatgttaatt acgggcatga   2694

agcaaaaggt tttctttaaa aaaaaaaaa                                     2723
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<213> Homo sapiens

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<222> (81)..(752)

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<223> n = a,t,c or g

<400> 217

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ccccccccgc anngnaaaat tgatactgan agctagcgca agactaccgg accggaatcc     60

cgggtcgacg atttcgtgtg    atg gcg gct ggt gat ggg gac gtg aag cta      110
                         Met Ala Ala Gly Asp Gly Asp Val Lys Leu
                           1               5

ggc acc ctg ggg agt ggc agc gag agc agc aac gac ggc ggc agc gag      158
Gly Thr Leu Gly Ser Gly Ser Glu Ser Ser Asn Asp Gly Gly Ser Glu
 11                  16                  21                  26

agt cca ggc gac gcg gga gcg gca gcg gaa ggg gga ggc tgg gcg gcg      206
Ser Pro Gly Asp Ala Gly Ala Ala Ala Glu Gly Gly Gly Trp Ala Ala
 27                  32                  37                  42

gcg gcg ttg gcg ctt ctg acg ggg ggc ggg gaa atg ctg ctg aac gtg      254
Ala Ala Leu Ala Leu Leu Thr Gly Gly Gly Glu Met Leu Leu Asn Val
 43                  48                  53                  58

gcg ctg gtg gct ctg gtg ctg ctg ggg gcc tac cgg ctg tgg gtg cgc      302
Ala Leu Val Ala Leu Val Leu Leu Gly Ala Tyr Arg Leu Trp Val Arg
 59                  64                  69                  74

tgg ggg cgg cgg ggt ctg ggg gcc ggg gcc ggg gcg ggc gag gag agc      350
Trp Gly Arg Arg Gly Leu Gly Ala Gly Ala Gly Ala Gly Glu Glu Ser
```

```
 75                  80                  85                  90

ccc gcc acc tct ctg cct cgc atg aag aag cgg gac ttc agc ttg gag      398
Pro Ala Thr Ser Leu Pro Arg Met Lys Lys Arg Asp Phe Ser Leu Glu
 91                  96                 101                 106

cag ctg cgc cag tac gac ggc tcc cgc aac ccg cgc atc ctg ctc gcg      446
Gln Leu Arg Gln Tyr Asp Gly Ser Arg Asn Pro Arg Ile Leu Leu Ala
107                 112                 117                 122

gtc aat ggg aaa gtc ttc gac gtg acc aaa ggc agc aag ttc tac ggc      494
Val Asn Gly Lys Val Phe Asp Val Thr Lys Gly Ser Lys Phe Tyr Gly
123                 128                 133                 138

ccg gcg ggt cca tat gga ata ttt gct ggt agg gat gcc tcc aga gga      542
Pro Ala Gly Pro Tyr Gly Ile Phe Ala Gly Arg Asp Ala Ser Arg Gly
139                 144                 149                 154

ctg gcc aca ttt tgc cta gat aaa gat gca ctt aga gat gaa tat gat      590
Leu Ala Thr Phe Cys Leu Asp Lys Asp Ala Leu Arg Asp Glu Tyr Asp
155                 160                 165                 170

gat ctc tca gat ttg aat gca gta caa atg gag agt gtt cga gaa tgg      638
Asp Leu Ser Asp Leu Asn Ala Val Gln Met Glu Ser Val Arg Glu Trp
171                 176                 181                 186

gaa atg cag ttt aaa gaa aaa tat gat tat gta ggc aga ctc cta aaa      686
Glu Met Gln Phe Lys Glu Lys Tyr Asp Tyr Val Gly Arg Leu Leu Lys
187                 192                 197                 202

cca gga gaa gaa cca tca gaa tat aca gat gaa gaa gat acc aag gat      734
Pro Gly Glu Glu Pro Ser Glu Tyr Thr Asp Glu Glu Asp Thr Lys Asp
203                 208                 213                 218

cac aat aaa cag gat tga actttg taaacaacca aagtcagggg ccttcagaac      788
His Asn Lys Gln Asp  *
219                 224

tgcaattctt actccctttc acagactgtc cggagtcttt gggtttgatt cacctgctgc    848

gaaaaacatt caacaaattg tgtacaagat aaattaatct cactatgaag atttgaataa    908

ctagacatta tttatgctgc caaactcatt tgttgcagtt gtttgtaatg tctagtgggg    968

cttcatcatc ctgaaaagaa ggagacaggg attttttaa agagcaagaa agtcacaata   1028

ttacttcttt ccttcctttt ttccttcttt cctttcttct ttctctttct ttctttttaa   1088

aatatattga agacaaccag atatgtattt gctactcaag tgtacagatc tcctcaagaa   1148

acatcaaggg actcctgtgt cacatactgt gtttttattt taacatgggt gagggaggcg   1208

acctgatcag gggaggtggg ggtacacatc aatttgagtt gttcaggcta ctgaaacatt   1268

aaaatgtgaa ttcccaaact tttctttttg gctttgtcag ggaaaagaaa aatatcttta   1328

taaagaaatc tttggaaatt aggagaagga atttcaggtg ggtttaagtc agagctagtt   1388
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ccccaacaga aagatcattt gaaaccagtt tttatccctt ctctttcctt ccctttccct   1448

aaatcaaatc aatattaatt gtgccttatt tcacttaaca tagacttgaa ttatttttag   1508

ggaaagcccc tataatgaat tcagaaatca ctacaagcag cattaagact gaagttggaa   1568

tattctgttg accataaaac cttgatatca ttctgtgtat atagaatgta aaaggaatat   1628

tacagtgtta actgccatat atgtaatata cacaaactca attagcattg taatggccaa   1688

atgcattccc ccatgctttt ctgttttcaa aaaaattgaa aaacaaatca actcttatcc   1748

ccaacagctg cctaatttta ggagtctgac cctccacatc tcactggtgt gggtgcatgg   1808

ggctgtggag tgggtgtcag tatggatgtg tctgaatgtg tgaggccttg gaagggactc   1868

tttctgcaga tactgtaaat acaagtacca ttttaataaa gcatgtacaa taaaccaaaa   1928

aaaaaaaa                                                           1936
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<211> 2717
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (289)..(2511)

<400> 218

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aggcggcgtc cagaagccct aggtcccaga ggtccgctca gcggcaggcg cataaggcgg    120

ggccggcgcg ggcctttcct tccatcggaa ccgttctccc ggggctgagt ccctgcccgg    180

actccgaacg ccgaagacca ggggccggaa gcgcgcgccg ccactgccac gccgtgtcag    240

tcgggaggga gggagcgagc aggcgaagcc gcggaggacg gggtgaag atg gcg gcc     297
                                                      Met Ala Ala
                                                        1

ttc tcc gag atg ggt gta atg cct gag att gca caa gct gtg gaa gag      345
Phe Ser Glu Met Gly Val Met Pro Glu Ile Ala Gln Ala Val Glu Glu
  4                   9                  14                  19

atg gat tgg ctc ctc cca act gat atc cag gct gaa tct atc cca ctg      393
Met Asp Trp Leu Leu Pro Thr Asp Ile Gln Ala Glu Ser Ile Pro Leu
 20                  25                  30                  35

atc tta gga gga ggt gat gta ctt atg gct gca gaa aca gga agt ggc      441
Ile Leu Gly Gly Gly Asp Val Leu Met Ala Ala Glu Thr Gly Ser Gly
 36                  41                  46                  51
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```
aaa act ggt gct ttt agt att cca gtt atc cag ata gtt tat gaa act      489
Lys Thr Gly Ala Phe Ser Ile Pro Val Ile Gln Ile Val Tyr Glu Thr
 52                  57                  62                  67

ctg aaa gac caa cag gaa ggc aaa aaa gga aaa aca aca att aaa act      537
Leu Lys Asp Gln Gln Glu Gly Lys Lys Gly Lys Thr Thr Ile Lys Thr
 68                  73                  78                  83

ggt gct tca gtg ctg aac aaa tgg cag atg aac cca tat gac aga gga      585
Gly Ala Ser Val Leu Asn Lys Trp Gln Met Asn Pro Tyr Asp Arg Gly
 84                  89                  94                  99

tct gct ttt gca att ggg tca gat ggt ctt tgt tgt caa agc aga gaa      633
Ser Ala Phe Ala Ile Gly Ser Asp Gly Leu Cys Cys Gln Ser Arg Glu
100                 105                 110                 115

gta aag gaa tgg cat ggg tgt aga gct act aaa gga tta atg aaa ggg      681
Val Lys Glu Trp His Gly Cys Arg Ala Thr Lys Gly Leu Met Lys Gly
116                 121                 126                 131

aaa cac tac tat gaa gta tcc tgt cat gac caa ggg tta tgc agg gtc      729
Lys His Tyr Tyr Glu Val Ser Cys His Asp Gln Gly Leu Cys Arg Val
132                 137                 142                 147

ggg tgg tct acc atg cag gcc tct ttg gac cta ggt act gac aag ttt      777
Gly Trp Ser Thr Met Gln Ala Ser Leu Asp Leu Gly Thr Asp Lys Phe
148                 153                 158                 163

gga ttt ggc ttt ggt gga aca gga aag aaa tcc cat aac aaa caa ttt      825
Gly Phe Gly Phe Gly Gly Thr Gly Lys Lys Ser His Asn Lys Gln Phe
164                 169                 174                 179

gat aat tat gga gag gaa ttc act atg cat gat acc att gga tgt tac      873
Asp Asn Tyr Gly Glu Glu Phe Thr Met His Asp Thr Ile Gly Cys Tyr
180                 185                 190                 195

ctg gat ata gat aag gga cat gtc aag ttc tcc aaa aat gga aaa gat      921
Leu Asp Ile Asp Lys Gly His Val Lys Phe Ser Lys Asn Gly Lys Asp
196                 201                 206                 211

ctt ggt ctg gca ttt gaa ata cca cca cat atg aaa aac caa gcc ctc      969
Leu Gly Leu Ala Phe Glu Ile Pro Pro His Met Lys Asn Gln Ala Leu
212                 217                 222                 227

ttt cct gcc tgt gtt ttg aag aat gct gaa ctg aaa ttt aac ttc ggt     1017
Phe Pro Ala Cys Val Leu Lys Asn Ala Glu Leu Lys Phe Asn Phe Gly
228                 233                 238                 243

gaa gag gaa ttt aag ttt cca cca aaa gat ggc ttt gtt gct ctt tcc     1065
Glu Glu Glu Phe Lys Phe Pro Pro Lys Asp Gly Phe Val Ala Leu Ser
244                 249                 254                 259

aag gca ccg gat ggt tac att gtc aaa tca cag cac tca ggt aat gca     1113
Lys Ala Pro Asp Gly Tyr Ile Val Lys Ser Gln His Ser Gly Asn Ala
260                 265                 270                 275
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cag gtg aca caa aca aag ttt ctc ccc aat gct ccg aaa gct ctc att     1161
Gln Val Thr Gln Thr Lys Phe Leu Pro Asn Ala Pro Lys Ala Leu Ile
276                 281                 286                 291

gtt gaa cct tcc cgg gag tta gct gaa caa act ttg aac aac atc aag     1209
Val Glu Pro Ser Arg Glu Leu Ala Glu Gln Thr Leu Asn Asn Ile Lys
292                 297                 302                 307

cag ttt aag aaa tac att gat aat cct aaa tta agg gag ctt ctg ata     1257
Gln Phe Lys Lys Tyr Ile Asp Asn Pro Lys Leu Arg Glu Leu Leu Ile
308                 313                 318                 323

att gga ggt gtt gca gcc cgg gat cag ctc tct gtt ttg gaa aat gga     1305
Ile Gly Gly Val Ala Ala Arg Asp Gln Leu Ser Val Leu Glu Asn Gly
324                 329                 334                 339

gta gat ata gtt gta ggt act ccg gga aga cta gat gac ttg gtg tca     1353
Val Asp Ile Val Val Gly Thr Pro Gly Arg Leu Asp Asp Leu Val Ser
340                 345                 350                 355

act gga aag ctg aac tta tct caa gtt aga ttc ctg gtc ctg gat gaa     1401
Thr Gly Lys Leu Asn Leu Ser Gln Val Arg Phe Leu Val Leu Asp Glu
356                 361                 366                 371

gct gat ggg ctt ctt tct caa ggt tat tct gat ttt ata aat agg atg     1449
Ala Asp Gly Leu Leu Ser Gln Gly Tyr Ser Asp Phe Ile Asn Arg Met
372                 377                 382                 387

cac aat cag att cct cag gtt acc tct gat gga aaa aga ctt cag gtg     1497
His Asn Gln Ile Pro Gln Val Thr Ser Asp Gly Lys Arg Leu Gln Val
388                 393                 398                 403

att gtt tgc tct gcc act ttg cat tct ttc gat gta aag aaa ctg tcc     1545
Ile Val Cys Ser Ala Thr Leu His Ser Phe Asp Val Lys Lys Leu Ser
404                 409                 414                 419

gag aag ata atg cat ttt cct aca tgg gtt gac tta aaa gga gaa gac     1593
Glu Lys Ile Met His Phe Pro Thr Trp Val Asp Leu Lys Gly Glu Asp
420                 425                 430                 435

tct gtt cca gat act gta cac cat gtt gtt gtc cca gta aat ccc aaa     1641
Ser Val Pro Asp Thr Val His His Val Val Val Pro Val Asn Pro Lys
436                 441                 446                 451

act gac aga ctc tgg gaa agg ctt gga aag agc cac att aga act gat     1689
Thr Asp Arg Leu Trp Glu Arg Leu Gly Lys Ser His Ile Arg Thr Asp
452                 457                 462                 467

gat gta cat gca aaa gat aac aca aga cct ggt gct aat agt cca gag     1737
Asp Val His Ala Lys Asp Asn Thr Arg Pro Gly Ala Asn Ser Pro Glu
468                 473                 478                 483

atg tgg tct gaa gct att aaa atc ctg aaa ggg gag tat gct gtc cgg     1785
Met Trp Ser Glu Ala Ile Lys Ile Leu Lys Gly Glu Tyr Ala Val Arg
484                 489                 494                 499

gca atc aag gaa cat aag atg gat caa gca att atc ttc tgt aga acc     1833
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Ala Ile Lys Glu His Lys Met Asp Gln Ala Ile Ile Phe Cys Arg Thr
500                 505                 510                 515

aaa att gac tgt gat aac ttg gag cag tac ttt ata caa caa gga gga     1881
Lys Ile Asp Cys Asp Asn Leu Glu Gln Tyr Phe Ile Gln Gln Gly Gly
516                 521                 526                 531

gga cct gat aaa aaa gga cac cag ttc tca tgt gtt tgt ctt cat ggt     1929
Gly Pro Asp Lys Lys Gly His Gln Phe Ser Cys Val Cys Leu His Gly
532                 537                 542                 547

gac aga aag cct cat gag aga aag caa aac ttg gaa aga ttt aag aaa     1977
Asp Arg Lys Pro His Glu Arg Lys Gln Asn Leu Glu Arg Phe Lys Lys
548                 553                 558                 563

gga gat gta aga ttc ttg att tgc aca gat gta gct gct aga gga att     2025
Gly Asp Val Arg Phe Leu Ile Cys Thr Asp Val Ala Ala Arg Gly Ile
564                 569                 574                 579

gat atc cac ggt gtt cct tat gtt ata aat gtc act ctg ccc gat gaa     2073
Asp Ile His Gly Val Pro Tyr Val Ile Asn Val Thr Leu Pro Asp Glu
580                 585                 590                 595

aag caa aac tac gta cat cga att ggc aga gta gga aga gct gaa agg     2121
Lys Gln Asn Tyr Val His Arg Ile Gly Arg Val Gly Arg Ala Glu Arg
596                 601                 606                 611

atg ggt ctg gca att tcc ctg gtg gca aca gaa aaa gaa aag gtt tgg     2169
Met Gly Leu Ala Ile Ser Leu Val Ala Thr Glu Lys Glu Lys Val Trp
612                 617                 622                 627

tac cat gta tgt agc agc cgt gga aaa ggg tgt tat aac aca aga ctc     2217
Tyr His Val Cys Ser Ser Arg Gly Lys Gly Cys Tyr Asn Thr Arg Leu
628                 633                 638                 643

aag gaa gat gga ggc tgt acc ata tgg tac aac gag atg cag tta cta     2265
Lys Glu Asp Gly Gly Cys Thr Ile Trp Tyr Asn Glu Met Gln Leu Leu
644                 649                 654                 659

tct gag ata gaa gaa cac ctg aac tgt acc att tct cag gtt gag ccg     2313
Ser Glu Ile Glu Glu His Leu Asn Cys Thr Ile Ser Gln Val Glu Pro
660                 665                 670                 675

gat ata aag gta cca gtg gat gaa ttt gat ggg aaa gtt acc tac ggt     2361
Asp Ile Lys Val Pro Val Asp Glu Phe Asp Gly Lys Val Thr Tyr Gly
676                 681                 686                 691

cag aaa agg gct gct ggt ggt gga agc tat aaa ggc cat gtg gat att     2409
Gln Lys Arg Ala Ala Gly Gly Gly Ser Tyr Lys Gly His Val Asp Ile
692                 697                 702                 707

ttg gca cct act gtt caa gag ttg gct gcc ctt gaa aag gag gcg cag     2457
Leu Ala Pro Thr Val Gln Glu Leu Ala Ala Leu Glu Lys Glu Ala Gln
708                 713                 718                 723

aca tct ttc ctg cat ctt ggc tac ctt cct aac cag ctg ttc aga acc     2505
Thr Ser Phe Leu His Leu Gly Tyr Leu Pro Asn Gln Leu Phe Arg Thr
```

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724                 729                 734                 739

ttc tga tttttacatt tactgaataa gatttgagta atgaaagtct gtagtcttaa      2561
Phe  *
740

aactctaaaa cagttgtact gcttccaagc agcagtattt atagtaacgt aagctattaa   2621

tgctaactct tgcatgtcaa gaaacattag tcttaggaat tcttcaaaaa atggcatccc   2681

aatgaaaata aatttgatga ctataaaaaa aaaaaa                              2717



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gaggagaagt cagcctggca gagagactct gaaatgaggg attagaggtg ttcaaggagc    120

aagagcttca gcctgaagac aagggagcag tccctgaaga cgcttctact gagaggtctg    180

cc   atg gcc tct ctt ggc ctc caa ctt gtg ggc tac atc cta ggc ctt      227
     Met Ala Ser Leu Gly Leu Gln Leu Val Gly Tyr Ile Leu Gly Leu
       1               5                  10

ctg ggg ctt ttg ggc aca ctg gtt gcc atg ctg ctc ccc agc tgg aaa      275
Leu Gly Leu Leu Gly Thr Leu Val Ala Met Leu Leu Pro Ser Trp Lys
 16                  21                  26                  31

aca agt tct tat gtc ggt gcc agc att gtg aca gca gtt ggc ttc tcc      323
Thr Ser Ser Tyr Val Gly Ala Ser Ile Val Thr Ala Val Gly Phe Ser
 32                  37                  42                  47

aag ggc ctc tgg atg gaa tgt gcc aca cac agc aca ggc atc acc cag      371
Lys Gly Leu Trp Met Glu Cys Ala Thr His Ser Thr Gly Ile Thr Gln
 48                  53                  58                  63

tgt gac atc tat agc acc ctt ctg ggc ctg ccc gct gac atc cag gct      419
Cys Asp Ile Tyr Ser Thr Leu Leu Gly Leu Pro Ala Asp Ile Gln Ala
 64                  69                  74                  79

gcc cag gcc atg atg gtg aca tcc agt gca atc tcc tcc ctg gcc tgc      467
Ala Gln Ala Met Met Val Thr Ser Ser Ala Ile Ser Ser Leu Ala Cys
 80                  85                  90                  95

att atc tct gtg gtg ggc atg aga tgc aca gtc ttc tgc cag gaa tcc      515
Ile Ile Ser Val Val Gly Met Arg Cys Thr Val Phe Cys Gln Glu Ser
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 96                  101                 106                 111

cga gcc aaa gac aga gtg gcg gta gca ggt gga gtc ttt ttc atc ctt      563
Arg Ala Lys Asp Arg Val Ala Val Ala Gly Gly Val Phe Phe Ile Leu
112                 117                 122                 127

gga ggc ctc ctg gga ttc att cct gtt gcc tgg aat ctt cat ggg atc      611
Gly Gly Leu Leu Gly Phe Ile Pro Val Ala Trp Asn Leu His Gly Ile
128                 133                 138                 143

cta cgg gac ttc tac tca cca ctg gtg cct gac agc atg aaa ttt gag      659
Leu Arg Asp Phe Tyr Ser Pro Leu Val Pro Asp Ser Met Lys Phe Glu
144                 149                 154                 159

att gga gag gct ctt tac ttg ggc att att tct tcc ctg ttc tcc ctg      707
Ile Gly Glu Ala Leu Tyr Leu Gly Ile Ile Ser Ser Leu Phe Ser Leu
160                 165                 170                 175

ata gct gga atc atc ctc tgc ttt tcc tgc tca tgc cag aga aat cgc      755
Ile Ala Gly Ile Ile Leu Cys Phe Ser Cys Ser Cys Gln Arg Asn Arg
176                 181                 186                 191

tcc aac tac tac gat gcc tac caa gcc caa cct ctt gcc aca agg agc      803
Ser Asn Tyr Tyr Asp Ala Tyr Gln Ala Gln Pro Leu Ala Thr Arg Ser
192                 197                 202                 207

tct cca agg cct ggt caa cct ccc aaa gtc aag agt gag ttc aat tcc      851
Ser Pro Arg Pro Gly Gln Pro Pro Lys Val Lys Ser Glu Phe Asn Ser
208                 213                 218                 223

tac agc ctg aca ggg tat gtg tga agaaccaggg gccagagctg gggggtggct     905
Tyr Ser Leu Thr Gly Tyr Val  *
224                 229

gggtctgtga aaaacagtgg acagcacccc gagggccaca ggtgagggac actaccactg    965

gatcgtgtca gaaggtgctg ctgaggatag actgactttg gccattggat tgagcaaagg   1025

cagaaatggg ggctagtgta acagcatgca ggttgaattg ccaaggatgc tcgccatgcc   1085

agcctttctg ttttcctcac cttgctgctc ccctgcccta agtccccaac cctcaacttg   1145

aaaccccatt cccttaagcc aggactcaga ggatcccttt gccctctggt ttacctggga   1205

ctccatcccc caaacccact aatcacatcc cactgactga ccctctgtga tcaaagaccc   1265

tctctctggc tgaggttggc tcttagctca ttgctgggga tgggaaggag aagcagtggc   1325

ttttgtgggc attgctctaa cctacttctc aagcttccct ccaaagaaac tgattggccc   1385

tggaacctcc atcccactct tgttatgact ccacagtgtc cagactaatt tgtgcatgaa   1445

ctgaaataaa accatcctac ggtatccagg gaacagaaag caggatgcag gatgggagga   1505

caggaaggca gcctgggaca tttaaaaaaa aaaaa                              1540
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cagcgtggcc atgaagctcc ttcaccaagt aagcaagctg tgtgggaagt gcagccccac 120

tgacgtggac atcctgcagc cctccttcaa cttcctgtat tggagccttc atcagaccac 180

acccagcagt cagaaaagag gtgcaggggc ccgggctggg acagtgaaga gtgctgggca 240

gtctgtggtc ctctgtatct caacttttc atcttaaaaa aacaaatagg gttgtgtgtg 300

tggctggtgg tcataaggtc ctttctggct ctaataacct gagcttctgt tatgaagctg 360

ggacccttag agcctcagga tgatcctctg tttgtttgtg aagccccaat caggtgctaa 420

gcaccatagt ggcacttagc tgaagctcct ctgtaactcc tgtgggccct gccttgccca 480

cccccgacag ctgctgcagt gctcctgagc agcacaggcc tg atg gag ctt ctg 534
Met Glu Leu Leu
1

gag aag atg ctg gcc ctc acc ttg gca aag gca gat tct ccc agg act 582
Glu Lys Met Leu Ala Leu Thr Leu Ala Lys Ala Asp Ser Pro Arg Thr
5 10 15 20

gca ctc ctc tgc tct gcc tgg ctg ctc act gcc tcc ttc tct gcc cag 630
Ala Leu Leu Cys Ser Ala Trp Leu Leu Thr Ala Ser Phe Ser Ala Gln
21 26 31 36

cag cac aag ggc agt ttg cag aag gac cct cta ttg tcc cag gcc tgt 678
Gln His Lys Gly Ser Leu Gln Lys Asp Pro Leu Leu Ser Gln Ala Cys
37 42 47 52

gtt ggc tgc ctg gag gcc ttg ctt gac tac ctg gat gcc cgg agc cca 726
Val Gly Cys Leu Glu Ala Leu Leu Asp Tyr Leu Asp Ala Arg Ser Pro
53 58 63 68

gac att gct ctc cac gtg gcc tca cag cct tgg aat cgg ttt ttg ctg 774
Asp Ile Ala Leu His Val Ala Ser Gln Pro Trp Asn Arg Phe Leu Leu
69 74 79 84

ttt acc ctc ttg gat gct gga gag aat tcc ttc ctc aga cct gag att 822
Phe Thr Leu Leu Asp Ala Gly Glu Asn Ser Phe Leu Arg Pro Glu Ile
85 90 95 100

ttg agg ctc atg acc ctg ctc cag agc atg gga cac ctg gct gac cac 870

```
Leu Arg Leu Met Thr Leu Leu Gln Ser Met Gly His Leu Ala Asp His
101                 106                 111                 116

agc atg gcc cag acc ctg cag gcc ttc ctt gga ggg cct tcc ccc tag      918
Ser Met Ala Gln Thr Leu Gln Ala Phe Leu Gly Gly Pro Ser Pro  *
117                 122                 127                 132

cacctcctca ggccagccac ccctgcagga catgctctgc ctgggagggg tggctgtatc    978

cctgtcccac atcagaaact gatcctcagg acttgaaggc ccagaagtgg agagagaatg   1038

agacctggag acaaagggca taattgttgg ggaaatggat gacagctgaa gctattcata   1098

tggagccata tactctattg ttgaaataga ataaggaaat aaaatgatac actcacataa   1158

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gcgcgacagg gaaaataaaa gaagcaaaaa caggccctgc tgtgagggac cacgaggcag    180

tgccaggatg aaagagttgg agtaacctag gtgattctga gtgaatcagt caggaggcct    240

tcctggaggg ggctgaggcc ccagcttgtg gccaccacaa cgtatcaagc tatctccagg    300

gttgggctca ggactcagag ctgacgcagc tggggtgccc cttggttctg gagg  atg     357
                                                            Met
                                                              1

agg ctc ctc cgc aga cgc cac atg ccc ctg cgc ctg gcc atg gtg ggc      405
Arg Leu Leu Arg Arg Arg His Met Pro Leu Arg Leu Ala Met Val Gly
  2                   7                  12                  17

tgc gcc ttt gtg ctc ttc ctc ttc ctc ctg cat agg gat gtg agc agc      453
Cys Ala Phe Val Leu Phe Leu Phe Leu Leu His Arg Asp Val Ser Ser
 18                  23                  28                  33

aga gag gag gcc aca gag aag ccg tgg ctg aag tcc ctg gtg agc cgg      501
Arg Glu Glu Ala Thr Glu Lys Pro Trp Leu Lys Ser Leu Val Ser Arg
 34                  39                  44                  49

aag gat cac gtc ctg gac ctc atg ctg gag gcc atg aac aac ctt aga      549
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```
Lys Asp His Val Leu Asp Leu Met Leu Glu Ala Met Asn Asn Leu Arg
 50                  55                  60                  65

gat tca atg ccc aag ctc caa atc agg gct cca gaa gcc cag cag act      597
Asp Ser Met Pro Lys Leu Gln Ile Arg Ala Pro Glu Ala Gln Gln Thr
 66                  71                  76                  81

ctg ttc tcc ata aat cag tcc tgc ctc cct ggg ttc tat acc cca gct      645
Leu Phe Ser Ile Asn Gln Ser Cys Leu Pro Gly Phe Tyr Thr Pro Ala
 82                  87                  92                  97

gaa ctg aag ccc ttc tgg gaa cgg cca cca cag gac ccc aat gcc cct      693
Glu Leu Lys Pro Phe Trp Glu Arg Pro Pro Gln Asp Pro Asn Ala Pro
 98                 103                 108                 113

ggg gca gat gga aaa gca ttt cag aag agc aag tgg acc ccc ctg gag      741
Gly Ala Asp Gly Lys Ala Phe Gln Lys Ser Lys Trp Thr Pro Leu Glu
114                 119                 124                 129

acc cag gaa aag gaa gaa ggc tat aag aag cac tgt ttc aat gcc ttt      789
Thr Gln Glu Lys Glu Glu Gly Tyr Lys Lys His Cys Phe Asn Ala Phe
130                 135                 140                 145

gcc agc gac cgg atc tcc ctg cag agg tcc ctg ggg cca gac acc cga      837
Ala Ser Asp Arg Ile Ser Leu Gln Arg Ser Leu Gly Pro Asp Thr Arg
146                 151                 156                 161

cca cct gag tgt gtg gac cag aag ttc cgg cgc tgc ccc cca ctg gcc      885
Pro Pro Glu Cys Val Asp Gln Lys Phe Arg Arg Cys Pro Pro Leu Ala
162                 167                 172                 177

acc acc agc gtg atc att gtg ttc cac aac gaa gcc tgg tcc aca ctg      933
Thr Thr Ser Val Ile Ile Val Phe His Asn Glu Ala Trp Ser Thr Leu
178                 183                 188                 193

ctg cga aca gtg tac agc gtc cta cac acc acc cct gcc atc ttg ctc      981
Leu Arg Thr Val Tyr Ser Val Leu His Thr Thr Pro Ala Ile Leu Leu
194                 199                 204                 209

aag gag atc ata ctg gtg gat gat gcc agc aca gag gag cac cta aag     1029
Lys Glu Ile Ile Leu Val Asp Asp Ala Ser Thr Glu Glu His Leu Lys
210                 215                 220                 225

gag aag ctg gag cag tac gtg aag cag ctg cag gtg gtg agg gtg gtg     1077
Glu Lys Leu Glu Gln Tyr Val Lys Gln Leu Gln Val Val Arg Val Val
226                 231                 236                 241

cgg cag gag gag cgg aag ggg ctg atc acc gcc cgg ctg ctg ggg gcc     1125
Arg Gln Glu Glu Arg Lys Gly Leu Ile Thr Ala Arg Leu Leu Gly Ala
242                 247                 252                 257

agc gtg gca cag gcg gag gtg ctc acg ttc ctg gat gcc cac tgt gag     1173
Ser Val Ala Gln Ala Glu Val Leu Thr Phe Leu Asp Ala His Cys Glu
258                 263                 268                 273

tgc ttc cac ggc tgg ctg gag ccc ctc ctg gct cga atc gct gag gac     1221
Cys Phe His Gly Trp Leu Glu Pro Leu Leu Ala Arg Ile Ala Glu Asp
```

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274                 279                 284                 289

aag aca gtg gtg gtg agc cca gac atc gtc acc atc gac ctt aat act     1269
Lys Thr Val Val Val Ser Pro Asp Ile Val Thr Ile Asp Leu Asn Thr
290                 295                 300                 305

ttt gag ttc gcc aag ccc gtc cag agg ggc aga gtc cat agc cga ggc     1317
Phe Glu Phe Ala Lys Pro Val Gln Arg Gly Arg Val His Ser Arg Gly
306                 311                 316                 321

aac ttt gac tgg agc ctg acc ttc ggc tgg gaa aca ctt cct cca cat     1365
Asn Phe Asp Trp Ser Leu Thr Phe Gly Trp Glu Thr Leu Pro Pro His
322                 327                 332                 337

gag aag cag agg cgc aag gat gaa acc tac ccc atc aaa tcc ccg acg     1413
Glu Lys Gln Arg Arg Lys Asp Glu Thr Tyr Pro Ile Lys Ser Pro Thr
338                 343                 348                 353

ttt gct ggt ggc ctc ttc tcc atc tcc aag tcc tac ttt gag cac atc     1461
Phe Ala Gly Gly Leu Phe Ser Ile Ser Lys Ser Tyr Phe Glu His Ile
354                 359                 364                 369

ggt acc tat gat aat cag atg gag atc tgg gga ggg gag aac gtg gaa     1509
Gly Thr Tyr Asp Asn Gln Met Glu Ile Trp Gly Gly Glu Asn Val Glu
370                 375                 380                 385

atg tcc ttc cgg gtg tgg cag tgt ggg ggc cag ctg gag atc atc ccc     1557
Met Ser Phe Arg Val Trp Gln Cys Gly Gly Gln Leu Glu Ile Ile Pro
386                 391                 396                 401

tgc tct gtc gta ggc cat gtg ttc cgg acc aag agc ccc cac acc ttc     1605
Cys Ser Val Val Gly His Val Phe Arg Thr Lys Ser Pro His Thr Phe
402                 407                 412                 417

ccc aag ggc act agt gtc att gct cgc aat caa gtg cgc ctg gca gag     1653
Pro Lys Gly Thr Ser Val Ile Ala Arg Asn Gln Val Arg Leu Ala Glu
418                 423                 428                 433

gtc tgg atg gac agc tac aag aag att ttc tat agg aga aat ctg cag     1701
Val Trp Met Asp Ser Tyr Lys Lys Ile Phe Tyr Arg Arg Asn Leu Gln
434                 439                 444                 449

gca gca aag atg gcc caa gag aaa tcc ttc ggt gac att tcg gaa cga     1749
Ala Ala Lys Met Ala Gln Glu Lys Ser Phe Gly Asp Ile Ser Glu Arg
450                 455                 460                 465

ctg cag ctg agg gaa caa ctg cac tgt cac aac ttt tcc tgg tac ctg     1797
Leu Gln Leu Arg Glu Gln Leu His Cys His Asn Phe Ser Trp Tyr Leu
466                 471                 476                 481

cac aat gtc tac cca gag atg ttt gtt cct gac ctg acg ccc acc ttc     1845
His Asn Val Tyr Pro Glu Met Phe Val Pro Asp Leu Thr Pro Thr Phe
482                 487                 492                 497

tat ggt gcc atc aag aac ctc ggc acc aac caa tgc ctg gat gtg ggt     1893
Tyr Gly Ala Ile Lys Asn Leu Gly Thr Asn Gln Cys Leu Asp Val Gly
498                 503                 508                 513
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gag aac aac cgc ggg ggg aag ccc ctc atc atg tac tcc tgc cac ggc     1941
Glu Asn Asn Arg Gly Gly Lys Pro Leu Ile Met Tyr Ser Cys His Gly
514                 519                 524                 529

ctt ggc ggc aac cag tac ttt gag tac aca act cag agg gac ctt cgc     1989
Leu Gly Gly Asn Gln Tyr Phe Glu Tyr Thr Thr Gln Arg Asp Leu Arg
530                 535                 540                 545

cac aac atc gca aag cag ctg tgt cta cat gtc agc aag ggt gct ctg     2037
His Asn Ile Ala Lys Gln Leu Cys Leu His Val Ser Lys Gly Ala Leu
546                 551                 556                 561

ggc ctt ggg agc tgt cac ttc act ggc aag aat agc cag gtc ccc aag     2085
Gly Leu Gly Ser Cys His Phe Thr Gly Lys Asn Ser Gln Val Pro Lys
562                 567                 572                 577

gac gag gaa tgg gaa ttg gcc cag gat cag ctc atc agg aac tca gga     2133
Asp Glu Glu Trp Glu Leu Ala Gln Asp Gln Leu Ile Arg Asn Ser Gly
578                 583                 588                 593

tct ggt acc tgc ctg aca tcc cag gac aaa aag cca gcc atg gcc ccc     2181
Ser Gly Thr Cys Leu Thr Ser Gln Asp Lys Lys Pro Ala Met Ala Pro
594                 599                 604                 609

tgc aat ccc agt gac ccc cat cag ttg tgg ctc ttt gtc tag gacccag     2230
Cys Asn Pro Ser Asp Pro His Gln Leu Trp Leu Phe Val  *
610                 615                 620

atcatcccca gagagagccc ccacaagctc ctcaggaaac aggattgctg atgtctggga   2290

acctgatcac cagcttctct ggaggccgta aagatggatt tctaaaccca ctgggtggca   2350

aggcaggacc ttcctaatcc ttgcaacaac attgggccca ttttctttcc ttcacaccga   2410

tggaagagac cattaggaca tatatttagc ctagcgtttt cctgttctag aaatagaggc   2470

tcccaaagta gggaaggcag ctgggggagg gttcagggca gcaatgctga gttcaagaaa   2530

agtacttcag gctgggcaca gtggctcatg cctgaaatcc tagcactttg ggaagacaat   2590

gtgggagaat ggcttgagcc caggagttca agaccggcct gagcaacata gtgaggatcc   2650

catctctacg cccaccctcc ccccggcaaa aaaaaaagct gggtatggtg gcttatgcct   2710

gtagtcgcag ctactcagaa ggctgaggtg ggaggattgc ttgttccccg gaggttgaag   2770

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catcttggat ttgaaagttg agagcagc atg ttt tgc cca ctg aaa ctc atc 172
Met Phe Cys Pro Leu Lys Leu Ile
1 5

ctg ctg cca gtg tta ctg gat tat tcc ttg ggc ctg aat gac ttg aat 220
Leu Leu Pro Val Leu Leu Asp Tyr Ser Leu Gly Leu Asn Asp Leu Asn
9 14 19 24

gtt tcc ccg cct gag cta aca gtc cat gtg ggt gat tca gct ctg atg 268
Val Ser Pro Pro Glu Leu Thr Val His Val Gly Asp Ser Ala Leu Met
25 30 35 40

gga tgt gtt ttc cag agc aca gaa gac aaa tgt ata ttc aag ata gac 316
Gly Cys Val Phe Gln Ser Thr Glu Asp Lys Cys Ile Phe Lys Ile Asp
41 46 51 56

tgg act ctg tca cca gga gag cac gcc aag gac gaa tat gtg cta tac 364
Trp Thr Leu Ser Pro Gly Glu His Ala Lys Asp Glu Tyr Val Leu Tyr
57 62 67 72

tat tac tcc aat ctc agt gtg cct att ggg cgc ttc cag aac cgc gta 412
Tyr Tyr Ser Asn Leu Ser Val Pro Ile Gly Arg Phe Gln Asn Arg Val
73 78 83 88

cac ttg atg ggg gac atc tta tgc aat gat ggc tct ctc ctg ctc caa 460
His Leu Met Gly Asp Ile Leu Cys Asn Asp Gly Ser Leu Leu Leu Gln
89 94 99 104

gat gtg caa gag gct gac cag gga acc tat atc tgt gaa atc cgc ctc 508
Asp Val Gln Glu Ala Asp Gln Gly Thr Tyr Ile Cys Glu Ile Arg Leu
105 110 115 120

aaa ggg gag agc cag gtg ttc aag aag gcg gtg gta ctg cat gtg ctt 556
Lys Gly Glu Ser Gln Val Phe Lys Lys Ala Val Val Leu His Val Leu
121 126 131 136

cca gag gag ccc aaa gag ctc atg gtc cat gtg ggt gga ttg att cag 604
Pro Glu Glu Pro Lys Glu Leu Met Val His Val Gly Gly Leu Ile Gln
137 142 147 152

atg gga tgt gtt ttc cag agc aca gaa gtg aaa cac gtg acc aag gta 652
Met Gly Cys Val Phe Gln Ser Thr Glu Val Lys His Val Thr Lys Val
153 158 163 168

gaa tgg ata ttt tca gga cgg cgc gca aag gag gag att gta ttt cgt 700
Glu Trp Ile Phe Ser Gly Arg Arg Ala Lys Glu Glu Ile Val Phe Arg

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169                 174                 179                 184

tac tac cac aaa ctc agg atg tct gtg gag tac tcc cag agc tgg ggc      748
Tyr Tyr His Lys Leu Arg Met Ser Val Glu Tyr Ser Gln Ser Trp Gly
185                 190                 195                 200

cac ttc cag aat cgt gtg aac ctg gtg ggg gac att ttc cgc aat gac      796
His Phe Gln Asn Arg Val Asn Leu Val Gly Asp Ile Phe Arg Asn Asp
201                 206                 211                 216

ggt tcc atc atg ctt caa gga gtg agg gag tca gat gga gga aac tac      844
Gly Ser Ile Met Leu Gln Gly Val Arg Glu Ser Asp Gly Gly Asn Tyr
217                 222                 227                 232

acc tgc agt atc cac cta ggg aac ctg gtg ttc aag aaa acc att gtg      892
Thr Cys Ser Ile His Leu Gly Asn Leu Val Phe Lys Lys Thr Ile Val
233                 238                 243                 248

ctg cat gtc agc ccg gaa gag cct cga aca ctg gtg acc ccg gca gcc      940
Leu His Val Ser Pro Glu Glu Pro Arg Thr Leu Val Thr Pro Ala Ala
249                 254                 259                 264

ctg agg cct ctg gtc ttg ggt ggt aat cag ttg gtg atc att gtg gga      988
Leu Arg Pro Leu Val Leu Gly Gly Asn Gln Leu Val Ile Ile Val Gly
265                 270                 275                 280

att gtc tgt gcc aca atc ctg ctg ctc cct gtt ctg ata ttg atc gtg     1036
Ile Val Cys Ala Thr Ile Leu Leu Leu Pro Val Leu Ile Leu Ile Val
281                 286                 291                 296

aag aag acc tgt gga aat aag agt tca gtg aat tct aca gtc ttg gtg     1084
Lys Lys Thr Cys Gly Asn Lys Ser Ser Val Asn Ser Thr Val Leu Val
297                 302                 307                 312

aag aac acg aag aag act aat cca gag ata aaa gaa aaa ccc tgc cat     1132
Lys Asn Thr Lys Lys Thr Asn Pro Glu Ile Lys Glu Lys Pro Cys His
313                 318                 323                 328

ttt gaa aga tgt gaa ggg gag aaa cac att tac tcc cca ata att gta     1180
Phe Glu Arg Cys Glu Gly Glu Lys His Ile Tyr Ser Pro Ile Ile Val
329                 334                 339                 344

cgg gag gtg atc gag gaa gaa gaa cca agt gaa aaa tca gag gcc acc     1228
Arg Glu Val Ile Glu Glu Glu Glu Pro Ser Glu Lys Ser Glu Ala Thr
345                 350                 355                 360

tac atg acc atg cac cca gtt tgg cct tct ctg agg tca gat cgg aac     1276
Tyr Met Thr Met His Pro Val Trp Pro Ser Leu Arg Ser Asp Arg Asn
361                 366                 371                 376

aac tca ctt gaa aaa aag tca ggt ggg gga atg cca aaa aca cag caa     1324
Asn Ser Leu Glu Lys Lys Ser Gly Gly Gly Met Pro Lys Thr Gln Gln
377                 382                 387                 392

gcc ttt tga gaagaat ggagagtccc ttcatctcag cagcgggggga gactctctcc     1380
Ala Phe  *
393
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tgtgtgtgtc ctgggccact ctaccagtga tttcagactt cccgctctcc cagctgtcct   1440

cctgtctcat tgtttggtca atacactgaa gaa                                1473
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gtccgcggcg gttgagagc atg gcc tct cca ggg gca ggt agg gcg cct ccg      112
                    Met Ala Ser Pro Gly Ala Gly Arg Ala Pro Pro
                      1               5

gag tta ccg gag cgg aac tgc ggg tac cgc gaa gtc gag tac tgg gat      160
Glu Leu Pro Glu Arg Asn Cys Gly Tyr Arg Glu Val Glu Tyr Trp Asp
 12                  17                  22                  27

cag cgc tac caa ggc gca gcc gat tct gcc ccc tac gat tgg ttc ggg      208
Gln Arg Tyr Gln Gly Ala Ala Asp Ser Ala Pro Tyr Asp Trp Phe Gly
 28                  33                  38                  43

gac ttc tcc tcc ttc cgt gcc ctc cta gag ccg gag ctg cgg ccc gag      256
Asp Phe Ser Ser Phe Arg Ala Leu Leu Glu Pro Glu Leu Arg Pro Glu
 44                  49                  54                  59

gac cgt atc ctt gtg cta ggt tgc ggg aac agt gcc ctg agc tac gag      304
Asp Arg Ile Leu Val Leu Gly Cys Gly Asn Ser Ala Leu Ser Tyr Glu
 60                  65                  70                  75

ctg ttc ctc gga ggc ttc cct aat gtg acc agt gtg gac tac tca tca      352
Leu Phe Leu Gly Gly Phe Pro Asn Val Thr Ser Val Asp Tyr Ser Ser
 76                  81                  86                  91

gtc gtg gtg gct gcc atg cag gct cgc tat gcc cat gtg ccg cag ctg      400
Val Val Val Ala Ala Met Gln Ala Arg Tyr Ala His Val Pro Gln Leu
 92                  97                 102                 107

cgc tgg gag acc atg gat gtg cgg aag ctg gac ttc ccc agt gct tct      448
Arg Trp Glu Thr Met Asp Val Arg Lys Leu Asp Phe Pro Ser Ala Ser
108                 113                 118                 123

ttt gat gtg gtg ctc gag aag ggc acg ctg gat gcc ctg ctg gct ggg      496
Phe Asp Val Val Leu Glu Lys Gly Thr Leu Asp Ala Leu Leu Ala Gly
124                 129                 134                 139

gaa cga gat ccc tgg acc gtg tcc tct gaa ggt gtc cac act gtg gac      544
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Glu Arg Asp Pro Trp Thr Val Ser Ser Glu Gly Val His Thr Val Asp
140                 145                 150                 155

cag gtg ttg agt gag gtg agc cgc gtg ctt gtc cct gga ggc cgg ttt      592
Gln Val Leu Ser Glu Val Ser Arg Val Leu Val Pro Gly Gly Arg Phe
156                 161                 166                 171

atc tca atg act tct gct gcc ccc cac ttt cgg acc aga cac tat gcc      640
Ile Ser Met Thr Ser Ala Ala Pro His Phe Arg Thr Arg His Tyr Ala
172                 177                 182                 187

caa gcc tat tat ggc tgg tcc ctg agg cat gct acc tat ggc agc ggt      688
Gln Ala Tyr Tyr Gly Trp Ser Leu Arg His Ala Thr Tyr Gly Ser Gly
188                 193                 198                 203

ttc cac ttc cat ctc tac ctc atg cac aag ggc ggg aag ctc agt gtg      736
Phe His Phe His Leu Tyr Leu Met His Lys Gly Gly Lys Leu Ser Val
204                 209                 214                 219

gcc cag ctg gct ctg ggg gcc caa atc ctc tca ccc ccc aga cct ccc      784
Ala Gln Leu Ala Leu Gly Ala Gln Ile Leu Ser Pro Pro Arg Pro Pro
220                 225                 230                 235

acc tca cct tgc ttc ctt cag gac tca gat cat gag gac ttc ctt agt      832
Thr Ser Pro Cys Phe Leu Gln Asp Ser Asp His Glu Asp Phe Leu Ser
236                 241                 246                 251

gcc att cag ctc tga ggccagagca tggtcctcca cccttcctgc cattctgccc      887
Ala Ile Gln Leu  *
252

tgggctcctc aggtagttgg aattcctgac ttaggacttg gggttgggtc caaggtgctt    947

acatcccagg ggcctcatgc ctaagataga gggtgggagc gaacccacat gaaccaatac   1007

agcccagctc caactagaaa aaaaaaaaa                                     1036
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09650756 - 07-06-2006

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gctggcccgg cacggcggtg gtcttgcggg aggcgtgggc tgggattgcg gtgcctgtgc    120

ttcccggtgc cagggtgtc atg gaa ggg ctg ctg aca aga tgc aga gca ttg      172
                    Met Glu Gly Leu Leu Thr Arg Cys Arg Ala Leu
                      1               5
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ccc gcc ctg gcc acc tgc agc cgc cag ctc tct ggg tat gtt cct tgc      220
Pro Ala Leu Ala Thr Cys Ser Arg Gln Leu Ser Gly Tyr Val Pro Cys
 12                  17                  22                  27

agg ttt cac cac tgt gcc cca aga aga ggg cgg cgc ctg ctg ctg tct      268
Arg Phe His His Cys Ala Pro Arg Arg Gly Arg Arg Leu Leu Leu Ser
 28                  33                  38                  43

cgt gtg ttc cag cca cag aac ctt cgg gaa gac cgg gtg ctc tcc ctg      316
Arg Val Phe Gln Pro Gln Asn Leu Arg Glu Asp Arg Val Leu Ser Leu
 44                  49                  54                  59

cag gac aaa tct gat gac ctg acc tgt aag agc cag cgg ctg atg ctg      364
Gln Asp Lys Ser Asp Asp Leu Thr Cys Lys Ser Gln Arg Leu Met Leu
 60                  65                  70                  75

cag gtg ggc ctg atc tac cca gca agc ccc ggc tgt tac cac ctc ctg      412
Gln Val Gly Leu Ile Tyr Pro Ala Ser Pro Gly Cys Tyr His Leu Leu
 76                  81                  86                  91

cca tat acc gtc cgt gcc atg gag aag ctc gtg cga gtg ata gac cag      460
Pro Tyr Thr Val Arg Ala Met Glu Lys Leu Val Arg Val Ile Asp Gln
 92                  97                 102                 107

gag atg cag gcc atc ggg ggc cag aaa gtc aac atg ccc agc ctc agc      508
Glu Met Gln Ala Ile Gly Gly Gln Lys Val Asn Met Pro Ser Leu Ser
108                 113                 118                 123

ccg gca gag ctc tgg caa gcc acc aac cgg tgg gac ttg atg ggc aaa      556
Pro Ala Glu Leu Trp Gln Ala Thr Asn Arg Trp Asp Leu Met Gly Lys
124                 129                 134                 139

gag ctg cta aga ctt aga gac agg cat ggc aag gaa tac tgc tta gga      604
Glu Leu Leu Arg Leu Arg Asp Arg His Gly Lys Glu Tyr Cys Leu Gly
140                 145                 150                 155

cca act cac gag gaa gcc att acg gcc tta att gcc tcc cag aag aaa      652
Pro Thr His Glu Glu Ala Ile Thr Ala Leu Ile Ala Ser Gln Lys Lys
156                 161                 166                 171

ctg tcc tac aag cag ctt ccc ttc ctg ctg tac caa gtg aca agg aag      700
Leu Ser Tyr Lys Gln Leu Pro Phe Leu Leu Tyr Gln Val Thr Arg Lys
172                 177                 182                 187

ttt cgg gat gag ccc agg ccc cgc ttt ggt ctt ctc cgt ggc cga gag      748
Phe Arg Asp Glu Pro Arg Pro Arg Phe Gly Leu Leu Arg Gly Arg Glu
188                 193                 198                 203

ttt tac atg aag gat atg tac acc ttt gac tcc tcc cca gag gct gcc      796
Phe Tyr Met Lys Asp Met Tyr Thr Phe Asp Ser Ser Pro Glu Ala Ala
204                 209                 214                 219

cag cag acc tac agc ctg gtg tgt gat gcc tac tgc agc ctg ttc aac      844
Gln Gln Thr Tyr Ser Leu Val Cys Asp Ala Tyr Cys Ser Leu Phe Asn
220                 225                 230                 235
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aag cta ggg ctg cca ttt gtc aag gtc cag gcc gat gtg ggc acc atc      892
Lys Leu Gly Leu Pro Phe Val Lys Val Gln Ala Asp Val Gly Thr Ile
236                 241                 246                 251

ggg ggc aca gtg tct cat gag ttc cag ctc cca gtg gat att gga gag      940
Gly Gly Thr Val Ser His Glu Phe Gln Leu Pro Val Asp Ile Gly Glu
252                 257                 262                 267

gac cgg ctt gcc atc tgt ccc cgc tgc agc ttc tca gcc aac atg gag      988
Asp Arg Leu Ala Ile Cys Pro Arg Cys Ser Phe Ser Ala Asn Met Glu
268                 273                 278                 283

aca cta gac ttg tca caa atg aac tgc cct gct tgc cag ggc cca ttg     1036
Thr Leu Asp Leu Ser Gln Met Asn Cys Pro Ala Cys Gln Gly Pro Leu
284                 289                 294                 299

act aaa acc aaa ggc att gag gtg ggg cac aca ttt tac ctg ggt acc     1084
Thr Lys Thr Lys Gly Ile Glu Val Gly His Thr Phe Tyr Leu Gly Thr
300                 305                 310                 315

aag tac tca tcc att ttc aat gcc cag ttt acc aat gtc tgt ggc aaa     1132
Lys Tyr Ser Ser Ile Phe Asn Ala Gln Phe Thr Asn Val Cys Gly Lys
316                 321                 326                 331

cca acc ctg gct gaa atg ggg tgc tat ggc ttg ggt gtg aca cgg atc     1180
Pro Thr Leu Ala Glu Met Gly Cys Tyr Gly Leu Gly Val Thr Arg Ile
332                 337                 342                 347

ttg gct gct gcc att gaa gtc ctc tct aca gaa gac tgt gtc cgc tgg     1228
Leu Ala Ala Ala Ile Glu Val Leu Ser Thr Glu Asp Cys Val Arg Trp
348                 353                 358                 363

ccc agc cta ctg gcc cct tac caa gcc tgc ctc atc ccc cct aag aag     1276
Pro Ser Leu Leu Ala Pro Tyr Gln Ala Cys Leu Ile Pro Pro Lys Lys
364                 369                 374                 379

ggc agt aag gag cag gcg gcc tcc gag ctc ata ggg cag ctg tac gac     1324
Gly Ser Lys Glu Gln Ala Ala Ser Glu Leu Ile Gly Gln Leu Tyr Asp
380                 385                 390                 395

cac atc aca gag gca gtg cct cag ctt cac ggg gag gtg ctc ctg gac     1372
His Ile Thr Glu Ala Val Pro Gln Leu His Gly Glu Val Leu Leu Asp
396                 401                 406                 411

gac agg acc cat ctg acc atc gga aac aga ctg aaa gat gcc aac aag     1420
Asp Arg Thr His Leu Thr Ile Gly Asn Arg Leu Lys Asp Ala Asn Lys
412                 417                 422                 427

ttt ggc tac ccc ttt gtg ata atc gct ggc aag agg gcc ctg gag gac     1468
Phe Gly Tyr Pro Phe Val Ile Ile Ala Gly Lys Arg Ala Leu Glu Asp
428                 433                 438                 443

cct gca cat ttt gag gtt tgg tgt cag aac act ggt gag gtg gcc ttc     1516
Pro Ala His Phe Glu Val Trp Cys Gln Asn Thr Gly Glu Val Ala Phe
444                 449                 454                 459

ctc acc aaa gat gga gtc atg gat tta ctg acc cca gtg cag act gtc     1564
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Leu Thr Lys Asp Gly Val Met Asp Leu Leu Thr Pro Val Gln Thr Val
460                 465                 470                 475

taa atgc ccccagccca cccctgcccc catttgcagc cttggtgttc gttctaacac     1621
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476

tgcattttcc tacacccctt tcctggactg ctctctccag aaacagcaca gctcatggag   1681

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09550210 - 09550210

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catatttgga gttaaaagaa ccaaatatta ctaagtaagc agacgcgggc acgcgctgca    180

taccgggatt tgtagtccct tccggggcgg ggtacagcgc gcctgcgcag aggggccgtc    240

gctcttccgg gcgc  atg cgt gcg gca gcg gcg cca gga ctg act gcg ccg      290
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tgg agg ctg ctg cag tgt tgt gag ttg gaa gct ggg gag ctc ggc atg      338
Trp Arg Leu Leu Gln Cys Cys Glu Leu Glu Ala Gly Glu Leu Gly Met
 13                  18                  23                  28

gcg gtc ccc gct gca gcc atg ggg ccc tcg gcg ttg ggc cag agc ggc      386
Ala Val Pro Ala Ala Ala Met Gly Pro Ser Ala Leu Gly Gln Ser Gly
 29                  34                  39                  44

ccc ggc tcg atg gcc ccg tgg tgc tca gtg agc agc ggc ccg tcg cgc      434
Pro Gly Ser Met Ala Pro Trp Cys Ser Val Ser Ser Gly Pro Ser Arg
 45                  50                  55                  60

tac gtg ctt ggg atg cag gag ctg ttc cgg ggc cac agc aag acg cgc      482
Tyr Val Leu Gly Met Gln Glu Leu Phe Arg Gly His Ser Lys Thr Arg
 61                  66                  71                  76

gag ttc ctg gcg cac agc gcc aag gtg cac tcg gtg gcc tgg agt tgc      530
Glu Phe Leu Ala His Ser Ala Lys Val His Ser Val Ala Trp Ser Cys
 77                  82                  87                  92

gac ggg cgt cgc cta gcc tcg ggg tcc ttc gac aag acg gcc agc gtc      578
Asp Gly Arg Arg Leu Ala Ser Gly Ser Phe Asp Lys Thr Ala Ser Val
 93                  98                 103                 108

ttc ttg ctg gag aag gac cgg ttg gtc aaa gaa aac aat tat cgg gga      626
Phe Leu Leu Glu Lys Asp Arg Leu Val Lys Glu Asn Asn Tyr Arg Gly
109                 114                 119                 124

cat ggg gat agt gtg gac cag ctt tgt tgg cat cca agt aat cct gac      674
His Gly Asp Ser Val Asp Gln Leu Cys Trp His Pro Ser Asn Pro Asp
125                 130                 135                 140

cta ttt gtt acg gcg tcc gga gat aaa acc att cgc atc tgg gat gtg      722
Leu Phe Val Thr Ala Ser Gly Asp Lys Thr Ile Arg Ile Trp Asp Val
141                 146                 151                 156

agg act aca aaa tgc att gcc act gtg aac act aaa ggg gag aac att      770
Arg Thr Thr Lys Cys Ile Ala Thr Val Asn Thr Lys Gly Glu Asn Ile
157                 162                 167                 172

aat atc tgc tgg agt cct gat ggg cag acc att gct gta ggc aac aag      818
Asn Ile Cys Trp Ser Pro Asp Gly Gln Thr Ile Ala Val Gly Asn Lys
173                 178                 183                 188

gat gat gtg gtg acc ttt att gat gcc aag aca cac cgt tcc aaa gca      866
Asp Asp Val Val Thr Phe Ile Asp Ala Lys Thr His Arg Ser Lys Ala
189                 194                 199                 204

gaa gag cag ttc aag ttc gag gtc aac gaa atc tcc tgg aac aat gac      914
Glu Glu Gln Phe Lys Phe Glu Val Asn Glu Ile Ser Trp Asn Asn Asp
205                 210                 215                 220

aat aat atg ttc ttc ctg aca aat ggc aat ggt tgt atc aac atc ctc      962
Asn Asn Met Phe Phe Leu Thr Asn Gly Asn Gly Cys Ile Asn Ile Leu
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agc tac cca gaa ctg aag cct gtg cag tcc atc aac gcc cat cct tcc     1010
Ser Tyr Pro Glu Leu Lys Pro Val Gln Ser Ile Asn Ala His Pro Ser
237                 242                 247                 252

aac tgc atc tgt atc aag ttt gac ccc atg ggg aag tac ttt gcc aca     1058
Asn Cys Ile Cys Ile Lys Phe Asp Pro Met Gly Lys Tyr Phe Ala Thr
253                 258                 263                 268

gga agt gca gat gct ttg gtc agc ctc tgg gat gtg gat gag tta gtg     1106
Gly Ser Ala Asp Ala Leu Val Ser Leu Trp Asp Val Asp Glu Leu Val
269                 274                 279                 284

tgt gtt cgg tgc ttt tcc agg ctg gat tgg cct gta aga acc ctc agt     1154
Cys Val Arg Cys Phe Ser Arg Leu Asp Trp Pro Val Arg Thr Leu Ser
285                 290                 295                 300

ttc agc cat gat ggg aaa atg ctg gcg tca gca tcg gaa gat cat ttt     1202
Phe Ser His Asp Gly Lys Met Leu Ala Ser Ala Ser Glu Asp His Phe
301                 306                 311                 316

att gac att gct gaa gtg gag aca ggg gac aaa cta tgg gag gta cag     1250
Ile Asp Ile Ala Glu Val Glu Thr Gly Asp Lys Leu Trp Glu Val Gln
317                 322                 327                 332

tgt gag tct ccg acc ttc aca gtg gcg tgg cac ccc aaa agg cct ctg     1298
Cys Glu Ser Pro Thr Phe Thr Val Ala Trp His Pro Lys Arg Pro Leu
333                 338                 343                 348

ctg gca ttt gcc tgt gat gac aaa gac ggc aaa tat gac agc agc cgg     1346
Leu Ala Phe Ala Cys Asp Asp Lys Asp Gly Lys Tyr Asp Ser Ser Arg
349                 354                 359                 364

gaa gcc gga act gtg aag ctg ttt ggg ctt cct aat gat tct tga gag     1394
Glu Ala Gly Thr Val Lys Leu Phe Gly Leu Pro Asn Asp Ser  *
365                 370                 375

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Case No. 2015-0050

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ccgccgccgc cgttttcgcc tgcagctgct caccggatcc tcagtcttcc aca atg 236
Met
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Asn Pro Val Tyr Ser Pro Val Gln Pro Gly Ala Pro Tyr Gly Asn Pro
2 7 12 17

aag aac atg gcc tac acg ggt tac ccc aca gcc tat cca gca gct gcc 332
Lys Asn Met Ala Tyr Thr Gly Tyr Pro Thr Ala Tyr Pro Ala Ala Ala
18 23 28 33

cct gcc tac aat ccc agc ctg tac ccc acc aat agt ccc agt tat gct 380
Pro Ala Tyr Asn Pro Ser Leu Tyr Pro Thr Asn Ser Pro Ser Tyr Ala
34 39 44 49

cca gag ttt cag ttc ctg cat tca gct tat gca act ctg ctg atg aaa 428
Pro Glu Phe Gln Phe Leu His Ser Ala Tyr Ala Thr Leu Leu Met Lys
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cag gcc tgg cca cag aac tcg tct tcc tgt ggc act gaa ggc acc ttc 476
Gln Ala Trp Pro Gln Asn Ser Ser Ser Cys Gly Thr Glu Gly Thr Phe
66 71 76 81

cac ctc cca gtg gac acc ggg acc gag aac cga act tac caa gca tcc 524
His Leu Pro Val Asp Thr Gly Thr Glu Asn Arg Thr Tyr Gln Ala Ser
82 87 92 97

tct gcg gct ttc aga tat act gcg ggg aca cca tac aag gtc cca ccg 572
Ser Ala Ala Phe Arg Tyr Thr Ala Gly Thr Pro Tyr Lys Val Pro Pro
98 103 108 113

acc cag agt aac act gct cca ccc ccc tac tcc cca tca ccc aac ccc 620
Thr Gln Ser Asn Thr Ala Pro Pro Pro Tyr Ser Pro Ser Pro Asn Pro
114 119 124 129

tat cag acg gcc atg tat cca atc aga agt gcc tac ccc cag cag aat 668
Tyr Gln Thr Ala Met Tyr Pro Ile Arg Ser Ala Tyr Pro Gln Gln Asn
130 135 140 145

ctg tat gcc cag gga gcc tac tac aca cag ccg gtg tat gct gcc cag 716

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146                 151                 156                 161

cct cat gtc atc cac cac acc acg gtc gtc cag ccc aac agc att ccc      764
Pro His Val Ile His His Thr Thr Val Val Gln Pro Asn Ser Ile Pro
162                 167                 172                 177

tct gct atc tac cca gca cct gtt gcc gcc ccg agg acc aac ggt gtg      812
Ser Ala Ile Tyr Pro Ala Pro Val Ala Ala Pro Arg Thr Asn Gly Val
178                 183                 188                 193

gcc atg ggc atg gtg gca ggc acc acc atg gca atg tca gca ggt acc      860
Ala Met Gly Met Val Ala Gly Thr Thr Met Ala Met Ser Ala Gly Thr
194                 199                 204                 209

ctg ctg act aca ccc cag cac acg gcg att ggg gca cac cct gtc tcc      908
Leu Leu Thr Thr Pro Gln His Thr Ala Ile Gly Ala His Pro Val Ser
210                 215                 220                 225

atg cca aca tat agg gcc caa gga acc cct gcg tac agc tac gtg ccc      956
Met Pro Thr Tyr Arg Ala Gln Gly Thr Pro Ala Tyr Ser Tyr Val Pro
226                 231                 236                 241

cca cac tgg taa agc ctgcagccca tccaaatctg gagtcacaca ttgtatgcaa     1011
Pro His Trp  *
242

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gtcatagcat accatttatc gggctcggcg caggcccgcg gggagcgcag cccggcggag    180

agactg   atg gag agg cag aaa cgg aag gcg gac atc gag aaa ggg ctg      228
         Met Glu Arg Gln Lys Arg Lys Ala Asp Ile Glu Lys Gly Leu
           1               5                  10

cag ttc att cag tcg aca cta ccc cta aag caa gaa gaa tat gag gcc      276
Gln Phe Ile Gln Ser Thr Leu Pro Leu Lys Gln Glu Glu Tyr Glu Ala
 15                  20                  25                  30

ttt ctg ctc aag ctg gtg cag aat ctg ttt gct gag ggc aat gat ctg      324
Phe Leu Leu Lys Leu Val Gln Asn Leu Phe Ala Glu Gly Asn Asp Leu
 31                  36                  41                  46

ttc cgg gag aag gac tat aag cag gct ctg gtg cag tac atg gaa ggg      372
Phe Arg Glu Lys Asp Tyr Lys Gln Ala Leu Val Gln Tyr Met Glu Gly
 47                  52                  57                  62

ctg aac gtg gcc gac tac gct gcc tct gac cag gtg gcc ctg ccc cgg      420
Leu Asn Val Ala Asp Tyr Ala Ala Ser Asp Gln Val Ala Leu Pro Arg
 63                  68                  73                  78

gag ctg ctg tgc aag ctg cat gtc aat agg gcc gcc tgc tac ttc acc      468
Glu Leu Leu Cys Lys Leu His Val Asn Arg Ala Ala Cys Tyr Phe Thr
 79                  84                  89                  94

atg ggc ctg tat gag aag gcg ctg gag gac agc gag aag gcg ctg ggc      516
Met Gly Leu Tyr Glu Lys Ala Leu Glu Asp Ser Glu Lys Ala Leu Gly
 95                 100                 105                 110

ctg gac agt gag agt atc cgg gcg ttg ttc cgc aag gca cgc gct ctc      564
Leu Asp Ser Glu Ser Ile Arg Ala Leu Phe Arg Lys Ala Arg Ala Leu
111                 116                 121                 126

aat gaa ctg gga cgc cac aag gag gcc tac gag tgc agc agc cgg tgt      612
Asn Glu Leu Gly Arg His Lys Glu Ala Tyr Glu Cys Ser Ser Arg Cys
127                 132                 137                 142

tcc ctc gcc ctg ccc cac gat gaa agc gtg act cag ctt ggt cag gag      660
Ser Leu Ala Leu Pro His Asp Glu Ser Val Thr Gln Leu Gly Gln Glu
143                 148                 153                 158

ctg gcc cag aaa ctg ggg ctg cga gtt cgc aag gcg tat aag agg ccc      708
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Leu Ala Gln Lys Leu Gly Leu Arg Val Arg Lys Ala Tyr Lys Arg Pro
159                 164                 169                 174

cag gaa ttg gaa acc ttt tct ctg ctc agt aac ggc act gcg gct ggc      756
Gln Glu Leu Glu Thr Phe Ser Leu Leu Ser Asn Gly Thr Ala Ala Gly
175                 180                 185                 190

gtg gca gat cag gga act tct aat gga ttg ggg tcc ata gat gac atc      804
Val Ala Asp Gln Gly Thr Ser Asn Gly Leu Gly Ser Ile Asp Asp Ile
191                 196                 201                 206

gaa aca gac tgc tac gtg gac cct cga ggc tcc cca gcc ctt ctc ccc      852
Glu Thr Asp Cys Tyr Val Asp Pro Arg Gly Ser Pro Ala Leu Leu Pro
207                 212                 217                 222

tcc acg ccc acg atg ccc ctg ttc cct cac gtt ctg gac ctg ctg gcc      900
Ser Thr Pro Thr Met Pro Leu Phe Pro His Val Leu Asp Leu Leu Ala
223                 228                 233                 238

ccc ctg gac agc agc agg acc ctc ccc agc acc gac agc ctg gat gac      948
Pro Leu Asp Ser Ser Arg Thr Leu Pro Ser Thr Asp Ser Leu Asp Asp
239                 244                 249                 254

ttc tca gac ggg gat gtc ttt ggc cca gag ctg gac acc ctc ctg gac      996
Phe Ser Asp Gly Asp Val Phe Gly Pro Glu Leu Asp Thr Leu Leu Asp
255                 260                 265                 270

tcg ctg tct ctg gtc cag ggt ggc ctg tct ggc agc ggc gtg cct agt     1044
Ser Leu Ser Leu Val Gln Gly Gly Leu Ser Gly Ser Gly Val Pro Ser
271                 276                 281                 286

gag ttg ccc cag ctg ata ccc gtg ttc ccc ggc ggg acc cca ctg cta     1092
Glu Leu Pro Gln Leu Ile Pro Val Phe Pro Gly Gly Thr Pro Leu Leu
287                 292                 297                 302

cca cct gtg gtg ggt ggc tcc atc cct gtc tcc agc cca ctg ccc ccc     1140
Pro Pro Val Val Gly Gly Ser Ile Pro Val Ser Ser Pro Leu Pro Pro
303                 308                 313                 318

gcc tcc ttc ggc ttg gtc atg gac ccc tcc aag aag ctg gcc gcc tct     1188
Ala Ser Phe Gly Leu Val Met Asp Pro Ser Lys Lys Leu Ala Ala Ser
319                 324                 329                 334

gtg ctg gat gcc ctc gat ccc ccg ggc ccc acg ctg gac ccc ctg gac     1236
Val Leu Asp Ala Leu Asp Pro Pro Gly Pro Thr Leu Asp Pro Leu Asp
335                 340                 345                 350

ctg ctg ccg tac tcg gag acc cgg ctg gat gca ctc gac agc ttt ggg     1284
Leu Leu Pro Tyr Ser Glu Thr Arg Leu Asp Ala Leu Asp Ser Phe Gly
351                 356                 361                 366

tcg aca cga ggc tcc ctg gac aaa cct gac tcc ttc atg gag gag acc     1332
Ser Thr Arg Gly Ser Leu Asp Lys Pro Asp Ser Phe Met Glu Glu Thr
367                 372                 377                 382

aac tca cag gac cac cgt ccc cct agc ggt gct cag aaa cca gcc ccc     1380
Asn Ser Gln Asp His Arg Pro Pro Ser Gly Ala Gln Lys Pro Ala Pro
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383                 388                 393                 398

tcg cca gag ccc tgc atg ccc aac act gcc ttg ctc atc aag aac ccc     1428
Ser Pro Glu Pro Cys Met Pro Asn Thr Ala Leu Leu Ile Lys Asn Pro
399                 404                 409                 414

ttg gct gcc acc cac gag ttc aag cag gcc tgc cag ctc tgc tac ccc     1476
Leu Ala Ala Thr His Glu Phe Lys Gln Ala Cys Gln Leu Cys Tyr Pro
415                 420                 425                 430

aag aca ggc ccc cgg gct ggc gac tac acc tac cgt gag ggc ctt gag     1524
Lys Thr Gly Pro Arg Ala Gly Asp Tyr Thr Tyr Arg Glu Gly Leu Glu
431                 436                 441                 446

cac aag tgc aag cgg gac atc ctg ctc ggc cgg ctc cgg agc tcg gag     1572
His Lys Cys Lys Arg Asp Ile Leu Leu Gly Arg Leu Arg Ser Ser Glu
447                 452                 457                 462

gac cag acc tgg aag cgg atc cgg ccc cgg ccc act aag acc agc ttc     1620
Asp Gln Thr Trp Lys Arg Ile Arg Pro Arg Pro Thr Lys Thr Ser Phe
463                 468                 473                 478

gtg ggc tcc tac tac ctg tgc aaa gac atg att aac aag cag gac tgt     1668
Val Gly Ser Tyr Tyr Leu Cys Lys Asp Met Ile Asn Lys Gln Asp Cys
479                 484                 489                 494

aag tac ggg gat aac tgc acc ttc gcc tac cat cag gag gag atc gac     1716
Lys Tyr Gly Asp Asn Cys Thr Phe Ala Tyr His Gln Glu Glu Ile Asp
495                 500                 505                 510

gtg tgg acc gag gag cgg aag ggc acc ctc aac cgc gac ctg ctc ttc     1764
Val Trp Thr Glu Glu Arg Lys Gly Thr Leu Asn Arg Asp Leu Leu Phe
511                 516                 521                 526

gac ccg ctg ggg ggt gtt aag cgc ggc agc ctc acc atc gcc aag ctc     1812
Asp Pro Leu Gly Gly Val Lys Arg Gly Ser Leu Thr Ile Ala Lys Leu
527                 532                 537                 542

ctg aag gag cac cag ggc atc ttc acc ttc ctc tgc gag atc tgc ttt     1860
Leu Lys Glu His Gln Gly Ile Phe Thr Phe Leu Cys Glu Ile Cys Phe
543                 548                 553                 558

gac agt aaa ccc cgg atc atc agc aaa ggc acc aag gac tct ccg tct     1908
Asp Ser Lys Pro Arg Ile Ile Ser Lys Gly Thr Lys Asp Ser Pro Ser
559                 564                 569                 574

gtc tgc tcc aac ctg gct gcc aag cac agc ttc tac aac aac aag tgc     1956
Val Cys Ser Asn Leu Ala Ala Lys His Ser Phe Tyr Asn Asn Lys Cys
575                 580                 585                 590

ctg gtg cac atc gtc cgc tcc acc tcc ctc aag tac tcc aag atc cgc     2004
Leu Val His Ile Val Arg Ser Thr Ser Leu Lys Tyr Ser Lys Ile Arg
591                 596                 601                 606

cag ttc cag gag cac ttc cag ttc gac gtg tgc cgc cat gag gtg cgc     2052
Gln Phe Gln Glu His Phe Gln Phe Asp Val Cys Arg His Glu Val Arg
607                 612                 617                 622
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tac ggc tgc ctg cgg gag gac agc tgc cac ttc gcc cac agc ttc atc     2100
Tyr Gly Cys Leu Arg Glu Asp Ser Cys His Phe Ala His Ser Phe Ile
623                 628                 633                 638

gag ctc aag gtc tgg ctg ctg cag cag tac tca ggc atg acc cac gaa     2148
Glu Leu Lys Val Trp Leu Leu Gln Gln Tyr Ser Gly Met Thr His Glu
639                 644                 649                 654

gac atc gtt cag gag tct aag aag tac tgg cag cag atg gag gcg cat     2196
Asp Ile Val Gln Glu Ser Lys Lys Tyr Trp Gln Gln Met Glu Ala His
655                 660                 665                 670

gcg ggg aag gcc agc agc agc atg ggt gct ccg agg aca cat ggg ccc     2244
Ala Gly Lys Ala Ser Ser Ser Met Gly Ala Pro Arg Thr His Gly Pro
671                 676                 681                 686

agc acc ttt gac ctg cag atg aag ttt gta tgt ggc cag tgc tgg aga     2292
Ser Thr Phe Asp Leu Gln Met Lys Phe Val Cys Gly Gln Cys Trp Arg
687                 692                 697                 702

aac ggg cag gtg gtg gag cct gac aag gac ctc aag tac tgt agt gcc     2340
Asn Gly Gln Val Val Glu Pro Asp Lys Asp Leu Lys Tyr Cys Ser Ala
703                 708                 713                 718

aag gcc cgg cac tgc tgg acc aag gag cgg cgg gtc ctt ctg gtg atg     2388
Lys Ala Arg His Cys Trp Thr Lys Glu Arg Arg Val Leu Leu Val Met
719                 724                 729                 734

tcc aag gcc aag agg aaa tgg gtg tca gtg agg cca ctg cca tcc att     2436
Ser Lys Ala Lys Arg Lys Trp Val Ser Val Arg Pro Leu Pro Ser Ile
735                 740                 745                 750

cgt aac ttc cca cag caa tac gat ctc tgc atc cat gca cag aac ggc     2484
Arg Asn Phe Pro Gln Gln Tyr Asp Leu Cys Ile His Ala Gln Asn Gly
751                 756                 761                 766

cgc aag tgc caa tat gtg ggg aac tgc tcc ttc gca cac agc ccg gag     2532
Arg Lys Cys Gln Tyr Val Gly Asn Cys Ser Phe Ala His Ser Pro Glu
767                 772                 777                 782

gag agg gac atg tgg acc ttc atg aag gag aac aag atc ctg gac atg     2580
Glu Arg Asp Met Trp Thr Phe Met Lys Glu Asn Lys Ile Leu Asp Met
783                 788                 793                 798

cag cag acc tat gac atg tgg ctg aaa aaa cac aac cca gga aag cct     2628
Gln Gln Thr Tyr Asp Met Trp Leu Lys Lys His Asn Pro Gly Lys Pro
799                 804                 809                 814

gga gaa ggg acc ccc atc agt tct cgg gaa ggg gag aag cag atc cag     2676
Gly Glu Gly Thr Pro Ile Ser Ser Arg Glu Gly Glu Lys Gln Ile Gln
815                 820                 825                 830

atg ccc acg gac tac gcg gac atc atg atg ggc tac cac tgc tgg ctc     2724
Met Pro Thr Asp Tyr Ala Asp Ile Met Met Gly Tyr His Cys Trp Leu
831                 836                 841                 846
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tgc ggc aag aac agc aac agc aag aag cag tgg cag cag cac atc cag     2772
Cys Gly Lys Asn Ser Asn Ser Lys Lys Gln Trp Gln Gln His Ile Gln
847                 852                 857                 862

tcc gag aag cac aag gag aag gtc ttc acg tcc gac agt gac gcc agc     2820
Ser Glu Lys His Lys Glu Lys Val Phe Thr Ser Asp Ser Asp Ala Ser
863                 868                 873                 878

ggc tgg gcc ttc cgc ttc ccc atg ggc gag ttc cgg ctc tgc gac agg     2868
Gly Trp Ala Phe Arg Phe Pro Met Gly Glu Phe Arg Leu Cys Asp Arg
879                 884                 889                 894

ctc cag aag ggc aaa gcc tgc cca gat ggg gac aag tgc cgc tgc gcc     2916
Leu Gln Lys Gly Lys Ala Cys Pro Asp Gly Asp Lys Cys Arg Cys Ala
895                 900                 905                 910

cat gga cag gag gag ctc aac gag tgg ctg gac cgg cgc gag gtg ctg     2964
His Gly Gln Glu Glu Leu Asn Glu Trp Leu Asp Arg Arg Glu Val Leu
911                 916                 921                 926

aag cag aag ttg gcc aag gct cgc aag gac atg ctg ctg tgc cca cgg     3012
Lys Gln Lys Leu Ala Lys Ala Arg Lys Asp Met Leu Leu Cys Pro Arg
927                 932                 937                 942

gac gac gac ttt ggc aaa tac aac ttc ctg ctg caa gag gac ggg gac     3060
Asp Asp Asp Phe Gly Lys Tyr Asn Phe Leu Leu Gln Glu Asp Gly Asp
943                 948                 953                 958

ctt gcc ggt gcc acc cca gaa gcc cct gct gct gct gcc acc gcc acc     3108
Leu Ala Gly Ala Thr Pro Glu Ala Pro Ala Ala Ala Ala Thr Ala Thr
959                 964                 969                 974

act ggg gag tag ggc caggtgttgg ccgtgggtga agtcctgggg tcaggggtg     3163
Thr Gly Glu  *
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Gln Ile Ser Ala Leu Thr Arg Phe Lys Leu Ile Ser Gln Ala Tyr Glu
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gtg ctt tca gat cca aag aaa agg gat gtt tat gac caa ggc gga gag      328
Val Leu Ser Asp Pro Lys Lys Arg Asp Val Tyr Asp Gln Gly Gly Glu
 27                  32                  37                  42

cag gca att aaa gaa gga ggc tca ggc agc ccc agc ttc tct tca ccc      376
Gln Ala Ile Lys Glu Gly Gly Ser Gly Ser Pro Ser Phe Ser Ser Pro
 43                  48                  53                  58

atg gac atc ttt gac atg ttc ttt ggt ggt ggt gga cgg atg gct aga      424
Met Asp Ile Phe Asp Met Phe Phe Gly Gly Gly Gly Arg Met Ala Arg
 59                  64                  69                  74

gag aga aga ggc aag aat gtt gta cac cag tta tct gta act ctt gaa      472
Glu Arg Arg Gly Lys Asn Val Val His Gln Leu Ser Val Thr Leu Glu
 75                  80                  85                  90

gat cta tat aac gga gtc acg aag aaa ttg gcc ctc cag aaa aat gta      520
Asp Leu Tyr Asn Gly Val Thr Lys Lys Leu Ala Leu Gln Lys Asn Val
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att tgt gag aaa tgt gaa ggt gtt ggt ggg aag aag gga tcg gtg gag      568
Ile Cys Glu Lys Cys Glu Gly Val Gly Gly Lys Lys Gly Ser Val Glu
107                 112                 117                 122

aag tgc ccg ctg tgc aag ggg cgg ggg atg cag atc cac atc cag cag      616
Lys Cys Pro Leu Cys Lys Gly Arg Gly Met Gln Ile His Ile Gln Gln
123                 128                 133                 138

atc ggg ccg ggc atg gta cag cag atc cag acc gtg tgc atc gag tgc      664
Ile Gly Pro Gly Met Val Gln Gln Ile Gln Thr Val Cys Ile Glu Cys
139                 144                 149                 154

aag ggc cag ggt gag cgc atc aac ccc aag gac cgc tgc gag agc tgc      712
Lys Gly Gln Gly Glu Arg Ile Asn Pro Lys Asp Arg Cys Glu Ser Cys
155                 160                 165                 170

agc ggg gcc aag gtg atc cgt gag aag aag att atc gag gta cat gtt      760
Ser Gly Ala Lys Val Ile Arg Glu Lys Lys Ile Ile Glu Val His Val
171                 176                 181                 186

gaa aaa ggt atg aaa gat ggg caa aag ata cta ttt cat gga gaa gga      808
Glu Lys Gly Met Lys Asp Gly Gln Lys Ile Leu Phe His Gly Glu Gly
187                 192                 197                 202

gat cag gag cct gag ctg gag cct ggt gat gtc ata att gtg ctt gat      856
Asp Gln Glu Pro Glu Leu Glu Pro Gly Asp Val Ile Ile Val Leu Asp
203                 208                 213                 218

cag aag gat cat agt gtc ttt cag aga cga ggc cat gac ttg atc atg      904
Gln Lys Asp His Ser Val Phe Gln Arg Arg Gly His Asp Leu Ile Met
219                 224                 229                 234

aaa atg aaa att cag ctt tct gaa gct ctt tgt ggc ttc aag aag acg      952
Lys Met Lys Ile Gln Leu Ser Glu Ala Leu Cys Gly Phe Lys Lys Thr
235                 240                 245                 250

ata aaa aca ttg gac aat cga att ctt gtt att aca tcc aaa gca ggt     1000
Ile Lys Thr Leu Asp Asn Arg Ile Leu Val Ile Thr Ser Lys Ala Gly
251                 256                 261                 266

gag gtg ata aag cac ggg gac ctg aga tgc gtg cgc gat gaa gga atg     1048
Glu Val Ile Lys His Gly Asp Leu Arg Cys Val Arg Asp Glu Gly Met
267                 272                 277                 282

ccc atc tac aaa gca ccc ctg gaa aaa ggg att ctg atc ata cag ttt     1096
Pro Ile Tyr Lys Ala Pro Leu Glu Lys Gly Ile Leu Ile Ile Gln Phe
283                 288                 293                 298

tta gta atc ttt cct gaa aaa cac tgg ctt tct ctg gaa aag ctt cct     1144
Leu Val Ile Phe Pro Glu Lys His Trp Leu Ser Leu Glu Lys Leu Pro
299                 304                 309                 314

cag ctg gaa gct tta ctc cct cct cga cag aaa gtg agg att aca gat     1192
Gln Leu Glu Ala Leu Leu Pro Pro Arg Gln Lys Val Arg Ile Thr Asp
315                 320                 325                 330
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gac atg gat cag gtg gag ctg aag gag ttt tgt ccc aat gag cag aac     1240
Asp Met Asp Gln Val Glu Leu Lys Glu Phe Cys Pro Asn Glu Gln Asn
331                 336                 341                 346

tgg cgt cag cac agg gag gcc tac gag gag gac gaa gac ggg ccc cag     1288
Trp Arg Gln His Arg Glu Ala Tyr Glu Glu Asp Glu Asp Gly Pro Gln
347                 352                 357                 362

gct gga gtg cag tgc cag acg gca tga cgtgg tgcggggcag cgtggcccca     1340
Ala Gly Val Gln Cys Gln Thr Ala  *
363                 368

ccggactagc acatgatgaa tgtaaagttg gcacaatgaa aatgacatcg ctttaatggc   1400

cttgtgtttg ggatgtcctg tgtatgtgtt cagcattctt aattgctgag tgtcttttg    1460

gcttttcttt tggttgtaac ttaagttata gcttaattta tatttaaatg ttttaagtat   1520

aaatcaaaaa aaaaa                                                    1535
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US-15-050-520

<210> 229
<211> 1462
<212> DNA
<213> Homo sapiens

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<222> (49)..(1242)

<400> 229

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                                                    Met Val Lys
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gag acc cgg tac tat gac atc ctg ggc gtg aag ccc agc gcg tcc ccg      105
Glu Thr Arg Tyr Tyr Asp Ile Leu Gly Val Lys Pro Ser Ala Ser Pro
  4                   9                  14                  19

gag gag atc aag aag gcc tat cgg aag ctg gcg ctc aag tac cac ccg      153
Glu Glu Ile Lys Lys Ala Tyr Arg Lys Leu Ala Leu Lys Tyr His Pro
 20                  25                  30                  35

gac aag aac ccg gat gag ggc gag aag ttt aaa ctc ata tcc cag gca      201
Asp Lys Asn Pro Asp Glu Gly Glu Lys Phe Lys Leu Ile Ser Gln Ala
 36                  41                  46                  51

tat gaa gtg ctt tca gat cca aag aaa agg gat gtt tat gac caa ggc      249
Tyr Glu Val Leu Ser Asp Pro Lys Lys Arg Asp Val Tyr Asp Gln Gly
 52                  57                  62                  67

gga gag cag gca att aaa gaa gga ggc tca ggc agc ccc agc ttc tct      297
Gly Glu Gln Ala Ile Lys Glu Gly Gly Ser Gly Ser Pro Ser Phe Ser
 68                  73                  78                  83
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tca ccc atg gac atc ttt gac atg ttc ttt ggt ggt ggt gga cgg atg      345
Ser Pro Met Asp Ile Phe Asp Met Phe Phe Gly Gly Gly Gly Arg Met
 84                  89                  94                  99

gct aga gag aga aga ggc aag aat gtt gta cac cag tta tct gta act      393
Ala Arg Glu Arg Arg Gly Lys Asn Val Val His Gln Leu Ser Val Thr
100                 105                 110                 115

ctt gaa gat cta tat aac gga gtc acg aag aaa ttg gcc ctc cag aaa      441
Leu Glu Asp Leu Tyr Asn Gly Val Thr Lys Lys Leu Ala Leu Gln Lys
116                 121                 126                 131

aat gta att tgt gag aaa tgt gaa ggt gtt ggt ggg aag aag gga tcg      489
Asn Val Ile Cys Glu Lys Cys Glu Gly Val Gly Gly Lys Lys Gly Ser
132                 137                 142                 147

gtg gag aag tgc ccg ctg tgc aag ggg cgg ggg atg cag atc cac atc      537
Val Glu Lys Cys Pro Leu Cys Lys Gly Arg Gly Met Gln Ile His Ile
148                 153                 158                 163

cag cag atc ggg ccg ggc atg gta cag cag atc cag acc gtg tgc atc      585
Gln Gln Ile Gly Pro Gly Met Val Gln Gln Ile Gln Thr Val Cys Ile
164                 169                 174                 179

gag tgc aag ggc cag ggt gag cgc atc aac ccc aag gac cgc tgc gag      633
Glu Cys Lys Gly Gln Gly Glu Arg Ile Asn Pro Lys Asp Arg Cys Glu
180                 185                 190                 195

agc tgc agc ggg gcc aag gtg atc cgt gag aag aag att atc gag gta      681
Ser Cys Ser Gly Ala Lys Val Ile Arg Glu Lys Lys Ile Ile Glu Val
196                 201                 206                 211

cat gtt gaa aaa ggt atg aaa gat ggg caa aag ata cta ttt cat gga      729
His Val Glu Lys Gly Met Lys Asp Gly Gln Lys Ile Leu Phe His Gly
212                 217                 222                 227

gaa gga gat cag gag cct gag ctg gag cct ggt gat gtc ata att gtg      777
Glu Gly Asp Gln Glu Pro Glu Leu Glu Pro Gly Asp Val Ile Ile Val
228                 233                 238                 243

ctt gat cag aag gat cat agt gtc ttt cag aga cga ggc cat gac ttg      825
Leu Asp Gln Lys Asp His Ser Val Phe Gln Arg Arg Gly His Asp Leu
244                 249                 254                 259

atc atg aaa atg aaa att cag ctt tct gaa gct ctt tgt ggc ttc aag      873
Ile Met Lys Met Lys Ile Gln Leu Ser Glu Ala Leu Cys Gly Phe Lys
260                 265                 270                 275

aag acg ata aaa aca ttg gac aat cga att ctt gtt att aca tcc aaa      921
Lys Thr Ile Lys Thr Leu Asp Asn Arg Ile Leu Val Ile Thr Ser Lys
276                 281                 286                 291

gca ggt gag gtg ata aag cac ggg gac ctg aga tgc gtg cgc gat gaa      969
Ala Gly Glu Val Ile Lys His Gly Asp Leu Arg Cys Val Arg Asp Glu
292                 297                 302                 307
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gga atg ccc atc tac aaa gca ccc ctg gaa aaa ggg att ctg atc ata     1017
Gly Met Pro Ile Tyr Lys Ala Pro Leu Glu Lys Gly Ile Leu Ile Ile
308                 313                 318                 323

cag ttt tta gta atc ttt cct gaa aaa cac tgg ctt tct ctg gaa aag     1065
Gln Phe Leu Val Ile Phe Pro Glu Lys His Trp Leu Ser Leu Glu Lys
324                 329                 334                 339

ctt cct cag ctg gaa gct tta ctc cct cct cga cag aaa gtg agg att     1113
Leu Pro Gln Leu Glu Ala Leu Leu Pro Pro Arg Gln Lys Val Arg Ile
340                 345                 350                 355

aca gat gac atg gat cag gtg gag ctg aag gag ttt tgt ccc aat gag     1161
Thr Asp Asp Met Asp Gln Val Glu Leu Lys Glu Phe Cys Pro Asn Glu
356                 361                 366                 371

cag aac tgg cgt cag cac agg gag gcc tac gag gag gac gaa gac ggg     1209
Gln Asn Trp Arg Gln His Arg Glu Ala Tyr Glu Glu Asp Glu Asp Gly
372                 377                 382                 387

ccc cag gct gga gtg cag tgc cag acg gca tga cgtggtgc ggggcagcgt     1260
Pro Gln Ala Gly Val Gln Cys Gln Thr Ala  *
388                 393                 398

ggccccaccg gactagcaca tgatgaatgt aaagttggca caatgaaaat gacatcgctt   1320

taatggcctt gtgtttggga tgtcctgtgt atgtgttcag cattcttaat tgctgagtgt   1380

ctttttggct tttcttttgg ttgtaactta agttatagct taatttatat ttaaatgttt   1440

taagtataaa tcaaaaaaaa aa                                           1462
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09/15/2005 15:20:50 Page 5 of 50 Application No.: 10/549,000

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<222> (79)..(1815)

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                      Met Gly Gln Lys Gly His Lys Asp Ser Leu Tyr
                        1               5

cct tgt gga ggg act cct gag agc agc ctc cat gag gcc ctg gac cag      159
Pro Cys Gly Gly Thr Pro Glu Ser Ser Leu His Glu Ala Leu Asp Gln
 12                  17                  22                  27

tgc atg acc gcc ctg gac ctc ttc ctc acc aac cag ttc tca gaa gca      207
Cys Met Thr Ala Leu Asp Leu Phe Leu Thr Asn Gln Phe Ser Glu Ala
```

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 28                  33                  38                  43

ctc agc tac ctc aag ccc aga acc aag gaa agc atg tac cac tca ctg      255
Leu Ser Tyr Leu Lys Pro Arg Thr Lys Glu Ser Met Tyr His Ser Leu
 44                  49                  54                  59

aca tat gcc acc atc ctg gag atg cag gcc atg atg acc ttt gac cct      303
Thr Tyr Ala Thr Ile Leu Glu Met Gln Ala Met Met Thr Phe Asp Pro
 60                  65                  70                  75

cag gac atc ctg ctt gcc ggc aac atg atg aag gag gca cag atg ctg      351
Gln Asp Ile Leu Leu Ala Gly Asn Met Met Lys Glu Ala Gln Met Leu
 76                  81                  86                  91

tgt cag agg cac cgg agg aag tct tct gta aca gat tcc ttc agc agc      399
Cys Gln Arg His Arg Arg Lys Ser Ser Val Thr Asp Ser Phe Ser Ser
 92                  97                 102                 107

ctg gtg aac cgc ccc acg ctg ggc caa ttc act gaa gag gaa atc cac      447
Leu Val Asn Arg Pro Thr Leu Gly Gln Phe Thr Glu Glu Glu Ile His
108                 113                 118                 123

gct gag gtc tgc tat gca gag tgc ctg ctg cag cga gca gcc ctg acc      495
Ala Glu Val Cys Tyr Ala Glu Cys Leu Leu Gln Arg Ala Ala Leu Thr
124                 129                 134                 139

ttc ctg cag gac gag aac atg gtg agc ttc atc aaa ggc ggc atc aaa      543
Phe Leu Gln Asp Glu Asn Met Val Ser Phe Ile Lys Gly Gly Ile Lys
140                 145                 150                 155

gtt cga aac agc tac cag acc tac aag gag ctg gac agc ctt gtt cag      591
Val Arg Asn Ser Tyr Gln Thr Tyr Lys Glu Leu Asp Ser Leu Val Gln
156                 161                 166                 171

tcc tca caa tac tgc aag ggt gag aac cac ccg cac ttt gaa gga gga      639
Ser Ser Gln Tyr Cys Lys Gly Glu Asn His Pro His Phe Glu Gly Gly
172                 177                 182                 187

gtg aag ctt ggt gta ggg gcc ttc aac ctg aca ctg tcc atg ctt cct      687
Val Lys Leu Gly Val Gly Ala Phe Asn Leu Thr Leu Ser Met Leu Pro
188                 193                 198                 203

act agg atc ctg agg ctg ttg gag ttt gtg ggg ttt tca gga aac aag      735
Thr Arg Ile Leu Arg Leu Leu Glu Phe Val Gly Phe Ser Gly Asn Lys
204                 209                 214                 219

gac tat ggg ctg ctg cag ctg gag gag gga gcg tca ggg cac agc ttc      783
Asp Tyr Gly Leu Leu Gln Leu Glu Glu Gly Ala Ser Gly His Ser Phe
220                 225                 230                 235

cgc tct gtg ctc tgt gtc atg ctc ctg ctg tgc tac cac acc ttc ctc      831
Arg Ser Val Leu Cys Val Met Leu Leu Leu Cys Tyr His Thr Phe Leu
236                 241                 246                 251

acc ttc gtg ctc ggt act ggg aac gtc aac atc gag gag gcc gag aag      879
Thr Phe Val Leu Gly Thr Gly Asn Val Asn Ile Glu Glu Ala Glu Lys
252                 257                 262                 267
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ctc ttg aag ccc tac ctg aac cgg tac cct aag ggt gcc atc ttc ctg      927
Leu Leu Lys Pro Tyr Leu Asn Arg Tyr Pro Lys Gly Ala Ile Phe Leu
268                 273                 278                 283

ttc ctt gca ggg agg att gaa gtc att aaa ggc aac att gat gca gcc      975
Phe Leu Ala Gly Arg Ile Glu Val Ile Lys Gly Asn Ile Asp Ala Ala
284                 289                 294                 299

atc cgg cgt ttc gag gag tgc tgt gag gcc cag cag cac tgg aag cag     1023
Ile Arg Arg Phe Glu Glu Cys Cys Glu Ala Gln Gln His Trp Lys Gln
300                 305                 310                 315

ttc cac cac atg tgc tac tgg gag ctg atg tgg tgc ttc acc tac aag     1071
Phe His His Met Cys Tyr Trp Glu Leu Met Trp Cys Phe Thr Tyr Lys
316                 321                 326                 331

ggc cag tgg aag atg tcc tac ttc tac gcc gac ctg ctc agc aag gag     1119
Gly Gln Trp Lys Met Ser Tyr Phe Tyr Ala Asp Leu Leu Ser Lys Glu
332                 337                 342                 347

aac tgc tgg tcc aag gcc acc tac att tac atg aag gcc gcc tac ctc     1167
Asn Cys Trp Ser Lys Ala Thr Tyr Ile Tyr Met Lys Ala Ala Tyr Leu
348                 353                 358                 363

agc atg ttt ggg aag gag gac cac aag ccg ttc ggg gac gac gaa gtg     1215
Ser Met Phe Gly Lys Glu Asp His Lys Pro Phe Gly Asp Asp Glu Val
364                 369                 374                 379

gaa tta ttt cga gct gtg cca ggc ctg aag ctc aag att gct ggg aag     1263
Glu Leu Phe Arg Ala Val Pro Gly Leu Lys Leu Lys Ile Ala Gly Lys
380                 385                 390                 395

tct cta ccc aca gag aag ttt gcc atc cgg aag tcc cgg cgc tac ttc     1311
Ser Leu Pro Thr Glu Lys Phe Ala Ile Arg Lys Ser Arg Arg Tyr Phe
396                 401                 406                 411

tcc tcc aac cct atc tcg ctg cca gtg cct gct ctg gaa atg atg tac     1359
Ser Ser Asn Pro Ile Ser Leu Pro Val Pro Ala Leu Glu Met Met Tyr
412                 417                 422                 427

atc tgg aac ggc tac gcc gtg att ggg aag cag ccg aaa ctc acg gat     1407
Ile Trp Asn Gly Tyr Ala Val Ile Gly Lys Gln Pro Lys Leu Thr Asp
428                 433                 438                 443

ggg ata ctt gag att atc act aag gct gaa gag atg ctg gag aaa ggc     1455
Gly Ile Leu Glu Ile Ile Thr Lys Ala Glu Glu Met Leu Glu Lys Gly
444                 449                 454                 459

cca gag aac gag tac tca gtg gat gac gag tgc ttg gtg aaa ttg ttg     1503
Pro Glu Asn Glu Tyr Ser Val Asp Asp Glu Cys Leu Val Lys Leu Leu
460                 465                 470                 475

aaa ggc ctg tgt ctg aaa tac ctg ggc cgt gtc cag gag gcc gag gag     1551
Lys Gly Leu Cys Leu Lys Tyr Leu Gly Arg Val Gln Glu Ala Glu Glu
476                 481                 486                 491
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aat ttt agg agc atc tct gcc aat gaa aag aag att aaa tat gac cac     1599
Asn Phe Arg Ser Ile Ser Ala Asn Glu Lys Lys Ile Lys Tyr Asp His
492                 497                 502                 507

tac ttg atc cca aac gcc ctg ctg gag ctg gcc ctg ctg ctt atg gag     1647
Tyr Leu Ile Pro Asn Ala Leu Leu Glu Leu Ala Leu Leu Leu Met Glu
508                 513                 518                 523

caa gac aga aac gaa gag gcc atc aaa ctt ttg gaa tct gcc aag caa     1695
Gln Asp Arg Asn Glu Glu Ala Ile Lys Leu Leu Glu Ser Ala Lys Gln
524                 529                 534                 539

aac tac aag aat tac tcc atg gag tca agg aca cac ttt cga atc cag     1743
Asn Tyr Lys Asn Tyr Ser Met Glu Ser Arg Thr His Phe Arg Ile Gln
540                 545                 550                 555

gca gcc aca ctc caa gcc aag tct tcc cta gag aac agc agc aga tcc     1791
Ala Ala Thr Leu Gln Ala Lys Ser Ser Leu Glu Asn Ser Ser Arg Ser
556                 561                 566                 571

atg gtc tca tca gtg tcc ttg tag ctttgtgcag cagttccggg ctggaagaca    1845
Met Val Ser Ser Val Ser Leu  *
572                 577

gagacagctg gacagagctc ctgaaaacat ttcaaaatac cccctccccc tgccctgccc   1905

tgcctttggg gtccaccggc actccagttg gatggcacaa catagtgtat ccgtgcagaa   1965

gccgagctgg cattttcacc agtgtagcca agggcctttg ccaagggcag agcaggtgga   2025

gccctctgcc tgccctatca cacatacggg tacttgcttt tcactgtgat gtttaagaga   2085

atgtatgaac agtttacatt ttccttagaa atacattgat gggatcacag ttggctttaa   2145

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cttgtgtgac ggaaggtcct tcagaggacc tgaggaatgc ctgggagagg ctaagcctca   2325

ggcttcaatg cttctggggt tgggcatgag gatgtacaca gacacccact accttactac   2385

tcacacttca tttcactcct tttgtaaatt tccaatttaa aaatcaagca cgtcttttta   2445

gtgagataaa atctgagctc ttctgtagaa aaatcaatct ctaccagtag aaaatgccag   2505

ggcttgatgg aagagctgtg tagccctttc tatgccaaag ccaggaaatt tgggggggcag  2565

gaggaggttc tcagaatcca gtctgtatct ttgctgtatg ccaaactgaa accactggga   2625

ataatttatg aaacataaaa atcttctgta cttcactcca aggtacattt gcttactgac   2685

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Met Gly Gln Lys Gly His Lys Asp Ser Leu Tyr
1 5

cct tgt gga ggg act cct gag agc agc ctc cat gag gcc ctg gac cag 159
Pro Cys Gly Gly Thr Pro Glu Ser Ser Leu His Glu Ala Leu Asp Gln
12 17 22 27

tgc atg acc gcc ctg gac ctc ttc ctc acc aac cag ttc tca gaa gca 207
Cys Met Thr Ala Leu Asp Leu Phe Leu Thr Asn Gln Phe Ser Glu Ala
28 33 38 43

ctc agc tac ctc aag ccc aga acc aag gaa agc atg tac cac tca ctg 255
Leu Ser Tyr Leu Lys Pro Arg Thr Lys Glu Ser Met Tyr His Ser Leu
44 49 54 59

aca tat gcc acc atc ctg gag atg cag gcc atg atg acc ttt gac cct 303
Thr Tyr Ala Thr Ile Leu Glu Met Gln Ala Met Met Thr Phe Asp Pro
60 65 70 75

cag gac atc ctg ctt gcc ggc aac atg atg aag gag gca cag atg ctg 351
Gln Asp Ile Leu Leu Ala Gly Asn Met Met Lys Glu Ala Gln Met Leu
76 81 86 91

tgt cag agg cac cgg agg aag tct tct gta aca gat tcc ttc agc agc 399
Cys Gln Arg His Arg Arg Lys Ser Ser Val Thr Asp Ser Phe Ser Ser
92 97 102 107

ctg gtg aac cgc ccc acg ctg ggc caa ttc act gaa gag gaa atc cac 447
Leu Val Asn Arg Pro Thr Leu Gly Gln Phe Thr Glu Glu Glu Ile His
108 113 118 123

gct gag gtc tgc tat gca gag tgc ctg ctg cag cga gca gcc ctg acc 495
Ala Glu Val Cys Tyr Ala Glu Cys Leu Leu Gln Arg Ala Ala Leu Thr
124 129 134 139

ttc ctg cag ggt tcc tca cac gga ggg gca gtc agg ccc aga gcc ttg 543
Phe Leu Gln Gly Ser Ser His Gly Gly Ala Val Arg Pro Arg Ala Leu
140 145 150 155

cat gat ccc tct cac gcc tgc agc tgc cca cct ggg cca ggc cgt cag 591
His Asp Pro Ser His Ala Cys Ser Cys Pro Pro Gly Pro Gly Arg Gln
156 161 166 171

cat ctt ttc ctc ctg cag gac gag aac atg gtg agc ttc atc aaa ggc 639

```
His Leu Phe Leu Leu Gln Asp Glu Asn Met Val Ser Phe Ile Lys Gly
172                 177                 182                 187

ggc atc aaa gtt cga aac agc tac cag acc tac aag gag ctg gac agc      687
Gly Ile Lys Val Arg Asn Ser Tyr Gln Thr Tyr Lys Glu Leu Asp Ser
188                 193                 198                 203

ctt gtt cag tcc tca caa tac tgc aag ggt gag aac cac ccg cac ttt      735
Leu Val Gln Ser Ser Gln Tyr Cys Lys Gly Glu Asn His Pro His Phe
204                 209                 214                 219

gaa gga gga gtg aag ctt ggt gta ggg gcc ttc aac ctg aca ctg tcc      783
Glu Gly Gly Val Lys Leu Gly Val Gly Ala Phe Asn Leu Thr Leu Ser
220                 225                 230                 235

atg ctt cct act agg atc ctg agg ctg ttg gag ttt gtg ggg ttt tca      831
Met Leu Pro Thr Arg Ile Leu Arg Leu Leu Glu Phe Val Gly Phe Ser
236                 241                 246                 251

gga aac aag gac tat ggg ctg ctg cag ctg gag gag gga gcg tca ggg      879
Gly Asn Lys Asp Tyr Gly Leu Leu Gln Leu Glu Glu Gly Ala Ser Gly
252                 257                 262                 267

cac agc ttc cgc tct gtg ctc tgt gtc atg ctc ctg ctg tgc tac cac      927
His Ser Phe Arg Ser Val Leu Cys Val Met Leu Leu Leu Cys Tyr His
268                 273                 278                 283

acc ttc ctc acc ttc gtg ctc ggt act ggg aac gtc aac atc gag gag      975
Thr Phe Leu Thr Phe Val Leu Gly Thr Gly Asn Val Asn Ile Glu Glu
284                 289                 294                 299

gcc gag aag ctc ttg aag ccc tac ctg aac cgg tac cct aag ggt gcc     1023
Ala Glu Lys Leu Leu Lys Pro Tyr Leu Asn Arg Tyr Pro Lys Gly Ala
300                 305                 310                 315

atc ttc ctg ttc ctt gca ggg agg att gaa gtc att aaa ggc aac att     1071
Ile Phe Leu Phe Leu Ala Gly Arg Ile Glu Val Ile Lys Gly Asn Ile
316                 321                 326                 331

gat gca gcc atc cgg cgt ttc gag gag tgc tgt gag gcc cag cag cac     1119
Asp Ala Ala Ile Arg Arg Phe Glu Glu Cys Cys Glu Ala Gln Gln His
332                 337                 342                 347

tgg aag cag ttc cac cac atg tgc tac tgg gag ctg atg tgg tgc ttc     1167
Trp Lys Gln Phe His His Met Cys Tyr Trp Glu Leu Met Trp Cys Phe
348                 353                 358                 363

acc tac aag ggc cag tgg aag atg tcc tac ttc tac gcc gac ctg ctc     1215
Thr Tyr Lys Gly Gln Trp Lys Met Ser Tyr Phe Tyr Ala Asp Leu Leu
364                 369                 374                 379

agc aag gag aac tgc tgg tcc aag gcc acc tac att tac atg aag gcc     1263
Ser Lys Glu Asn Cys Trp Ser Lys Ala Thr Tyr Ile Tyr Met Lys Ala
380                 385                 390                 395

gcc tac ctc agc atg ttt ggg aag gag gac cac aag ccg ttc ggg gac     1311
Ala Tyr Leu Ser Met Phe Gly Lys Glu Asp His Lys Pro Phe Gly Asp
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396                 401                 406                 411

gac gaa gtg gaa tta ttt cga gct gtg cca ggc ctg aag ctc aag att     1359
Asp Glu Val Glu Leu Phe Arg Ala Val Pro Gly Leu Lys Leu Lys Ile
412                 417                 422                 427

gct ggg aag tct cta ccc aca gag aag ttt gcc atc cgg aag tcc cgg     1407
Ala Gly Lys Ser Leu Pro Thr Glu Lys Phe Ala Ile Arg Lys Ser Arg
428                 433                 438                 443

cgc tac ttc tcc tcc aac cct atc tcg ctg cca gtg cct gct ctg gaa     1455
Arg Tyr Phe Ser Ser Asn Pro Ile Ser Leu Pro Val Pro Ala Leu Glu
444                 449                 454                 459

atg atg tac atc tgg aac ggc tac gcc gtg att ggg aag cag ccg aaa     1503
Met Met Tyr Ile Trp Asn Gly Tyr Ala Val Ile Gly Lys Gln Pro Lys
460                 465                 470                 475

ctc acg gat ggg ata ctt gag att atc act aag gct gaa gag atg ctg     1551
Leu Thr Asp Gly Ile Leu Glu Ile Ile Thr Lys Ala Glu Glu Met Leu
476                 481                 486                 491

gag aaa ggc cca gag aac gag tac tca gtg gat gac gag tgc ttg gtg     1599
Glu Lys Gly Pro Glu Asn Glu Tyr Ser Val Asp Asp Glu Cys Leu Val
492                 497                 502                 507

aaa ttg ttg aaa ggc ctg tgt ctg aaa tac ctg ggc cgt gtc cag gag     1647
Lys Leu Leu Lys Gly Leu Cys Leu Lys Tyr Leu Gly Arg Val Gln Glu
508                 513                 518                 523

gcc gag gag aat ttt agg agc atc tct gcc aat gaa aag aag att aaa     1695
Ala Glu Glu Asn Phe Arg Ser Ile Ser Ala Asn Glu Lys Lys Ile Lys
524                 529                 534                 539

tat gac cac tac ttg atc cca aac gcc ctg ctg gag ctg gcc ctg ctg     1743
Tyr Asp His Tyr Leu Ile Pro Asn Ala Leu Leu Glu Leu Ala Leu Leu
540                 545                 550                 555

ctt atg gag caa gac aga aac gaa gag gcc atc aaa ctt ttg gaa tct     1791
Leu Met Glu Gln Asp Arg Asn Glu Glu Ala Ile Lys Leu Leu Glu Ser
556                 561                 566                 571

gcc aag caa aac tac aag aat tac tcc atg gag tca agg aca cac ttt     1839
Ala Lys Gln Asn Tyr Lys Asn Tyr Ser Met Glu Ser Arg Thr His Phe
572                 577                 582                 587

cga atc cag gca gcc aca ctc caa gcc aag tct tcc cta gag aac agc     1887
Arg Ile Gln Ala Ala Thr Leu Gln Ala Lys Ser Ser Leu Glu Asn Ser
588                 593                 598                 603

agc aga tcc atg gtc tca tca gtg tcc ttg tag ctttgtgc agcagttccg     1938
Ser Arg Ser Met Val Ser Ser Val Ser Leu  *
604                 609                 614

ggctggaaga cagagacagc tggacagagc tcctgaaaac atttcaaaat acccccctccc   1998

cctgccctgc cctgcctttg gggtccaccg gcactccagt tggatggcac aacatagtgt   2058
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atccgtgcag aagccgagct ggcattttca ccagtgtagc caagggcctt tgccaagggc 2118

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catctggagg taaatctctt tatatgatga tgccaaaggg caaattgctt ttcaaattca 2358

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ctaccttact actcacactt catttcactc cttttgtaaa tttccaattt aaaaatcaag 2538

cacgtctttt tagtgagata aaatctgagc tcttctgtag aaaaatcaat ctctaccagt 2598

agaaaatgcc agggcttgat ggaagagctg tgtagccctt tctatgccaa agccaggaaa 2658

tttgggggggc aggaggaggt tctcagaatc cagtctgtat ctttgctgta tgccaaactg 2718

aaaccactgg gaataattta tgaaacataa aaatcttctg tacttcactc caaggtacat 2778

ttgcttactg acagcatttt tgttaaaact gttattcttg aaaaaaaaaa aa 2830

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<213> Homo sapiens

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gacgcgggag gctgtatcgg ccgaccggac gcaggggggct ggcgggaacg tgaagctccg 120

cggtgcctga tggggccgtt gggcggccgg tagctgttgc tgttggggga ccccctcatt 180

cctgccgctg ccgtccctgc tgcctc atg gcg gcc atc gga gtt cac ctg ggc 233
Met Ala Ala Ile Gly Val His Leu Gly
1 5

tgc acc tca gcc tgt gtg gcc gtc tat aag gat ggc cgg gct ggt gtg 281
Cys Thr Ser Ala Cys Val Ala Val Tyr Lys Asp Gly Arg Ala Gly Val
10 15 20 25

gtt gca aat gat gcc ggt gac cga gtt act cca gct gtt gtt gct tac 329
Val Ala Asn Asp Ala Gly Asp Arg Val Thr Pro Ala Val Val Ala Tyr
26 31 36 41

```
tca gaa aat gaa gag att gtt gga ttg gca gca aaa caa agt aga ata      377
Ser Glu Asn Glu Glu Ile Val Gly Leu Ala Ala Lys Gln Ser Arg Ile
 42                  47                  52                  57

aga aat att tca aat aca gta atg aaa gta aag cag atc ctg ggc aga      425
Arg Asn Ile Ser Asn Thr Val Met Lys Val Lys Gln Ile Leu Gly Arg
 58                  63                  68                  73

agc tcc agt gat cca caa gct cag aaa tac atc gcg gaa agt aaa tgt      473
Ser Ser Ser Asp Pro Gln Ala Gln Lys Tyr Ile Ala Glu Ser Lys Cys
 74                  79                  84                  89

tta gtc att gaa aaa aat ggg aaa tta cga tat gaa ata gat act gga      521
Leu Val Ile Glu Lys Asn Gly Lys Leu Arg Tyr Glu Ile Asp Thr Gly
 90                  95                 100                 105

gaa gaa aca aaa ttt gtt aac cca gaa gat gtt gcc aga ctg ata ttt      569
Glu Glu Thr Lys Phe Val Asn Pro Glu Asp Val Ala Arg Leu Ile Phe
106                 111                 116                 121

agt aaa atg aaa gaa acg gca cat tct gta ttg ggc tca gat gca aat      617
Ser Lys Met Lys Glu Thr Ala His Ser Val Leu Gly Ser Asp Ala Asn
122                 127                 132                 137

gat gta gtt att act gtc ccg ttt gat ttt gga gaa aag caa aaa aat      665
Asp Val Val Ile Thr Val Pro Phe Asp Phe Gly Glu Lys Gln Lys Asn
138                 143                 148                 153

gct ctt gga gaa gca gct aga gct gct gga ttt aat gtt ttg cga tta      713
Ala Leu Gly Glu Ala Ala Arg Ala Ala Gly Phe Asn Val Leu Arg Leu
154                 159                 164                 169

att cac gaa ccg tct gca gct ctt ctt gct tat gga att gga caa gac      761
Ile His Glu Pro Ser Ala Ala Leu Leu Ala Tyr Gly Ile Gly Gln Asp
170                 175                 180                 185

tcc cct act gga aaa agc aat att ttg gtg ttt aag ctt gga gga aca      809
Ser Pro Thr Gly Lys Ser Asn Ile Leu Val Phe Lys Leu Gly Gly Thr
186                 191                 196                 201

tcc tta tct ctc agc gtc atg gaa gtt aac agt gga ata tat cgg gtt      857
Ser Leu Ser Leu Ser Val Met Glu Val Asn Ser Gly Ile Tyr Arg Val
202                 207                 212                 217

ctt tca aca aac act gat gat aac atc ggt ggt gca cat ttc aca gaa      905
Leu Ser Thr Asn Thr Asp Asp Asn Ile Gly Gly Ala His Phe Thr Glu
218                 223                 228                 233

acc tta gca cag tat cta gct tct gag ttc caa aga tcc ttc aaa cat      953
Thr Leu Ala Gln Tyr Leu Ala Ser Glu Phe Gln Arg Ser Phe Lys His
234                 239                 244                 249

gat gtg aga gga aat gcg cga gcc atg atg aaa tta acg aac agt gct     1001
Asp Val Arg Gly Asn Ala Arg Ala Met Met Lys Leu Thr Asn Ser Ala
250                 255                 260                 265
```

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gaa gta gcg aaa cat tct ttg tca acc ttg gga agt gcc aac tgt ttt     1049
Glu Val Ala Lys His Ser Leu Ser Thr Leu Gly Ser Ala Asn Cys Phe
266                 271                 276                 281

ctt gac tca tta tat gaa ggt caa gat ttt gat tgc aat gtg tcc aga     1097
Leu Asp Ser Leu Tyr Glu Gly Gln Asp Phe Asp Cys Asn Val Ser Arg
282                 287                 292                 297

gca aga ttt gaa ctt ctt tgt tct cca ctt ttt aat aag tgt ata gaa     1145
Ala Arg Phe Glu Leu Leu Cys Ser Pro Leu Phe Asn Lys Cys Ile Glu
298                 303                 308                 313

gca atc aga gga ctc tta gat caa aat gga ttt aca gca gat gat atc     1193
Ala Ile Arg Gly Leu Leu Asp Gln Asn Gly Phe Thr Ala Asp Asp Ile
314                 319                 324                 329

aac aag gtt gtc ctt tgt gga ggg tct tct cga atc cca aag cta cag     1241
Asn Lys Val Val Leu Cys Gly Gly Ser Ser Arg Ile Pro Lys Leu Gln
330                 335                 340                 345

caa ctg att aaa gat ctt ttc cca gct gtt gag ctt ctc aat tct atc     1289
Gln Leu Ile Lys Asp Leu Phe Pro Ala Val Glu Leu Leu Asn Ser Ile
346                 351                 356                 361

cct cct gat gaa gtg atc cct att ggt gca gct ata gaa gca gga att     1337
Pro Pro Asp Glu Val Ile Pro Ile Gly Ala Ala Ile Glu Ala Gly Ile
362                 367                 372                 377

ctt att ggg aaa gaa aac ctg ttg gtg gaa gac tct ctt atg ata gag     1385
Leu Ile Gly Lys Glu Asn Leu Leu Val Glu Asp Ser Leu Met Ile Glu
378                 383                 388                 393

tgt tca gcc aga gat att tta gtt aag ggt gtg gac gaa tca gga gcc     1433
Cys Ser Ala Arg Asp Ile Leu Val Lys Gly Val Asp Glu Ser Gly Ala
394                 399                 404                 409

agt aga ttc aca gtg ctg ttt cca tca ggg act cct ttg cca gct cga     1481
Ser Arg Phe Thr Val Leu Phe Pro Ser Gly Thr Pro Leu Pro Ala Arg
410                 415                 420                 425

aga caa cac aca ttg caa gcc cct gga agc ata tct tca gtg tgc ctt     1529
Arg Gln His Thr Leu Gln Ala Pro Gly Ser Ile Ser Ser Val Cys Leu
426                 431                 436                 441

gaa ctc tat gag tct gat ggg aag aac tct gcc aaa gag gaa acc aag     1577
Glu Leu Tyr Glu Ser Asp Gly Lys Asn Ser Ala Lys Glu Glu Thr Lys
442                 447                 452                 457

ttt gca cag gtt gta ctc cag gat tta gat aaa aaa gaa aat gga tta     1625
Phe Ala Gln Val Val Leu Gln Asp Leu Asp Lys Lys Glu Asn Gly Leu
458                 463                 468                 473

cgt gat ata tta gct gtt ctt act atg aaa agg gat gga tct tta cat     1673
Arg Asp Ile Leu Ala Val Leu Thr Met Lys Arg Asp Gly Ser Leu His
474                 479                 484                 489

gtg aca tgc aca gat caa gaa act gga aaa tgt gaa gca atc tct att     1721
```

```
Val Thr Cys Thr Asp Gln Glu Thr Gly Lys Cys Glu Ala Ile Ser Ile
490                 495                 500                 505

gag ata gca tct tag tgttttagag aaatcaagaa tttttaaaaa caagaatatc     1776
Glu Ile Ala Ser  *
506

aacatttggt tttgtgtata agtggtgttt gtattaaaat acttttttcaa tgaactgtat   1836

aaactatgtt ttattaaact acaatatatc agtaaaaaaa aaaaa                    1881
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ccgggtcgac ccacgcgtcc gcgacgccgc cacctccgga acaagcc  atg gtg gcg      56
                                                     Met Val Ala
                                                       1

gcg acg gtg gca gcg gcg tgg ctg ctc ctg tgg gct gcg gcc tgc gcg      104
Ala Thr Val Ala Ala Ala Trp Leu Leu Leu Trp Ala Ala Ala Cys Ala
  4                   9                  14                  19

cag cag gag cag gac ttc tac gac ttc aag gcg gtc aac atc cgg ggc      152
Gln Gln Glu Gln Asp Phe Tyr Asp Phe Lys Ala Val Asn Ile Arg Gly
 20                  25                  30                  35

aaa ctg gtg tcg ctg gag aag tac cgc gga tcg gtg tcc ctg gtg gtg      200
Lys Leu Val Ser Leu Glu Lys Tyr Arg Gly Ser Val Ser Leu Val Val
 36                  41                  46                  51

aat gtg gcc agc gag tgc ggc ttc aca gac cag cac tac cga gcc ctg      248
Asn Val Ala Ser Glu Cys Gly Phe Thr Asp Gln His Tyr Arg Ala Leu
 52                  57                  62                  67

cag cag ctg cag cga gac ctg ggc ccc cac cac ttc aac gtg ctc gcc      296
Gln Gln Leu Gln Arg Asp Leu Gly Pro His His Phe Asn Val Leu Ala
 68                  73                  78                  83

ttc ccc tgc aac cag ttt ggc caa cag gag cct gac agc aac aag gag      344
Phe Pro Cys Asn Gln Phe Gly Gln Gln Glu Pro Asp Ser Asn Lys Glu
 84                  89                  94                  99

att gag agc ttt gcc cgc cgc acc tac agt gtc tca ttc ccc atg ttt      392
Ile Glu Ser Phe Ala Arg Arg Thr Tyr Ser Val Ser Phe Pro Met Phe
100                 105                 110                 115

agc aag att gca gtc acc ggt act ggt gcc cat cct gcc ttc aag tac      440
```

```
Ser Lys Ile Ala Val Thr Gly Thr Gly Ala His Pro Ala Phe Lys Tyr
116                 121                 126                 131

ctg gcc cag act tct ggg aag gag ccc acc tgg aac ttc tgg aag tac      488
Leu Ala Gln Thr Ser Gly Lys Glu Pro Thr Trp Asn Phe Trp Lys Tyr
132                 137                 142                 147

cta gta gcc cca gat gga aag gtg gta ggg gct tgg gac cca act gtg      536
Leu Val Ala Pro Asp Gly Lys Val Val Gly Ala Trp Asp Pro Thr Val
148                 153                 158                 163

tca gtg gag gag gtc aga ccc cag atc aca gcg ctc gtg agg aag ctc      584
Ser Val Glu Glu Val Arg Pro Gln Ile Thr Ala Leu Val Arg Lys Leu
164                 169                 174                 179

atc cta ctg aag cga gaa gac tta taa ccacc gcgtctcctc ctccaccacc      636
Ile Leu Leu Lys Arg Glu Asp Leu  *
180                 185

tcatcccgcc cacctgtgtg gggctgacca atgcaaactc aaatggtgct tcaaagggag    696

agacccactg actctccttc ctttactctt atgccattgg tcccatcatt cttgtggggg    756

aaaaattcta gtattttgat tatttgaatc ttacagcaac aaataggaac tcctggccaa    816

tgagagctct tgaccagtga atcaccagcc gatacgaacg tcttgccaac aaaaatgtgt    876

ggcaaataga agtatatcaa gcaataatct cccacccaag gcttctgtaa actgggacca    936

atgattacct catagggctg ttgtgaggat taggatgaaa tacctgtgaa agtgcctagg    996

cagtgccagc caaataggag gcattcaatg aacatttttt gcatataaaa caaaaaataa   1056

cttgttatca ataaaaactt gcatccaaca tgaaaaaaaa aaaa                    1100
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<210> 234
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<222> (1)...(1991)
<223> n = a,t,c or g

<400> 234

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agtacttann tagtnngnnc naggagnccn nncctgatac ccctgatacc gctccgaagn     60

gcnaccggtc cggaattccc gggtcgaccc acgcgtccgg ggtgcggcag cactgccagg    120
```

```
ggaagagggt gatccgaccc ggggaaggtc gctgggcagg gcgagttggg aaagcggcag    180

cccccgccgc ccccgcagcc ccttctcctc ctttctccca cgtcctatct gcctctcgct    240

ggaggccagg ccgtgcagca tcgaagacag gaggaactgg agcctcattg gccggcccgg    300

ggcgccggcc tcgggcttaa ataggagctc cgggctctgg ctgggacccg accgctgccg    360

gccgcgctcc cgctgctcct gccgggtg   atg gaa aac ccc agc ccg gcc gcc     412
                                 Met Glu Asn Pro Ser Pro Ala Ala
                                   1               5

gcc ctg ggc aag gcc ctc tgc gct ctc ctc ctg gcc act ctc ggc gcc     460
Ala Leu Gly Lys Ala Leu Cys Ala Leu Leu Leu Ala Thr Leu Gly Ala
  9                  14                  19                  24

gcc ggc cag cct ctt ggg gga gaa tcc atc tgt tcc gcc aga gcc ccg     508
Ala Gly Gln Pro Leu Gly Gly Glu Ser Ile Cys Ser Ala Arg Ala Pro
 25                  30                  35                  40

gcc aaa tac agc atc acc ttc acg ggc aag tgg agc cag acg gcc ttc     556
Ala Lys Tyr Ser Ile Thr Phe Thr Gly Lys Trp Ser Gln Thr Ala Phe
 41                  46                  51                  56

ccc aag cag tac ccc ctg ttc cgc ccc cct gcg cag tgg tct tcg ctg     604
Pro Lys Gln Tyr Pro Leu Phe Arg Pro Pro Ala Gln Trp Ser Ser Leu
 57                  62                  67                  72

ctg ggg gcc gcg cat agc tcc gac tac agc atg tgg agg aag aac cag     652
Leu Gly Ala Ala His Ser Ser Asp Tyr Ser Met Trp Arg Lys Asn Gln
 73                  78                  83                  88

tac gtc agt aac ggg ctg cgc gac ttt gcg gag cgc ggc gag gcc tgg     700
Tyr Val Ser Asn Gly Leu Arg Asp Phe Ala Glu Arg Gly Glu Ala Trp
 89                  94                  99                 104

gcg ctg atg aag gag atc gag gcg gcg ggg gag gcg ctg cag agc gtg     748
Ala Leu Met Lys Glu Ile Glu Ala Ala Gly Glu Ala Leu Gln Ser Val
105                 110                 115                 120

cac gcg gtg ttt tcg gcg ccc gcc gtc ccc agc ggc acc ggg cag acg     796
His Ala Val Phe Ser Ala Pro Ala Val Pro Ser Gly Thr Gly Gln Thr
121                 126                 131                 136

tcg gcg gag ctg gag gtg cag cgc agg cac tcg ctg gtc tcg ttt gtg     844
Ser Ala Glu Leu Glu Val Gln Arg Arg His Ser Leu Val Ser Phe Val
137                 142                 147                 152

gtg cgc atc gtg ccc agc ccc gac tgg ttc gtg ggc gtg gac agc ctg     892
Val Arg Ile Val Pro Ser Pro Asp Trp Phe Val Gly Val Asp Ser Leu
153                 158                 163                 168

gac ctg tgc gac ggg gac cgt tgg cgg gaa cag gcg gcg ctg gac ctg     940
Asp Leu Cys Asp Gly Asp Arg Trp Arg Glu Gln Ala Ala Leu Asp Leu
169                 174                 179                 184

tac ccc tac gac gcc ggg acg gac agc ggc ttc acc ttc tcc tcc ccc     988
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US 2005/0250147 A1

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Tyr Pro Tyr Asp Ala Gly Thr Asp Ser Gly Phe Thr Phe Ser Ser Pro
185                 190                 195                 200

aac ttc gcc acc atc ccg cag gac acg gtg acc gag ata acg tcc tcc     1036
Asn Phe Ala Thr Ile Pro Gln Asp Thr Val Thr Glu Ile Thr Ser Ser
201                 206                 211                 216

tct ccc agc cac ccg gcc aac tcc ttc tac tac ccg cgg ctg aag gcc     1084
Ser Pro Ser His Pro Ala Asn Ser Phe Tyr Tyr Pro Arg Leu Lys Ala
217                 222                 227                 232

ctg cct ccc atc gcc agg gtg aca ctg ctg cgg ctg cga cag agc ccc     1132
Leu Pro Pro Ile Ala Arg Val Thr Leu Leu Arg Leu Arg Gln Ser Pro
233                 238                 243                 248

agg gcc ttc atc cct ccc gcc cca gtc ctg ccc agc agg gac aat gag     1180
Arg Ala Phe Ile Pro Pro Ala Pro Val Leu Pro Ser Arg Asp Asn Glu
249                 254                 259                 264

att gta gac agc gcc tca gtt cca gaa acg ccg ctg gac tgc gag gtc     1228
Ile Val Asp Ser Ala Ser Val Pro Glu Thr Pro Leu Asp Cys Glu Val
265                 270                 275                 280

tcc ctg tgg tcg tcc tgg gga ctg tgc gga ggc cac tgt ggg agg ctc     1276
Ser Leu Trp Ser Ser Trp Gly Leu Cys Gly Gly His Cys Gly Arg Leu
281                 286                 291                 296

ggg acc aag agc agg act cgc tac gtc cgg gtc cag ccc gcc aac aac     1324
Gly Thr Lys Ser Arg Thr Arg Tyr Val Arg Val Gln Pro Ala Asn Asn
297                 302                 307                 312

ggg agc ccc tgc ccc gag ctc gaa gaa gag gct gag tgc gtc cct gat     1372
Gly Ser Pro Cys Pro Glu Leu Glu Glu Glu Ala Glu Cys Val Pro Asp
313                 318                 323                 328

aac tgc gtc taa gac cagagccccg cagcccctgg ggccccccgg agccatgggg     1427
Asn Cys Val  *
329

tgtcgggggc tcctgtgcag gctcatgctg caggcggccg agggcacagg gggtttcgcg   1487

ctgctcctga ccgcggtgag gccgcgccga ccatctctgc actgaagggc cctctggtgg   1547

ccggcacggg cattgggaaa cagcctcctc ctttcccaac cttgcttctt aggggccccc   1607

gtgtcccgtc tgctctcagc ctcctcctcc tgcaggataa agtcatcccc aaggctccag   1667

ctactctaaa ttatgtctcc ttataagtta ttgctgctcc aggagattgt ccttcatcgt   1727

ccaggggcct ggctcccacg tggttgcaga tacctcagac ctggtgctct aggctgtgct   1787

gagcccactc tcccgagggc gcatccaagc gggggccact tgagaagtga ataaatgggg   1847

cggtttcgga agcgtcagtg tttccatgtt atggatctct ctgcgtttga ataaagacta   1907

tctctgttgc tcacaaaaaa aaaaaaaaaa aaaaaagggg gggccctttt aaggggccca   1967
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US 6,756,480 B2

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ggttttcctc gccggggttg gaaa                                              1991



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     <211> 1046
     <212> DNA
     <213> Homo sapiens

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     <221> CDS
     <222> (174)..(962)

     <400> 235
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cggcgggacc ctgcagaggc ggcggggctc ctcctcccgc tcctcctcgg cctccccttc     120

gggcgctctc gcgctaactg tgctcctccg gggccctccg cctgctccca gcc   atg      176
                                                             Met
                                                               1

gtg gcc tgg cgc tcg gcg ttc ctt gtc tgc ctc gct ttc tcc ttg gcc      224
Val Ala Trp Arg Ser Ala Phe Leu Val Cys Leu Ala Phe Ser Leu Ala
  2                   7                  12                  17

acc ctg gtc cag cga gga tct ggg gac ttt gat gat ttt aac ctg gag      272
Thr Leu Val Gln Arg Gly Ser Gly Asp Phe Asp Asp Phe Asn Leu Glu
 18                  23                  28                  33

gat gca gtg aaa gaa act tcc tca gta aag cag cca tgg gac cac acc      320
Asp Ala Val Lys Glu Thr Ser Ser Val Lys Gln Pro Trp Asp His Thr
 34                  39                  44                  49

acc acc acc aca acc aat agg cca gga acc acc aga gct ccg gca aaa      368
Thr Thr Thr Thr Thr Asn Arg Pro Gly Thr Thr Arg Ala Pro Ala Lys
 50                  55                  60                  65

cct cca ggt agt gga ttg gac ttg gct gat gct ttg gat gat caa gat      416
Pro Pro Gly Ser Gly Leu Asp Leu Ala Asp Ala Leu Asp Asp Gln Asp
 66                  71                  76                  81

gat ggc cgc agg aaa ccg ggt ata gga gga aga gag aga tgg aac cat      464
Asp Gly Arg Arg Lys Pro Gly Ile Gly Gly Arg Glu Arg Trp Asn His
 82                  87                  92                  97

gta acc acc acg acc aag agg cca gta acc acc aga gct cca gca aat      512
Val Thr Thr Thr Thr Lys Arg Pro Val Thr Thr Arg Ala Pro Ala Asn
 98                 103                 108                 113

act tta gga aat gat ttt gac ttg gct gat gcc ctg gat gat cga aat      560
Thr Leu Gly Asn Asp Phe Asp Leu Ala Asp Ala Leu Asp Asp Arg Asn
114                 119                 124                 129

gat cga gat gat ggc cgc agg aaa cca att gct gga gga gga ggt ttt      608
Asp Arg Asp Asp Gly Arg Arg Lys Pro Ile Ala Gly Gly Gly Gly Phe
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130                 135                 140                 145

tca gac aag gat ctt gaa gac ata gta ggg ggt gga gaa tac aaa cct      656
Ser Asp Lys Asp Leu Glu Asp Ile Val Gly Gly Gly Glu Tyr Lys Pro
146                 151                 156                 161

gac aag ggt aaa ggt gat ggc cgg tac ggc agc aat gac gac cct gga      704
Asp Lys Gly Lys Gly Asp Gly Arg Tyr Gly Ser Asn Asp Asp Pro Gly
162                 167                 172                 177

tct ggc atg gtg gca gag cct ggc acc att gcc ggg gtg gcc agc gcc      752
Ser Gly Met Val Ala Glu Pro Gly Thr Ile Ala Gly Val Ala Ser Ala
178                 183                 188                 193

ctg gcc atg gcc ctc atc ggt gcc gtc tcc agc tac atc tcc tac cag      800
Leu Ala Met Ala Leu Ile Gly Ala Val Ser Ser Tyr Ile Ser Tyr Gln
194                 199                 204                 209

cag aag aag ttc tgc ttc agc att cag cag ggt ctc aac gca gac tac      848
Gln Lys Lys Phe Cys Phe Ser Ile Gln Gln Gly Leu Asn Ala Asp Tyr
210                 215                 220                 225

gtg aag gga gag aac ctg gaa gcc gtg gta tgt gag gaa ccc caa gtg      896
Val Lys Gly Glu Asn Leu Glu Ala Val Val Cys Glu Glu Pro Gln Val
226                 231                 236                 241

aaa tac tcc acg ttg cac acg cag tct gca gag ccg ccg ccg ccg ccc      944
Lys Tyr Ser Thr Leu His Thr Gln Ser Ala Glu Pro Pro Pro Pro Pro
242                 247                 252                 257

gaa cca gcc cgg atc tga gggccc tgtccagctg caggcatgca caatggtgcc      998
Glu Pro Ala Arg Ile  *
258                 263

accgcttgtc acccggctcc ccccacccct tcatttggac acgcagct               1046
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09650.P2

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<213> Homo sapiens

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<400> 236

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gcggaggaat tctgccacga acaggccaat aaggagggag cagtgcgggg tttaaatctg     60

aggctaggct ggctcttctc ggcgtgctgc ggcggaacgg ctgttggttt ctgctggttg    120

taggtccttg gctggtcggg cctccggtgt tctgcttctc cccgctgagc tgctgcctgg    180

tgaagaggaa gcc   atg gcg ctc cga gtc acc agg aac tcg aaa att aat      229
                Met Ala Leu Arg Val Thr Arg Asn Ser Lys Ile Asn
```

```
                    1               5                  10

gct gaa aat aag gcg aag atc aac atg gca ggc gca aag cgc gtt cct      277
Ala Glu Asn Lys Ala Lys Ile Asn Met Ala Gly Ala Lys Arg Val Pro
 13                  18                  23                  28

acg gcc cct gct gca acc tcc aag ccc gga ctg agg cca aga aca gct      325
Thr Ala Pro Ala Ala Thr Ser Lys Pro Gly Leu Arg Pro Arg Thr Ala
 29                  34                  39                  44

ctt ggg gac att ggt aac aaa gtc agt gaa caa ctg cag gcc aaa atg      373
Leu Gly Asp Ile Gly Asn Lys Val Ser Glu Gln Leu Gln Ala Lys Met
 45                  50                  55                  60

cct atg aag aag gaa gca aaa cct tca gct act gga aaa gtc att gat      421
Pro Met Lys Lys Glu Ala Lys Pro Ser Ala Thr Gly Lys Val Ile Asp
 61                  66                  71                  76

aaa aaa cta cca aaa cct ctt gaa aag gta cct atg ctg gtg cca gtg      469
Lys Lys Leu Pro Lys Pro Leu Glu Lys Val Pro Met Leu Val Pro Val
 77                  82                  87                  92

cca gtg tct gag cca gtg cca gag cca gaa cct gag cca gaa cct gag      517
Pro Val Ser Glu Pro Val Pro Glu Pro Glu Pro Glu Pro Glu Pro Glu
 93                  98                 103                 108

cct gtt aaa gaa gaa aaa ctt tcg cct gag cct att ttg gtt gat act      565
Pro Val Lys Glu Glu Lys Leu Ser Pro Glu Pro Ile Leu Val Asp Thr
109                 114                 119                 124

gcc tct cca agc cca atg gaa aca tct gga tgt gcc cct gca gaa gaa      613
Ala Ser Pro Ser Pro Met Glu Thr Ser Gly Cys Ala Pro Ala Glu Glu
125                 130                 135                 140

gac ctg tgt cag gct ttc tct gat gta att ctt gca gta aat gat gtg      661
Asp Leu Cys Gln Ala Phe Ser Asp Val Ile Leu Ala Val Asn Asp Val
141                 146                 151                 156

gat gca gaa gat gga gct gat cca aac ctt tgt agt gaa tat gtg aaa      709
Asp Ala Glu Asp Gly Ala Asp Pro Asn Leu Cys Ser Glu Tyr Val Lys
157                 162                 167                 172

gat att tat gct tat ctg aga caa ctt gag gaa gag caa gca gtc aga      757
Asp Ile Tyr Ala Tyr Leu Arg Gln Leu Glu Glu Glu Gln Ala Val Arg
173                 178                 183                 188

cca aaa tac cta ctg ggt cgg gaa gtc act gga aac atg aga gcc atc      805
Pro Lys Tyr Leu Leu Gly Arg Glu Val Thr Gly Asn Met Arg Ala Ile
189                 194                 199                 204

cta att gac tgg cta gta cag gtt caa atg aaa ttc agg ttg ttg cag      853
Leu Ile Asp Trp Leu Val Gln Val Gln Met Lys Phe Arg Leu Leu Gln
205                 210                 215                 220

gag acc atg tac atg act gtc tcc att att gat cgg ttc atg cag aat      901
Glu Thr Met Tyr Met Thr Val Ser Ile Ile Asp Arg Phe Met Gln Asn
221                 226                 231                 236
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Doc No. 7,166,566

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aat tgt gtg ccc aag aag atg ctg cag ctg gtt ggt gtc act gcc atg      949
Asn Cys Val Pro Lys Lys Met Leu Gln Leu Val Gly Val Thr Ala Met
237                 242                 247                 252

ttt att gca agc aaa tat gaa gaa atg tac cct cca gaa att ggt gac      997
Phe Ile Ala Ser Lys Tyr Glu Glu Met Tyr Pro Pro Glu Ile Gly Asp
253                 258                 263                 268

ttt gct ttt gtg act gac aac act tat act aag cac caa atc aga cag     1045
Phe Ala Phe Val Thr Asp Asn Thr Tyr Thr Lys His Gln Ile Arg Gln
269                 274                 279                 284

atg gaa atg aag att cta aga gct tta aac ttt ggt ctg ggt cgg cct     1093
Met Glu Met Lys Ile Leu Arg Ala Leu Asn Phe Gly Leu Gly Arg Pro
285                 290                 295                 300

cta cct ttg cac ttc ctt cgg aga gca tct aag att gga gag gtt gat     1141
Leu Pro Leu His Phe Leu Arg Arg Ala Ser Lys Ile Gly Glu Val Asp
301                 306                 311                 316

gtc gag caa cat act ttg gcc aaa tac ctg atg gaa cta act atg ttg     1189
Val Glu Gln His Thr Leu Ala Lys Tyr Leu Met Glu Leu Thr Met Leu
317                 322                 327                 332

gac tat gac atg gtg cac ttt cct cct tct caa att gca gca gga gct     1237
Asp Tyr Asp Met Val His Phe Pro Pro Ser Gln Ile Ala Ala Gly Ala
333                 338                 343                 348

ttt tgc tta gca ctg aaa att ctg gat aat ggt gaa tgg aca cca act     1285
Phe Cys Leu Ala Leu Lys Ile Leu Asp Asn Gly Glu Trp Thr Pro Thr
349                 354                 359                 364

cta caa cat tac ctg tca tat act gaa gaa tct ctt ctt cca gtt atg     1333
Leu Gln His Tyr Leu Ser Tyr Thr Glu Glu Ser Leu Leu Pro Val Met
365                 370                 375                 380

cag cac ctg gct aag aat gta gtc atg gta aat caa gga ctt aca aag     1381
Gln His Leu Ala Lys Asn Val Val Met Val Asn Gln Gly Leu Thr Lys
381                 386                 391                 396

cac atg act gtc aag aac aag tat gcc aca tcg aag cat gct aag atc     1429
His Met Thr Val Lys Asn Lys Tyr Ala Thr Ser Lys His Ala Lys Ile
397                 402                 407                 412

agc act cta cca cag ctg aat tct gca cta gtt caa gat tta gcc aag     1477
Ser Thr Leu Pro Gln Leu Asn Ser Ala Leu Val Gln Asp Leu Ala Lys
413                 418                 423                 428

gct gtg gca aag gtg taa cttgta aacttgagtt ggagtactat atttacaaat     1531
Ala Val Ala Lys Val  *
429                 434

aaaattggca ccatgtgcca tctgtacaaa aaaaaaaaa                          1570
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acccacgacc gcagcccagc aactcgcaaa cgcaacctga agcctgggct gcgcagtgtg 180

ggagggcttc gcgatcttgg gggacccatt ccgaacttgc agaggaccgt agctctcctg 240

gcctggagag tgtgaacagg attgtggact cttccaagat tcacaatgat atggtgaatc 300

caaagactgg aaccaaaaag atttactcag tgctttagtt ttaacaacag taaattgtct 360

accaacaccc atc atg gct aaa agt gcg gag gtc aaa ctg gca ata ttt 409
Met Ala Lys Ser Ala Glu Val Lys Leu Ala Ile Phe
1 5 10

ggg aga gca ggc gtg ggc aag tca gct ctt gta gtg aga ttt ctg acc 457
Gly Arg Ala Gly Val Gly Lys Ser Ala Leu Val Val Arg Phe Leu Thr
13 18 23 28

aaa cgg ttc atc tgg gaa tat gat ccc acc ctc gaa tca acc tac cga 505
Lys Arg Phe Ile Trp Glu Tyr Asp Pro Thr Leu Glu Ser Thr Tyr Arg
29 34 39 44

cac caa gca acc atc gat gat gaa gtt gtt tcc atg gag ata cta gac 553
His Gln Ala Thr Ile Asp Asp Glu Val Val Ser Met Glu Ile Leu Asp
45 50 55 60

act gct ggt cag gaa gat acc att cag agg gag ggg cac atg cga tgg 601
Thr Ala Gly Gln Glu Asp Thr Ile Gln Arg Glu Gly His Met Arg Trp
61 66 71 76

ggg gaa ggc ttt gtg ctg gtc tac gac att act gac cga gga agt ttt 649
Gly Glu Gly Phe Val Leu Val Tyr Asp Ile Thr Asp Arg Gly Ser Phe
77 82 87 92

gag gaa gtg ctg cca ctt aag aac atc cta gat gag atc aaa aag ccc 697
Glu Glu Val Leu Pro Leu Lys Asn Ile Leu Asp Glu Ile Lys Lys Pro
93 98 103 108

aag aat gtg act ctc atc ttg gtt gga aac aaa gct gac ttg gac cac 745
Lys Asn Val Thr Leu Ile Leu Val Gly Asn Lys Ala Asp Leu Asp His
109 114 119 124

tcc agg cag gtt agc aca gaa gaa gga gag aag ctg gcc aca gaa ttg 793
Ser Arg Gln Val Ser Thr Glu Glu Gly Glu Lys Leu Ala Thr Glu Leu

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125                 130                 135                 140

gct tgt gct ttt tac gag tgc tct gcc tgc act gga gaa ggg aac atc      841
Ala Cys Ala Phe Tyr Glu Cys Ser Ala Cys Thr Gly Glu Gly Asn Ile
141                 146                 151                 156

aca gag ata ttc tat gaa ttg tgt cga gag gtg cgt cgc cgg agg atg      889
Thr Glu Ile Phe Tyr Glu Leu Cys Arg Glu Val Arg Arg Arg Arg Met
157                 162                 167                 172

gtg cag ggc aag acg agg cga cgc agc tcc acc acg cat gtc aag caa      937
Val Gln Gly Lys Thr Arg Arg Arg Ser Ser Thr Thr His Val Lys Gln
173                 178                 183                 188

gcc att aac aag atg ctc acc aaa atc agt agt tag gcag cccagctgag      987
Ala Ile Asn Lys Met Leu Thr Lys Ile Ser Ser  *
189                 194                 199

gtggaccaac taattggaaa cactcttccc cttctgttcc cctttcaaaa ataaaacaaa   1047

atattgcatt ctttgtttgg attctgagaa atgtctgggc ttcccattgt ttctggcctc   1107

taataggttg ggaagtttta gcgtgtttta tgcaatttca gtgctaacaa tttcttcctt   1167

tcctgcttga ataagataca ctctaatggc atttgaacat gtaatcacca gagattctga   1227

aatgactggt ttatgttaag ctatttttag gcatcttcac cttgctttaa gtaggttgaa   1287

gtttttgcaa aggcatttaa aaattcaatt tcttgtcaga tactacaaat aattttctta   1347

aaagtctaag atagcagaaa atacagtaaa aacacaggag aagaagctga gctattggaa   1407

caggaaatag aaggaactct agtttctgtt tgaagtgagg attttctgaa ttatctaata   1467

tcatctaggt tttctttaaa attttatttt gttcttcagt tcaagcatct tctcactaat   1527

gtttttcact ataacagaga attcatttca atttgagttg gttctctcaa tgatctattg   1587

atcattacac cctaactctc cttccttggc tcaaacaata ttttccctat aacaaaggca   1647

ataggacaca aaattcacat cctgctgggc ctttttttcat caagtcaggg tgatataaaa   1707

acattggaag tcttttcacc aaaccctgac tttattgaat gctagtagaa gatgtagaat   1767

tagagacatc tgatttgttt atcaccttag cagaaaaacc acagtccaaa agacaagcaa   1827

attaagaatg gagcttaacc atgcctccat tgggaagtct agactttgag ccaggtacag   1887

taagaaaaat tagcctctga ttcattaagt ttgccacatg acttattttg atattttgga   1947

tacattaact cacttaggag aattcagaaa agaatgggtg attaaagttc attacagctg   2007

aataaatgtg tctaaaacag actcttgtat tctgaaagta cagtctacaa ctgataaaac   2067

cttatgattc ttttctcccc cattatgccc ctatatatat caagatttgg gtactttatt   2127

ttagtagaaa atatatatct tttacatatg tatgtattta taaatgcata gatatatgta   2187
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Date Recue/Date Received 2020-05-26

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taaaaatttg taagcgttag cggcattaat tcaccaatgc atttggacaa cttgatgtaa   2247

ctgactttat tttatgtgac tataataaaa agcataattt tctc                    2291
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<400> 238

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                                        Met Ala Ala Glu Arg Gly
                                          1

gcg ggg cag caa cag tcg cag gag atg atg gag gtt gac agg cgg gtc     161
Ala Gly Gln Gln Gln Ser Gln Glu Met Met Glu Val Asp Arg Arg Val
  7                  12                  17                  22

gag tct gaa gaa tcc ggc gat gaa gaa ggg aag aaa cac agc agt ggc     209
Glu Ser Glu Glu Ser Gly Asp Glu Glu Gly Lys Lys His Ser Ser Gly
 23                  28                  33                  38

atc gtg gcc gac ctc agt gaa cag agc ctg aag gat ggg gag gag cgg     257
Ile Val Ala Asp Leu Ser Glu Gln Ser Leu Lys Asp Gly Glu Glu Arg
 39                  44                  49                  54

ggg gag gag gac cca gaa gaa gaa cat gag ctg cct gtg gac atg gaa     305
Gly Glu Glu Asp Pro Glu Glu Glu His Glu Leu Pro Val Asp Met Glu
 55                  60                  65                  70

acc atc aac ctg gac aga gat gca gag gat gtt gat ttg aat cac tat     353
Thr Ile Asn Leu Asp Arg Asp Ala Glu Asp Val Asp Leu Asn His Tyr
 71                  76                  81                  86

cgc ata ggg aag att gaa gga ttt gag gta ctg aag aaa gtg aag act     401
Arg Ile Gly Lys Ile Glu Gly Phe Glu Val Leu Lys Lys Val Lys Thr
 87                  92                  97                 102

ctc tgc ctc cgc caa aat tta att aaa tgc att gag aat ctg gag gag     449
Leu Cys Leu Arg Gln Asn Leu Ile Lys Cys Ile Glu Asn Leu Glu Glu
103                 108                 113                 118

cta cag agt ctt cga gag ctg gat ctt tac gac aac cag atc aag aag     497
Leu Gln Ser Leu Arg Glu Leu Asp Leu Tyr Asp Asn Gln Ile Lys Lys
119                 124                 129                 134

att gag aat ctg gag gcg cta aca gag ctg gag att cta gat att tct     545
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Ile Glu Asn Leu Glu Ala Leu Thr Glu Leu Glu Ile Leu Asp Ile Ser
135                 140                 145                 150

ttt aat ctg ctg aga aac atc gaa ggg gtt gac aag ttg aca cga ctg      593
Phe Asn Leu Leu Arg Asn Ile Glu Gly Val Asp Lys Leu Thr Arg Leu
151                 156                 161                 166

aaa aaa ctc ttc ttg gtc aac aat aaa atc agt aaa att gag aac tta      641
Lys Lys Leu Phe Leu Val Asn Asn Lys Ile Ser Lys Ile Glu Asn Leu
167                 172                 177                 182

agc aac tta cat caa cta cag atg cta gag ctg gga tct aac cgc atc      689
Ser Asn Leu His Gln Leu Gln Met Leu Glu Leu Gly Ser Asn Arg Ile
183                 188                 193                 198

cgg gca atc gaa aat atc gac acc tta acc aac ctg gag agt ttg ttt      737
Arg Ala Ile Glu Asn Ile Asp Thr Leu Thr Asn Leu Glu Ser Leu Phe
199                 204                 209                 214

ttg ggg aaa aac aaa att act aaa ctt cag aac ctg gat gcg ctc acc      785
Leu Gly Lys Asn Lys Ile Thr Lys Leu Gln Asn Leu Asp Ala Leu Thr
215                 220                 225                 230

aac ctg aca gtc ctc agt atg cag agc aac cgg ctg acc aag atc gag      833
Asn Leu Thr Val Leu Ser Met Gln Ser Asn Arg Leu Thr Lys Ile Glu
231                 236                 241                 246

ggt ctg cag aac ctg gtg aac ctg cgg gag ctg tac ctt agc cac aat      881
Gly Leu Gln Asn Leu Val Asn Leu Arg Glu Leu Tyr Leu Ser His Asn
247                 252                 257                 262

ggc atc gag gtc atc gag ggc ctg gag aac aat aac aaa ctc acg atg      929
Gly Ile Glu Val Ile Glu Gly Leu Glu Asn Asn Asn Lys Leu Thr Met
263                 268                 273                 278

ttg gac att gca tca aat aga atc aaa aag att gaa aat atc agc cat      977
Leu Asp Ile Ala Ser Asn Arg Ile Lys Lys Ile Glu Asn Ile Ser His
279                 284                 289                 294

cta aca gag ctg caa gag ttc tgg atg aac gac aat ctc ctt gag agc     1025
Leu Thr Glu Leu Gln Glu Phe Trp Met Asn Asp Asn Leu Leu Glu Ser
295                 300                 305                 310

tgg agc gac ctc gac gag ctg aag gga gcc agg agc ctg gag aca gtg     1073
Trp Ser Asp Leu Asp Glu Leu Lys Gly Ala Arg Ser Leu Glu Thr Val
311                 316                 321                 326

tac ctg gag cgg aac ccc ttg cag aag gac ccc cag tac cgg cgg aag     1121
Tyr Leu Glu Arg Asn Pro Leu Gln Lys Asp Pro Gln Tyr Arg Arg Lys
327                 332                 337                 342

gtc atg ctc gcc ctc ccc tcc gtg cgg cag atc gat gcc acg ttc gtc     1169
Val Met Leu Ala Leu Pro Ser Val Arg Gln Ile Asp Ala Thr Phe Val
343                 348                 353                 358

agg ttc tga gtccttc ttggctcctc atgtggtccc tctcctcgga agaactgccc     1225
Arg Phe  *
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359

agccacgggt ttttaaccca cctgttgctc ctgaggtcgt cactatatca acagtcacaa 1285

acccaatggc aataaaggca ctgacgatag ctggcgcgcg cgacgccaca caccattttc 1345

agatgccgtt gcaattaaat cttgccacac tgtcaaaaaa aaaaaaa 1392

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Met Ala Ala Glu Arg Gly
1

gcg ggg cag caa cag tcg cag gag atg atg gag gtt gac agg cgg gtc 161
Ala Gly Gln Gln Gln Ser Gln Glu Met Met Glu Val Asp Arg Arg Val
7 12 17 22

gag tct gaa gaa tcc ggc gat gaa gaa ggg aag aaa cac agc agt ggc 209
Glu Ser Glu Glu Ser Gly Asp Glu Glu Gly Lys Lys His Ser Ser Gly
23 28 33 38

atc gtg gcc gac ctc agt gaa cag agc ctg aag gat ggg gag gag cgg 257
Ile Val Ala Asp Leu Ser Glu Gln Ser Leu Lys Asp Gly Glu Glu Arg
39 44 49 54

ggg gag gag gac cca gaa gaa gaa cat gag ctg cct gtg gac atg gaa 305
Gly Glu Glu Asp Pro Glu Glu Glu His Glu Leu Pro Val Asp Met Glu
55 60 65 70

acc atc aac ctg gac aga gat gca gag gat gtt gat ttg aat cac tat 353
Thr Ile Asn Leu Asp Arg Asp Ala Glu Asp Val Asp Leu Asn His Tyr
71 76 81 86

cgc ata ggg aag att gaa gga ttt gag act ctc tgc ctc cgc caa aat 401
Arg Ile Gly Lys Ile Glu Gly Phe Glu Thr Leu Cys Leu Arg Gln Asn
87 92 97 102

tta att aaa tgc att gag aat ctg gag gag cta cag agt ctt cga gag 449
Leu Ile Lys Cys Ile Glu Asn Leu Glu Glu Leu Gln Ser Leu Arg Glu
103 108 113 118

ctg gat ctt tac gac aac cag atc aag aag att gag aat ctg gag gcg 497
Leu Asp Leu Tyr Asp Asn Gln Ile Lys Lys Ile Glu Asn Leu Glu Ala

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119                 124                 129                 134

cta aca gag ctg gag att cta gat att tct ttt aat ctg ctg aga aac      545
Leu Thr Glu Leu Glu Ile Leu Asp Ile Ser Phe Asn Leu Leu Arg Asn
135                 140                 145                 150

atc gaa ggg gtt gac aag ttg aca cga ctg aaa aaa ctc ttc ttg gtc      593
Ile Glu Gly Val Asp Lys Leu Thr Arg Leu Lys Lys Leu Phe Leu Val
151                 156                 161                 166

aac aat aaa atc agt aaa att gag aac tta agc aac tta cat caa cta      641
Asn Asn Lys Ile Ser Lys Ile Glu Asn Leu Ser Asn Leu His Gln Leu
167                 172                 177                 182

cag atg cta gag ctg gga tct aac cgc atc cgg gca atc gaa aat atc      689
Gln Met Leu Glu Leu Gly Ser Asn Arg Ile Arg Ala Ile Glu Asn Ile
183                 188                 193                 198

gac acc tta acc aac ctg gag agt ttg ttt ttg ggg aaa aac aaa att      737
Asp Thr Leu Thr Asn Leu Glu Ser Leu Phe Leu Gly Lys Asn Lys Ile
199                 204                 209                 214

act aaa ctt cag aac ctg gat gcg ctc acc aac ctg aca gtc ctc agt      785
Thr Lys Leu Gln Asn Leu Asp Ala Leu Thr Asn Leu Thr Val Leu Ser
215                 220                 225                 230

atg cag agc aac cgg ctg acc aag atc gag ggt ctg cag aac ctg gtg      833
Met Gln Ser Asn Arg Leu Thr Lys Ile Glu Gly Leu Gln Asn Leu Val
231                 236                 241                 246

aac ctg cgg gag ctg tac ctt agc cac aat ggc atc gag gtc atc gag      881
Asn Leu Arg Glu Leu Tyr Leu Ser His Asn Gly Ile Glu Val Ile Glu
247                 252                 257                 262

ggc ctg gag aac aat aac aaa ctc acg atg ttg gac att gca tca aat      929
Gly Leu Glu Asn Asn Asn Lys Leu Thr Met Leu Asp Ile Ala Ser Asn
263                 268                 273                 278

aga atc aaa aag att gaa aat atc agc cat cta aca gag ctg caa gag      977
Arg Ile Lys Lys Ile Glu Asn Ile Ser His Leu Thr Glu Leu Gln Glu
279                 284                 289                 294

ttc tgg atg aac gac aat ctc ctt gag agc tgg agc gac ctc gac gag     1025
Phe Trp Met Asn Asp Asn Leu Leu Glu Ser Trp Ser Asp Leu Asp Glu
295                 300                 305                 310

ctg aag gga gcc agg agc ctg gag aca gtg tac ctg gag cgg aac ccc     1073
Leu Lys Gly Ala Arg Ser Leu Glu Thr Val Tyr Leu Glu Arg Asn Pro
311                 316                 321                 326

ttg cag aag gac ccc cag tac cgg cgg aag gtc atg ctc gcc ctc ccc     1121
Leu Gln Lys Asp Pro Gln Tyr Arg Arg Lys Val Met Leu Ala Leu Pro
327                 332                 337                 342

tcc gtg cgg cag atc gat gcc acg ttc gtc agg ttc tga gtccttcttg      1170
Ser Val Arg Gln Ile Asp Ala Thr Phe Val Arg Phe  *
343                 348                 353
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gctcctcatg tggtccctct cctcggaaga actgcccagc cacgggtttt taacccacct 1230

gttgctcctg aggtcgtcac tatatcaaca gtcacaaacc caatggcaat aaaggcactg 1290

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cccagggcct ggagacccgt ggggcggact ctgggatctg agcctatcgc cctggcctgg 180

agccccccctt tgtacctatt ccccattccc ctaccgagct gggcagttag ccagcccact 240

ccaactctcg gaacc atg ttt gca gac ttg gat tat gac atc gaa gag gat 291
Met Phe Ala Asp Leu Asp Tyr Asp Ile Glu Glu Asp
1 5 10

aaa ctc gga atc ccg act gtg cct ggg aag gtg acc ctg cag aag gat 339
Lys Leu Gly Ile Pro Thr Val Pro Gly Lys Val Thr Leu Gln Lys Asp
13 18 23 28

gct cag aac ctg atc ggg atc agc att gga gga ggg gcc cag tac tgt 387
Ala Gln Asn Leu Ile Gly Ile Ser Ile Gly Gly Gly Ala Gln Tyr Cys
29 34 39 44

ccc tgc ctc tat atc gtc cag gta ttt gac aac acc cca gca gcc ttg 435
Pro Cys Leu Tyr Ile Val Gln Val Phe Asp Asn Thr Pro Ala Ala Leu
45 50 55 60

gac ggc aca gtg gca gct ggc gat gag atc acc ggt gtc aat ggc agg 483
Asp Gly Thr Val Ala Ala Gly Asp Glu Ile Thr Gly Val Asn Gly Arg
61 66 71 76

tca atc aaa ggg aaa act aag gtg gag gtg gcg aag atg att cag gag 531
Ser Ile Lys Gly Lys Thr Lys Val Glu Val Ala Lys Met Ile Gln Glu
77 82 87 92

gtg aag ggg gag gtg acc atc cac tac aac aag ctg cag gcg gac ccc 579
Val Lys Gly Glu Val Thr Ile His Tyr Asn Lys Leu Gln Ala Asp Pro
93 98 103 108

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aag cag ggc atg tcc ctg gac att gtg ttg aag aaa gtc aag cac cgg      627
Lys Gln Gly Met Ser Leu Asp Ile Val Leu Lys Lys Val Lys His Arg
109                 114                 119                 124

ctg gtg gag aac atg agt tca ggg acc gca gat gct ctg ggc ctg agc      675
Leu Val Glu Asn Met Ser Ser Gly Thr Ala Asp Ala Leu Gly Leu Ser
125                 130                 135                 140

cgg gcc atc ctg tgc aat gat ggg ctt gtc aag agg cta gag gag ctg      723
Arg Ala Ile Leu Cys Asn Asp Gly Leu Val Lys Arg Leu Glu Glu Leu
141                 146                 151                 156

gag cgg acc gct gag cta tac aaa ggg atg acg gaa cac acc aag aac      771
Glu Arg Thr Ala Glu Leu Tyr Lys Gly Met Thr Glu His Thr Lys Asn
157                 162                 167                 172

ctc cta cgg gcc ttt tat gag ctg tcg cag act cac cgg gcc ttt ggg      819
Leu Leu Arg Ala Phe Tyr Glu Leu Ser Gln Thr His Arg Ala Phe Gly
173                 178                 183                 188

gac gtg ttc tcc gtg atc ggg gtg cgg gag ccc cag cca gct gcg agc      867
Asp Val Phe Ser Val Ile Gly Val Arg Glu Pro Gln Pro Ala Ala Ser
189                 194                 199                 204

gag gct ttt gtg aag ttc gcc gat gcc cac cgc agc atc gag aag ttc      915
Glu Ala Phe Val Lys Phe Ala Asp Ala His Arg Ser Ile Glu Lys Phe
205                 210                 215                 220

ggc att cgg ctt ctg aaa acc atc aag ccg atg ctg acg gat ctg aac      963
Gly Ile Arg Leu Leu Lys Thr Ile Lys Pro Met Leu Thr Asp Leu Asn
221                 226                 231                 236

acg tac ctc aac aaa gcc atc ccg gac act cgc ctc acc atc aag aag     1011
Thr Tyr Leu Asn Lys Ala Ile Pro Asp Thr Arg Leu Thr Ile Lys Lys
237                 242                 247                 252

tac ctg gac gtg aag ttt gag tac ctg tcg tac tgc ctg aag gtg aag     1059
Tyr Leu Asp Val Lys Phe Glu Tyr Leu Ser Tyr Cys Leu Lys Val Lys
253                 258                 263                 268

gag atg gat gac gag gaa tac agc tgc att gcc cta ggc gag ccc ctt     1107
Glu Met Asp Asp Glu Glu Tyr Ser Cys Ile Ala Leu Gly Glu Pro Leu
269                 274                 279                 284

tac cgg gtg agc acc ggc aac tat gag tac cgc ctg atc ctg cgc tgc     1155
Tyr Arg Val Ser Thr Gly Asn Tyr Glu Tyr Arg Leu Ile Leu Arg Cys
285                 290                 295                 300

cgc cag gag gcg cgc gcc cgc ttc tcc cag atg cgc aag gat gtg ctg     1203
Arg Gln Glu Ala Arg Ala Arg Phe Ser Gln Met Arg Lys Asp Val Leu
301                 306                 311                 316

gag aag atg gag ctg ctg gac cag aag cac gtc cag gac atc gtg ttc     1251
Glu Lys Met Glu Leu Leu Asp Gln Lys His Val Gln Asp Ile Val Phe
317                 322                 327                 332
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cag ctg cag cgc ctc gtg tcc acc atg tcc aag tac tac aac gac tgc     1299
Gln Leu Gln Arg Leu Val Ser Thr Met Ser Lys Tyr Tyr Asn Asp Cys
333                 338                 343                 348

tac gca gtg ctg cgg gat gcc gac gtc ttc ccc atc gag gta gac ctg     1347
Tyr Ala Val Leu Arg Asp Ala Asp Val Phe Pro Ile Glu Val Asp Leu
349                 354                 359                 364

gcg cac acc aca ttg gcc tat ggc ctc aac cag gag gag ttc aca gat     1395
Ala His Thr Thr Leu Ala Tyr Gly Leu Asn Gln Glu Glu Phe Thr Asp
365                 370                 375                 380

ggg gag gag gag gag gag gag gaa gac acg gca gct ggg gag ccg tcc     1443
Gly Glu Glu Glu Glu Glu Glu Glu Asp Thr Ala Ala Gly Glu Pro Ser
381                 386                 391                 396

agg gat aca cga ggg gct gct ggg ccc ttg gac aag ggt gga agc tgg     1491
Arg Asp Thr Arg Gly Ala Ala Gly Pro Leu Asp Lys Gly Gly Ser Trp
397                 402                 407                 412

tgt gac tcc tga gtg ccccgcggct gtggtgccgg gggcagggtg cgtgggagga     1546
Cys Asp Ser  *
413

cggagcctgg gagcggggcg gggccgccgc gcaaggggggc gacgcataaa ggcctgctgg   1606

cttggggcgc ctgcctccct gctcctctgt cctcgcacag cgaacctggg ctcctgccca   1666

ggacaggcac cagggtcatg gcctgggacc tggacactgg cccctccacc ctccctcccc   1726

tcccggctcc ccggccagag ggagagcttg gtctctggac ctgccttagg aaggagaggg   1786

agggcaggaa ggaaaagaaa ggacttggag gtggcaggag tccgagccct gctccttgtg   1846

ggcgctcaca ctgcccccgg agcctgctgg gagtggggcc agccgtggac agctgaggtt   1906

ggggtcaatg cctcctgggc acccttgcct cgccccagac cggcccgtcc agtccccatc   1966

acacctcggc ggcctttatt tattctgttc ccccagctcg gccacttctc tgaaggaggg   2026

ctgggttctg ggcctgtatc gaataaacac aaacctggat ggcgcaaaaa aaaaaaaa     2084
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<210> 241
<211> 812
<212> DNA
<213> Homo sapiens

<220>
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<222> (369)..(608)

<400> 241
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tattcgcttc cgggtgagag gtgcccggtc gccccagcaa ccaagtcgca cctggagctg    120

tcctagcgcc tagttctctc ccggccgcag agctggccgc ccaggggggag tcgcagagtt    180

tggaagatct ctctaacacc tctcggccaa cttcagaagt gtataagatc agctttatct    240

ttccaaatgg agacaagtat gatggtgact gtacaagaac atcttctgga atctacgaga    300

gaaatggaat aggtattcat accactccta atgggattgt ctacacagga agctggaaag    360

atgacaag atg aat ggt ttt gga aga ctt gag cat ttt tca gga gca gta      410
         Met Asn Gly Phe Gly Arg Leu Glu His Phe Ser Gly Ala Val
           1               5                  10

tat gaa gga caa ttt aag gat aat atg ttt cat gga ctg ggg act tac      458
Tyr Glu Gly Gln Phe Lys Asp Asn Met Phe His Gly Leu Gly Thr Tyr
 15                  20                  25                  30

aca ttc cca aat ggg gca aag tat act gga aat ttc aat gaa aat agg      506
Thr Phe Pro Asn Gly Ala Lys Tyr Thr Gly Asn Phe Asn Glu Asn Arg
 31                  36                  41                  46

gtg gaa ggt gaa ggg gaa tat act gat atc caa gga cta gaa tgg agt      554
Val Glu Gly Glu Gly Glu Tyr Thr Asp Ile Gln Gly Leu Glu Trp Ser
 47                  52                  57                  62

ggt aac ttt cat ttt aca gct gct cca gac ctg aaa tta aag ctt cac      602
Gly Asn Phe His Phe Thr Ala Ala Pro Asp Leu Lys Leu Lys Leu His
 63                  68                  73                  78

atg tag atgtgatgtt aaattaaagt tgaaatgtag taattgaagc ttttagttgt      658
Met  *
 79

aaggaaagca acttaatctg ttatttgaaa tgacttcata cactacccct ataagtttgc    718

caataaaacc atcacctgct tacacctttt tgaactttat attcattgtc ttacaattag    778

tttaaaataa atgacatgat tcaaaaaaaa aaaa                               812
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<210> 242
<211> 885
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (309)..(731)

<400> 242

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cgatttcgtg taagaaggca gcggacggac agtgctcgct ccccgcttca tggcggtcgg     60

tgaccctcac ccacgtcgaa tatcctgcag gtgatctctc cggccacctc cttgcctacc    120
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tgagcctcag ccctgtattt gtcatcgtcg gtttcgtgac cctcatcata tttaagcggg    180

agctgcacac gatctccttc cttgggggcc tggcactgaa cgaggggtc aactggctga    240

tcaaaaacgt catccaggag ccacggccct gtggaggccc ccacacagca gtgggcacca    300

agtacggg atg ccc tcc agc cat tcc cag ttt atg tgg ttc ttc tcc gtc     350
         Met Pro Ser Ser His Ser Gln Phe Met Trp Phe Phe Ser Val
           1               5                  10

tat tcc ttc ctt ttc ctg tat tta aga atg cac caa aca aac aac gcc      398
Tyr Ser Phe Leu Phe Leu Tyr Leu Arg Met His Gln Thr Asn Asn Ala
 15                  20                  25                  30

agg ttc ctg gac ttg ctg tgg agg cac gtg ctc tcc ctg gga ctc ctc      446
Arg Phe Leu Asp Leu Leu Trp Arg His Val Leu Ser Leu Gly Leu Leu
 31                  36                  41                  46

gct gtg gcc ttc cta gtc tcc tac agc agg gtc tac ctg ctg tac cac      494
Ala Val Ala Phe Leu Val Ser Tyr Ser Arg Val Tyr Leu Leu Tyr His
 47                  52                  57                  62

acc tgg agc cag gtg ctc tat gga ggc atc gct gga ggc ctc atg gcc      542
Thr Trp Ser Gln Val Leu Tyr Gly Gly Ile Ala Gly Gly Leu Met Ala
 63                  68                  73                  78

atc gcc tgg ttc atc ttc acc cag gag gtc ctc acc ccg ctg ttc ccc      590
Ile Ala Trp Phe Ile Phe Thr Gln Glu Val Leu Thr Pro Leu Phe Pro
 79                  84                  89                  94

agg ata gca gcc tgg cct gtc tcc gag ttc ttc cta atc cga gac aca      638
Arg Ile Ala Ala Trp Pro Val Ser Glu Phe Phe Leu Ile Arg Asp Thr
 95                 100                 105                 110

agc ctc att ccc aac gta ctc tgg ttt gag tac acg gta acc cgg gca      686
Ser Leu Ile Pro Asn Val Leu Trp Phe Glu Tyr Thr Val Thr Arg Ala
111                 116                 121                 126

gaa gcc agg aac aga caa cgc aag ctg ggg acg aaa ctg cag tga cca      734
Glu Ala Arg Asn Arg Gln Arg Lys Leu Gly Thr Lys Leu Gln  *
127                 132                 137

gtgggtgtgg ctgggtccag cctccagatc tggcccgcac gatgccttgc aggatggaca    794

ggatgacaga cagggacgaa gcagagacct ctacagaccc aagtgtattg cggccgctct    854

agaggatcca agcttacggg cgcggacgtc t                                   885
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<210> 243
<211> 2718
<212> DNA
<213> Homo sapiens

<220>

Docket No. 5050-0150-2

<221> CDS
<222> (548)..(2650)

<220>
<221> misc_feature
<222> (1)...(2718)
<223> n = a,t,c or g

<400> 243

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ccggaattcc cgggtcgacg atttcgtatg agaggctgtg tgagangctg cagccgccgg     60

cagaggagac ctcagcatca tctagagccc agcgctggcc ctgcctccgc ctgccccgcc    120

gccgccgtcg ccgtttctgt tcctgctact gtcccaccta aacaactccc gttacacgga    180

caagtgaaca actgtggctg tcctctcctt ttcttcctcc tcttccaact ccttctcctc    240

ctcccacttc ccagccgcag cagaaagccc ccaacccaac tgacactggc acaactgcaa    300

acggtgtcat ccgcacaact ttatctcgct cctcgggctc ccctaaggca ttggacccat    360

cgccgcgtct tttatttttt gcaaagttgc atcgctgtac atatttttgt ccccgccacc    420

tccctctgtc tctggagtgc cctacagccc cgcaaactcc tcctggagct gcgccctagt    480

gcccctgctg ggcagtggcg ttcccccccca tcctcccgcg cccagcccct gctgctctgg    540

gcagacg  atg ctg aag atg ctc tcc ttt aag ctg ctg ctg ctg gcc gtg      589
         Met Leu Lys Met Leu Ser Phe Lys Leu Leu Leu Leu Ala Val
           1               5                  10

gct ctg ggc ttc ttt gaa gga gat gct aag ttt ggg gaa aga aac gaa      637
Ala Leu Gly Phe Phe Glu Gly Asp Ala Lys Phe Gly Glu Arg Asn Glu
 15                  20                  25                  30

ggg agc gga gca agg agg aga agg tgc ctg aat ggg aac ccc ccg aag      685
Gly Ser Gly Ala Arg Arg Arg Arg Cys Leu Asn Gly Asn Pro Pro Lys
 31                  36                  41                  46

cgc ctg aaa agg aga gac agg agg atg atg tcc cag ctg gag ctg ctg      733
Arg Leu Lys Arg Arg Asp Arg Arg Met Met Ser Gln Leu Glu Leu Leu
 47                  52                  57                  62

agt ggg gga gag atg ctg tgc ggt ggc ttc tac cct cgg ctg tcc tgc      781
Ser Gly Gly Glu Met Leu Cys Gly Gly Phe Tyr Pro Arg Leu Ser Cys
 63                  68                  73                  78

tgc ctg cgg agt gac agc ccg ggg cta ggg cgc ctg gag aat aag ata      829
Cys Leu Arg Ser Asp Ser Pro Gly Leu Gly Arg Leu Glu Asn Lys Ile
 79                  84                  89                  94

ttt tct gtt acc aac aac aca gaa tgt ggg aag tta ctg gag gaa atc      877
Phe Ser Val Thr Asn Asn Thr Glu Cys Gly Lys Leu Leu Glu Glu Ile
 95                 100                 105                 110

aaa tgt gca ctt tgc tct cca cat tct caa agc ctg ttc cac tca cct      925
Lys Cys Ala Leu Cys Ser Pro His Ser Gln Ser Leu Phe His Ser Pro
```

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111                 116                 121                 126

gag aga gaa gtc ttg gaa aga gac cta gta ctt cct ctg ctc tgc aaa      973
Glu Arg Glu Val Leu Glu Arg Asp Leu Val Leu Pro Leu Leu Cys Lys
127                 132                 137                 142

gac tat tgc aaa gaa ttc ttt tac act tgc cga ggc cat att cca ggt     1021
Asp Tyr Cys Lys Glu Phe Phe Tyr Thr Cys Arg Gly His Ile Pro Gly
143                 148                 153                 158

ttc ctt caa aca act gcg gat gag ttt tgc ttt tac tat gca aga aaa     1069
Phe Leu Gln Thr Thr Ala Asp Glu Phe Cys Phe Tyr Tyr Ala Arg Lys
159                 164                 169                 174

gat ggt ggg ttg tgc ttt cca gat ttt cca aga aaa caa gtc aga gga     1117
Asp Gly Gly Leu Cys Phe Pro Asp Phe Pro Arg Lys Gln Val Arg Gly
175                 180                 185                 190

cca gca tct aac tac ttg gac cag atg gaa gaa tat gac aaa gtg gaa     1165
Pro Ala Ser Asn Tyr Leu Asp Gln Met Glu Glu Tyr Asp Lys Val Glu
191                 196                 201                 206

gag atc agc aga aag cac aaa cac aac tgc ttc tgt att cag gag gtt     1213
Glu Ile Ser Arg Lys His Lys His Asn Cys Phe Cys Ile Gln Glu Val
207                 212                 217                 222

gtg agt ggg ctg cgg cag ccc gtt ggt gcc ctg cat agt ggg gat ggc     1261
Val Ser Gly Leu Arg Gln Pro Val Gly Ala Leu His Ser Gly Asp Gly
223                 228                 233                 238

tcg caa cgt ctc ttc att ctg gaa aaa gaa ggt tat gtg aag ata ctt     1309
Ser Gln Arg Leu Phe Ile Leu Glu Lys Glu Gly Tyr Val Lys Ile Leu
239                 244                 249                 254

acc cct gaa gga gaa att ttc aag gag cct tat ttg gac att cac aaa     1357
Thr Pro Glu Gly Glu Ile Phe Lys Glu Pro Tyr Leu Asp Ile His Lys
255                 260                 265                 270

ctt gtt caa agt gga ata aag gga gga gat gaa aga gga ctg cta agc     1405
Leu Val Gln Ser Gly Ile Lys Gly Gly Asp Glu Arg Gly Leu Leu Ser
271                 276                 281                 286

ctc gca ttc cat ccc aat tac aag aaa aat gga aag ttg tat gtg tcc     1453
Leu Ala Phe His Pro Asn Tyr Lys Lys Asn Gly Lys Leu Tyr Val Ser
287                 292                 297                 302

tat acc acc aac caa gaa cgg tgg gct atc ggg cct cat gac cac att     1501
Tyr Thr Thr Asn Gln Glu Arg Trp Ala Ile Gly Pro His Asp His Ile
303                 308                 313                 318

ctt agg gtt gtg gaa tac aca gta tcc aga aaa aat cca cac caa gtt     1549
Leu Arg Val Val Glu Tyr Thr Val Ser Arg Lys Asn Pro His Gln Val
319                 324                 329                 334

gat ttg aga aca gcc aga gtc ttt ctt gaa gtt gca gaa ctc cac aga     1597
Asp Leu Arg Thr Ala Arg Val Phe Leu Glu Val Ala Glu Leu His Arg
335                 340                 345                 350
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aag cat ctg gga gga caa ctg ctc ttt ggc cct gac ggc ttt ttg tac     1645
Lys His Leu Gly Gly Gln Leu Leu Phe Gly Pro Asp Gly Phe Leu Tyr
351                 356                 361                 366

atc att ctt ggt gat ggg atg att aca ctg gat gat atg gaa gaa atg     1693
Ile Ile Leu Gly Asp Gly Met Ile Thr Leu Asp Asp Met Glu Glu Met
367                 372                 377                 382

gat ggg tta agt gat ttc aca ggc tca gtg cta cgg ctg gat gtg gac     1741
Asp Gly Leu Ser Asp Phe Thr Gly Ser Val Leu Arg Leu Asp Val Asp
383                 388                 393                 398

aca gac atg tgc aac gtg cct tat tcc ata cca agg agc aac cca cac     1789
Thr Asp Met Cys Asn Val Pro Tyr Ser Ile Pro Arg Ser Asn Pro His
399                 404                 409                 414

ttc aac agc acc aac cag ccc ccc gaa gtg ttt gct cat ggg ctc cac     1837
Phe Asn Ser Thr Asn Gln Pro Pro Glu Val Phe Ala His Gly Leu His
415                 420                 425                 430

gat cca ggc aga tgt gct gtg gat aga cat ccc act gat ata aac atc     1885
Asp Pro Gly Arg Cys Ala Val Asp Arg His Pro Thr Asp Ile Asn Ile
431                 436                 441                 446

aat tta acg ata ctg tgt tca gac tcc aat gga aaa aac aga tca tca     1933
Asn Leu Thr Ile Leu Cys Ser Asp Ser Asn Gly Lys Asn Arg Ser Ser
447                 452                 457                 462

gcc aga att cta cag ata ata aag ggg aaa gat tat gaa agt gag cca     1981
Ala Arg Ile Leu Gln Ile Ile Lys Gly Lys Asp Tyr Glu Ser Glu Pro
463                 468                 473                 478

tca ctt tta gaa ttc aag cca ttc agt aat ggt cct ttg gtt ggt gga     2029
Ser Leu Leu Glu Phe Lys Pro Phe Ser Asn Gly Pro Leu Val Gly Gly
479                 484                 489                 494

ttt gta tac cgg ggc tgc cag tca gaa aga ttg tat gga agc tac gtg     2077
Phe Val Tyr Arg Gly Cys Gln Ser Glu Arg Leu Tyr Gly Ser Tyr Val
495                 500                 505                 510

ttt gga gat cgt aat ggg aat ttc cta act ctc cag caa agt cct gtg     2125
Phe Gly Asp Arg Asn Gly Asn Phe Leu Thr Leu Gln Gln Ser Pro Val
511                 516                 521                 526

aca aag cag tgg caa gaa aaa cca ctc tgt ctc ggc act agt ggg tcc     2173
Thr Lys Gln Trp Gln Glu Lys Pro Leu Cys Leu Gly Thr Ser Gly Ser
527                 532                 537                 542

tgt aga ggc tac ttt tcc ggt cac atc ttg gga ttt gga gaa gat gaa     2221
Cys Arg Gly Tyr Phe Ser Gly His Ile Leu Gly Phe Gly Glu Asp Glu
543                 548                 553                 558

cta ggt gaa gtt tac att tta tca agc agt aaa agt atg acc cag act     2269
Leu Gly Glu Val Tyr Ile Leu Ser Ser Ser Lys Ser Met Thr Gln Thr
559                 564                 569                 574
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cac aat gga aaa ctc tac aaa att gta gat ccc aaa aga cct tta atg     2317
His Asn Gly Lys Leu Tyr Lys Ile Val Asp Pro Lys Arg Pro Leu Met
575                 580                 585                 590

cct gag gaa tgc aga gcc acg gta caa cct gca cag aca ctg act tca     2365
Pro Glu Glu Cys Arg Ala Thr Val Gln Pro Ala Gln Thr Leu Thr Ser
591                 596                 601                 606

gag tgc tcc agg ctc tgt cga aac ggc tac tgc acc ccc acg gga aag     2413
Glu Cys Ser Arg Leu Cys Arg Asn Gly Tyr Cys Thr Pro Thr Gly Lys
607                 612                 617                 622

tgc tgc tgc agt cca ggc tgg gag ggg gac ttc tgc aga act gca aaa     2461
Cys Cys Cys Ser Pro Gly Trp Glu Gly Asp Phe Cys Arg Thr Ala Lys
623                 628                 633                 638

tgt gag cca gca tgt cgt cat gga ggt gtc tgt gtt aga ccg aac aag     2509
Cys Glu Pro Ala Cys Arg His Gly Gly Val Cys Val Arg Pro Asn Lys
639                 644                 649                 654

tgc ctc tgt aaa aaa gga tat ctt ggt cct caa tgt gaa caa gtg gac     2557
Cys Leu Cys Lys Lys Gly Tyr Leu Gly Pro Gln Cys Glu Gln Val Asp
655                 660                 665                 670

aga aac atc cgc aga gtg acc agg gca ggt att ctt gat cag atc att     2605
Arg Asn Ile Arg Arg Val Thr Arg Ala Gly Ile Leu Asp Gln Ile Ile
671                 676                 681                 686

gac atg aca tct tac ttg ctg gat cta aca agt tac att gta tag ttt     2653
Asp Met Thr Ser Tyr Leu Leu Asp Leu Thr Ser Tyr Ile Val  *
687                 692                 697

ctgggactgt ttgaatattc tattccaatg ggcatttatt ttttatcctg tcattaaaaa   2713

aaaaa                                                               2718
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<210> 244
<211> 3042
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (548)..(2461)

<220>
<221> misc_feature
<222> (1)...(3042)
<223> n = a,t,c or g

<400> 244

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cagaggagac ctcagcatca tctagagccc agcgctggcc ctgcctccgc ctgccccgcc    120
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gccgccgtcg ccgtttctgt tcctgctact gtcccaccta aacaactccc gttacacgga    180

caagtgaaca actgtggctg tcctctcctt ttcttcctcc tcttccaact ccttctcctc    240

ctcccacttc ccagccgcag cagaaagccc ccaacccaac tgacactggc acaactgcaa    300

acggtgtcat ccgcacaact ttatctcgct cctcgggctc ccctaaggca ttggacccat    360

cgccgcgtct tttatttttt gcaaagttgc atcgctgtac atatttttgt ccccgccacc    420

tccctctgtc tctggagtgc cctacagccc cgcaaactcc tcctggagct gcgccctagt    480

gcccctgctg ggcagtggcg ttcccccccca tcctcccgcg cccagcccct gctgctctgg    540

gcagacg  atg ctg aag atg ctc tcc ttt aag ctg ctg ctg ctg gcc gtg      589
         Met Leu Lys Met Leu Ser Phe Lys Leu Leu Leu Leu Ala Val
           1               5                  10

gct ctg ggc ttc ttt gaa gga gat gct aag ttt ggg gaa aga aac gaa      637
Ala Leu Gly Phe Phe Glu Gly Asp Ala Lys Phe Gly Glu Arg Asn Glu
 15                  20                  25                  30

ggg agc gga gca agg agg aga agg tgc ctg aat ggg aac ccc ccg aag      685
Gly Ser Gly Ala Arg Arg Arg Arg Cys Leu Asn Gly Asn Pro Pro Lys
 31                  36                  41                  46

cgc ctg aaa agg aga gac agg agg atg atg tcc cag ctg gag ctg ctg      733
Arg Leu Lys Arg Arg Asp Arg Arg Met Met Ser Gln Leu Glu Leu Leu
 47                  52                  57                  62

agt ggg gga gag atg ctg tgc ggt ggc ttc tac cct cgg ctg tcc tgc      781
Ser Gly Gly Glu Met Leu Cys Gly Gly Phe Tyr Pro Arg Leu Ser Cys
 63                  68                  73                  78

tgc ctg cgg agt gac agc ccg ggg cta ggg cgc ctg gag aat aag ata      829
Cys Leu Arg Ser Asp Ser Pro Gly Leu Gly Arg Leu Glu Asn Lys Ile
 79                  84                  89                  94

ttt tct gtt acc aac aac aca gaa tgt ggg aag tta ctg gag gaa atc      877
Phe Ser Val Thr Asn Asn Thr Glu Cys Gly Lys Leu Leu Glu Glu Ile
 95                 100                 105                 110

aaa tgt gca ctt tgc tct cca cat tct caa agc ctg ttc cac tca cct      925
Lys Cys Ala Leu Cys Ser Pro His Ser Gln Ser Leu Phe His Ser Pro
111                 116                 121                 126

gag aga gaa gtc ttg gaa aga gac cta gta ctt cct ctg ctc tgc aaa      973
Glu Arg Glu Val Leu Glu Arg Asp Leu Val Leu Pro Leu Leu Cys Lys
127                 132                 137                 142

gac tat tgc aaa gaa ttc ttt tac act tgc cga ggc cat att cca ggt     1021
Asp Tyr Cys Lys Glu Phe Phe Tyr Thr Cys Arg Gly His Ile Pro Gly
143                 148                 153                 158

ttc ctt caa aca act gcg gat gag ttt tgc ttt tac tat gca aga aaa     1069
Phe Leu Gln Thr Thr Ala Asp Glu Phe Cys Phe Tyr Tyr Ala Arg Lys
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159                 164                 169                 174

gat ggt ggg ttg tgc ttt cca gat ttt cca aga aaa caa gtc aga gga     1117
Asp Gly Gly Leu Cys Phe Pro Asp Phe Pro Arg Lys Gln Val Arg Gly
175                 180                 185                 190

cca gca tct aac tac ttg gac cag atg gaa gaa tat gac aaa gtg gaa     1165
Pro Ala Ser Asn Tyr Leu Asp Gln Met Glu Glu Tyr Asp Lys Val Glu
191                 196                 201                 206

gag atc agc aga aag cac aaa cac aac tgc ttc tgt att cag gag gtt     1213
Glu Ile Ser Arg Lys His Lys His Asn Cys Phe Cys Ile Gln Glu Val
207                 212                 217                 222

gtg agt ggg ctg cgg cag ccc gtt ggt gcc ctg cat agt ggg gat ggc     1261
Val Ser Gly Leu Arg Gln Pro Val Gly Ala Leu His Ser Gly Asp Gly
223                 228                 233                 238

tcg caa cgt ctc ttc att ctg gaa aaa gaa ggt tat gtg aag ata ctt     1309
Ser Gln Arg Leu Phe Ile Leu Glu Lys Glu Gly Tyr Val Lys Ile Leu
239                 244                 249                 254

acc cct gaa gga gaa att ttc aag gag cct tat ttg gac att cac aaa     1357
Thr Pro Glu Gly Glu Ile Phe Lys Glu Pro Tyr Leu Asp Ile His Lys
255                 260                 265                 270

ctt gtt caa agt gga ata aag gga gga gat gaa aga gga ctg cta agc     1405
Leu Val Gln Ser Gly Ile Lys Gly Gly Asp Glu Arg Gly Leu Leu Ser
271                 276                 281                 286

ctc gca ttc cat ccc aat tac aag aaa aat gga aag ttg tat gtg tcc     1453
Leu Ala Phe His Pro Asn Tyr Lys Lys Asn Gly Lys Leu Tyr Val Ser
287                 292                 297                 302

tat acc acc aac caa gaa cgg tgg gct atc ggg cct cat gac cac att     1501
Tyr Thr Thr Asn Gln Glu Arg Trp Ala Ile Gly Pro His Asp His Ile
303                 308                 313                 318

ctt agg gtt gtg gaa tac aca gta tcc aga aaa aat cca cac caa gtt     1549
Leu Arg Val Val Glu Tyr Thr Val Ser Arg Lys Asn Pro His Gln Val
319                 324                 329                 334

gat ttg aga aca gcc aga gtc ttt ctt gaa gtt gca gaa ctc cac aga     1597
Asp Leu Arg Thr Ala Arg Val Phe Leu Glu Val Ala Glu Leu His Arg
335                 340                 345                 350

aag cat ctg gga gga caa ctg ctc ttt ggc cct gac ggc ttt ttg tac     1645
Lys His Leu Gly Gly Gln Leu Leu Phe Gly Pro Asp Gly Phe Leu Tyr
351                 356                 361                 366

atc att ctt ggt gat ggg atg att aca ctg gat gat atg gaa gaa atg     1693
Ile Ile Leu Gly Asp Gly Met Ile Thr Leu Asp Asp Met Glu Glu Met
367                 372                 377                 382

gat ggg tta agt gat ttc aca ggc tca gtg cta cgg ctg gat gtg gac     1741
Asp Gly Leu Ser Asp Phe Thr Gly Ser Val Leu Arg Leu Asp Val Asp
383                 388                 393                 398
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aca gac atg tgc aac gtg cct tat tcc ata cca agg agc aac cca cac     1789
Thr Asp Met Cys Asn Val Pro Tyr Ser Ile Pro Arg Ser Asn Pro His
399                 404                 409                 414

ttc aac agc acc aac cag ccc ccc gaa gtg ttt gct cat ggg ctc cac     1837
Phe Asn Ser Thr Asn Gln Pro Pro Glu Val Phe Ala His Gly Leu His
415                 420                 425                 430

gat cca ggc aga tgt gct gtg gat aga cat ccc act gat ata aac atc     1885
Asp Pro Gly Arg Cys Ala Val Asp Arg His Pro Thr Asp Ile Asn Ile
431                 436                 441                 446

aat tta acg ata ctg tgt tca gac tcc aat gga aaa aac aga tca tca     1933
Asn Leu Thr Ile Leu Cys Ser Asp Ser Asn Gly Lys Asn Arg Ser Ser
447                 452                 457                 462

gcc aga att cta cag ata ata aag ggg aaa gat tat gaa agt gag cca     1981
Ala Arg Ile Leu Gln Ile Ile Lys Gly Lys Asp Tyr Glu Ser Glu Pro
463                 468                 473                 478

tca ctt tta gaa ttc aag cca ttc agt aat ggt cct ttg gtt ggt gga     2029
Ser Leu Leu Glu Phe Lys Pro Phe Ser Asn Gly Pro Leu Val Gly Gly
479                 484                 489                 494

ttt gta tac cgg ggc tgc cag tca gaa aga ttg tat gga agc tac gtg     2077
Phe Val Tyr Arg Gly Cys Gln Ser Glu Arg Leu Tyr Gly Ser Tyr Val
495                 500                 505                 510

ttt gga gat cgt aat ggg aat ttc cta act ctc cag caa agt cct gtg     2125
Phe Gly Asp Arg Asn Gly Asn Phe Leu Thr Leu Gln Gln Ser Pro Val
511                 516                 521                 526

aca aag cag tgg caa gaa aaa cca ctc tgt ctc ggc act agt ggg tcc     2173
Thr Lys Gln Trp Gln Glu Lys Pro Leu Cys Leu Gly Thr Ser Gly Ser
527                 532                 537                 542

tgt aga ggc tac ttt tcc ggt cac atc ttg gga ttt gga gaa gat gaa     2221
Cys Arg Gly Tyr Phe Ser Gly His Ile Leu Gly Phe Gly Glu Asp Glu
543                 548                 553                 558

cta ggt gaa gtt tac att tta tca agc agt aaa agt atg acc cag act     2269
Leu Gly Glu Val Tyr Ile Leu Ser Ser Ser Lys Ser Met Thr Gln Thr
559                 564                 569                 574

cac aat gga aaa ctc tac aaa att gta gat ccc aaa aga cct tta atg     2317
His Asn Gly Lys Leu Tyr Lys Ile Val Asp Pro Lys Arg Pro Leu Met
575                 580                 585                 590

cct gag gaa tgc aga gcc acg gta caa cct gca cag aca ctg act tca     2365
Pro Glu Glu Cys Arg Ala Thr Val Gln Pro Ala Gln Thr Leu Thr Ser
591                 596                 601                 606

gag tgc tcc agg ctc tgt cga aac ggc tac tgc acc ccc acg gga aag     2413
Glu Cys Ser Arg Leu Cys Arg Asn Gly Tyr Cys Thr Pro Thr Gly Lys
607                 612                 617                 622
```

```
tgc tgc tgc agt cca ggc tgg gag ggg gac ttc tgc aga act ggg taa     2461
Cys Cys Cys Ser Pro Gly Trp Glu Gly Asp Phe Cys Arg Thr Gly  *
623                 628                 633                 638

ccctgaaaag gtttgctcag aacatccttt gctggccaac tgcactgact ccagaaagag   2521

acttctaagt gtaatcagag agcaaagcat atgctgtctg ccccctggaa gcaagaggaa   2581

ggaagaatcc aagggagttt atatggcgga tattccaccc aaccaaaatc caaaactgac   2641

tgttcctttc tgttgcactg gagttgcttg agcctctgtg tctccccctc aggctgggcc   2701

actcccatgt tgagatccta ccttgaagga atgggaacat agagcttggg aggccctctg   2761

tagagaatgc tcctgtgaag cagagatttc aaaggactaa aatcttcatt ttaaatagag   2821

ttaattttgc aaagggttgc aattgtttct catgatctct gcttctctag aaatgtctct   2881

cattctctgc tgagttcagg tctccaaata actatgggtg taaaagcctg tttcctactt   2941

gcatatttat ctttcagatc attttgtaac tatctccctc ctttttttccc tcgcttccct   3001

tattcagcaa atatttggtg gtctcatgct cagtcctggt t                       3042
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<210> 245
<211> 847
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (86)..(703)

<400> 245

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tggcctccat ttgaatgctg tcgcctgcac gaccggtccg gaattcccgg gtcgacccac     60

cgtccgcccc agccccccag gatac  atg tca gat caa gag gag gac atg tgc     112
                             Met Ser Asp Gln Glu Glu Asp Met Cys
                               1               5

ttt gaa gga atg aaa ccc gta aac caa act gca gcc tca aac aag gga      160
Phe Glu Gly Met Lys Pro Val Asn Gln Thr Ala Ala Ser Asn Lys Gly
 10                  15                  20                  25

ctc aga ggt ctc ctc cac cca cag cag ttg cac ttg ctg agc agg cag      208
Leu Arg Gly Leu Leu His Pro Gln Gln Leu His Leu Leu Ser Arg Gln
 26                  31                  36                  41

ctt gag gac cca aat ggt agc ttt tct aac gct gag atg agt gaa ctg      256
Leu Glu Asp Pro Asn Gly Ser Phe Ser Asn Ala Glu Met Ser Glu Leu
 42                  47                  52                  57

agt gtg gca cag aaa cca gaa aaa ctt ttg gag cgc tgc aag tac tgg      304
Ser Val Ala Gln Lys Pro Glu Lys Leu Leu Glu Arg Cys Lys Tyr Trp
```

```
 58                  63                  68                  73

cct gct tgt aaa aat ggg gat gag tgt gcc tac cat cac ccc atc tca      352
Pro Ala Cys Lys Asn Gly Asp Glu Cys Ala Tyr His His Pro Ile Ser
 74                  79                  84                  89

ccc tgc aaa gcc ttc ccc aat tgt aaa ttt gct gaa aaa tgt ttg ttt      400
Pro Cys Lys Ala Phe Pro Asn Cys Lys Phe Ala Glu Lys Cys Leu Phe
 90                  95                 100                 105

gtt cac cca aat tgt aaa tat gat gca aag tgt act aaa cca gat tgt      448
Val His Pro Asn Cys Lys Tyr Asp Ala Lys Cys Thr Lys Pro Asp Cys
106                 111                 116                 121

ccc ttc act cat gtg agt aga aga att cca gta ctg tct cca aaa cca      496
Pro Phe Thr His Val Ser Arg Arg Ile Pro Val Leu Ser Pro Lys Pro
122                 127                 132                 137

gca gtt gca cca cca gca cca cct tcc agt agt cag ctc tgc cgt tac      544
Ala Val Ala Pro Pro Ala Pro Pro Ser Ser Ser Gln Leu Cys Arg Tyr
138                 143                 148                 153

ttc cct gct tgt aag aag atg gaa tgt ccc ttc tat cat cca aaa cat      592
Phe Pro Ala Cys Lys Lys Met Glu Cys Pro Phe Tyr His Pro Lys His
154                 159                 164                 169

tgt agg ttt aac act caa tgt aca aga ccg gac tgc aca ttc tac cat      640
Cys Arg Phe Asn Thr Gln Cys Thr Arg Pro Asp Cys Thr Phe Tyr His
170                 175                 180                 185

ccc acc att aat gtc cca cca cga cat gcc ttg aaa tgg att cga cct      688
Pro Thr Ile Asn Val Pro Pro Arg His Ala Leu Lys Trp Ile Arg Pro
186                 191                 196                 201

caa acc agc gaa tag cacccagtcc tgcctggcag aagatcatgc agtttggaag      743
Gln Thr Ser Glu  *
202

ttttcatgta ctgatgaaag atactctaca gaacttgtca aatctttgaa acttggaata    803

tattgctttc ataatatgaa gttttattgc ctaaaaaaaa aaaa                     847
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<210> 246
<211> 844
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (86)..(700)

<400> 246
tggcctccat ttgaatgctg tcgcctgcac gaccggtccg gaattcccgg gtcgacccac 60

```
cgtccgcccc agccccccag gatac  atg tca gat caa gag gag gac atg tgc     112
                            Met Ser Asp Gln Glu Glu Asp Met Cys
                              1               5

ttt gaa gga atg aaa ccc gta aac caa act gca gcc tca aac aag gga     160
Phe Glu Gly Met Lys Pro Val Asn Gln Thr Ala Ala Ser Asn Lys Gly
 10                  15                  20                  25

ctc aga ggt ctc ctc cac cca cag cag ttg cac ttg ctg agc agg cag     208
Leu Arg Gly Leu Leu His Pro Gln Gln Leu His Leu Leu Ser Arg Gln
 26                  31                  36                  41

ctt gag gac cca aat ggt agc ttt tct aac gct gag atg agt gaa ctg     256
Leu Glu Asp Pro Asn Gly Ser Phe Ser Asn Ala Glu Met Ser Glu Leu
 42                  47                  52                  57

agt gtg gca cag aaa cca gaa aaa ctt ttg gag cgc tgc aag tac tgg     304
Ser Val Ala Gln Lys Pro Glu Lys Leu Leu Glu Arg Cys Lys Tyr Trp
 58                  63                  68                  73

cct gct tgt aaa aat ggg gat gag tgt gcc tac cat cac ccc atc tca     352
Pro Ala Cys Lys Asn Gly Asp Glu Cys Ala Tyr His His Pro Ile Ser
 74                  79                  84                  89

ccc tgc aaa gcc ttc ccc aat tgt aaa ttt gct gaa aaa tgt ttg ttt     400
Pro Cys Lys Ala Phe Pro Asn Cys Lys Phe Ala Glu Lys Cys Leu Phe
 90                  95                 100                 105

gtt cac cca aat tgt aaa tat gat gca aag tgt act aaa cca gat tgt     448
Val His Pro Asn Cys Lys Tyr Asp Ala Lys Cys Thr Lys Pro Asp Cys
106                 111                 116                 121

ccc ttc act cat gtg agt aga aga att cca gta ctg tct cca aaa cca     496
Pro Phe Thr His Val Ser Arg Arg Ile Pro Val Leu Ser Pro Lys Pro
122                 127                 132                 137

gtt gca cca cca gca cca cct tcc agt agt cag ctc tgc cgt tac ttc     544
Val Ala Pro Pro Ala Pro Pro Ser Ser Ser Gln Leu Cys Arg Tyr Phe
138                 143                 148                 153

cct gct tgt aag aag atg gaa tgt ccc ttc tat cat cca aaa cat tgt     592
Pro Ala Cys Lys Lys Met Glu Cys Pro Phe Tyr His Pro Lys His Cys
154                 159                 164                 169

agg ttt aac act caa tgt aca aga ccg gac tgc aca ttc tac cat ccc     640
Arg Phe Asn Thr Gln Cys Thr Arg Pro Asp Cys Thr Phe Tyr His Pro
170                 175                 180                 185

acc att aat gtc cca cca cga cat gcc ttg aaa tgg att cga cct caa     688
Thr Ile Asn Val Pro Pro Arg His Ala Leu Lys Trp Ile Arg Pro Gln
186                 191                 196                 201

acc agc gaa tag cac ccagtcctgc ctggcagaag atcatgcagt ttggaagttt     743
Thr Ser Glu  *
202

tcatgtactg atgaaagata ctctacagaa cttgtcaaat ctttgaaact tggaatatat    803
```

```
tgctttcata atatgaagtt ttattgccta aaaaaaaaaa a                          844
```

<210> 247
<211> 1368
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (353)..(787)

<400> 247

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gtggtaccgg tccggaatta ccgggtcgac gatttcgtgc cgcgggctct gtagctgagt      60

ggtggctggg tatggaggcg aaggcggcac ccaagccagc tgcaagcggc gcgtgctcgg     120

tgtcggcaga ggagaccgaa aagtggatgg aggaggcgat gcacatgata ctatgctatg     180

cacagtgttt tcatgtgggc catgttataa gccccacaga agccctatca gccatgagtg     240

gaagcttcct gaggccctca ctggaagcag atgctgatac catacttctt gtacagtctg     300

gagaactgcc aaagaagccc tcgaaaatac tgaagttcct gttggctgtc tt    atg      355
                                                            Met
                                                             1

gtc tac aac aat gaa gtt gta ggg aag ggg aga aat gaa gtt aac caa      403
Val Tyr Asn Asn Glu Val Val Gly Lys Gly Arg Asn Glu Val Asn Gln
  2                   7                  12                  17

acc aaa aat gct act cga cat gca gaa atg gtg gcc atc gat cag gtc      451
Thr Lys Asn Ala Thr Arg His Ala Glu Met Val Ala Ile Asp Gln Val
 18                  23                  28                  33

ctc gat tgg tgt cgt caa agt ggc aag agt ccc tct gaa gta ttt gaa      499
Leu Asp Trp Cys Arg Gln Ser Gly Lys Ser Pro Ser Glu Val Phe Glu
 34                  39                  44                  49

cac act gtg ttg tat gtc act gtg gag ccg tgc att atg tgt gca gct      547
His Thr Val Leu Tyr Val Thr Val Glu Pro Cys Ile Met Cys Ala Ala
 50                  55                  60                  65

gct ctc cgc ctg atg aaa atg ccg ctg gtt gta tat ggc tgt cag aat      595
Ala Leu Arg Leu Met Lys Met Pro Leu Val Val Tyr Gly Cys Gln Asn
 66                  71                  76                  81

gaa cga ttt ggt ggt tgt ggc tct gtt cta aat att gcc tct gct gac      643
Glu Arg Phe Gly Gly Cys Gly Ser Val Leu Asn Ile Ala Ser Ala Asp
 82                  87                  92                  97

cta cca aac act ggg aga cca ttt cag tgt atc cct gga tat cgg gct      691
Leu Pro Asn Thr Gly Arg Pro Phe Gln Cys Ile Pro Gly Tyr Arg Ala
 98                 103                 108                 113
```

```
gag gaa gca gtg gaa atg tta aag acc ttc tac aaa caa gaa aat cca      739
Glu Glu Ala Val Glu Met Leu Lys Thr Phe Tyr Lys Gln Glu Asn Pro
114                 119                 124                 129

aat gca cca aaa tcg aaa gtt cgg aaa aag gaa tgt cag aaa tct tga      787
Asn Ala Pro Lys Ser Lys Val Arg Lys Lys Glu Cys Gln Lys Ser  *
130                 135                 140                 145

acatgttctg atgaaagaac caagtgaccc aaagtgacct ggacaagatt catagactga    847

aagctgttga catcgttgaa tcatatgttt atatattgtt tttaatctgc aggaaaatgg    907

tgtctctcat catttgctct gttaagggaa caaattagca ctttttagaa gtctgacaat    967

tgtaaacagt tattagcttt tccagaagct gattcccatt ttaagatggg ggaaaattaa   1027

ggtttgaggt tttagaaatt agcaagtagt gcataccctt ctagccacaa gtgcccagtc   1087

caggcaagtg ctgacttctt agagaatgtg tggccagacc cagggacctg gagtgtgttt   1147

ggactgcagt ttgccaccct gagaacacct tctccaggac tggcatttca gaatcagatt   1207

cttcattttt tgcagctacg atgttcttcc agggcactgg gggctgtgac ttctctctaa   1267

attgtatata agttgtgtat atagagacca taattatatg gtccttagaa aagactttgc   1327

ttttataaag catttagaaa aaatgcatac ttttaaaaaa a                       1368
```

<210> 248
<211> 839
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (161)..(634)

<400> 248

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cgcctcgcgc gaccggtccg gaattcccgg gtcgacgatt tcgtggcggc gcagagctcc     60

ggggtagctt tgtggccgaa cgccgacctc gggcggagag cgcggctgtg cccagtatcc    120

catccccgcg acccccgcgc gctccggaga gaacaggact  atg ccc ggg gct ggg     175
                                              Met Pro Gly Ala Gly
                                                1

gac gga ggc aaa gcc ccg gcg aga tgg ctg ggc act ggg ctt ttg ggc      223
Asp Gly Gly Lys Ala Pro Ala Arg Trp Leu Gly Thr Gly Leu Leu Gly
  6                  11                  16                  21

ctc ttc ctg ctc ccc gta acc ctg tcg ctg gag gtg tct gtg gga aag      271
Leu Phe Leu Leu Pro Val Thr Leu Ser Leu Glu Val Ser Val Gly Lys
 22                  27                  32                  37
```

```
gcc acc gac atc tac gct gtc aat ggc acg gag atc ctg ctg ccc tgc      319
Ala Thr Asp Ile Tyr Ala Val Asn Gly Thr Glu Ile Leu Leu Pro Cys
 38                  43                  48                  53

acc ttc tcc agc tgc ttt ggc ttc gag gac ctc cac ttc cgg tgg acc      367
Thr Phe Ser Ser Cys Phe Gly Phe Glu Asp Leu His Phe Arg Trp Thr
 54                  59                  64                  69

tac aac agc agt gac gca ttc aag att ctc ata gag ggg act gtg aag      415
Tyr Asn Ser Ser Asp Ala Phe Lys Ile Leu Ile Glu Gly Thr Val Lys
 70                  75                  80                  85

aat gag aag tct gac ccc aag gtg acg ttg aaa gac gat gac cgc atc      463
Asn Glu Lys Ser Asp Pro Lys Val Thr Leu Lys Asp Asp Asp Arg Ile
 86                  91                  96                 101

act ctg gta ggc tct act aag gag aag agg aac aac att tcc att gtg      511
Thr Leu Val Gly Ser Thr Lys Glu Lys Arg Asn Asn Ile Ser Ile Val
102                 107                 112                 117

ctg agg gac ctg gag ttc agc gac acg ggc aaa tac acc tgc cat gtg      559
Leu Arg Asp Leu Glu Phe Ser Asp Thr Gly Lys Tyr Thr Cys His Val
118                 123                 128                 133

aag aac ccc aag gag aat aat ctc cag cac cac gcc acc atc ttt ctt      607
Lys Asn Pro Lys Glu Asn Asn Leu Gln His His Ala Thr Ile Phe Leu
134                 139                 144                 149

caa gtc gtt gat aga cgt atg cag tag gggct ggcacagggc agtggcgtgg      659
Gln Val Val Asp Arg Arg Met Gln  *
150                 155

gaaggacttg ggaggcaccc aactcatcat cacagtgaaa tggcaaaatg gaccgtgttg    719

gggttttctt ttgctttaca ctttccagag ctgctggagt tacatctaaa agctagaaga    779

gctcagcttg aacacttatt ctgctaccaa atagcttatg aaatactctt agcctctctc    839
```

<210> 249
<211> 1570
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (20)..(1432)

<220>
<221> misc_feature
<222> (1)...(1570)
<223> n = a,t,c or g

<400> 249

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gcacgagggc gctttccag atg cat cag aga tac ttt tgg act gac cag ggc      52
                       Met His Gln Arg Tyr Phe Trp Thr Asp Gln Gly
                         1               5

caa gtg gcg ctc ggc ggg cac tac atg gcg gag ggt gaa ggg tac ttc      100
Gln Val Ala Leu Gly Gly His Tyr Met Ala Glu Gly Glu Gly Tyr Phe
 12                  17                  22                  27

gcc atg tct gag gac gag ctg gcc tgc agc ccc tac atc ccc cta ggc      148
Ala Met Ser Glu Asp Glu Leu Ala Cys Ser Pro Tyr Ile Pro Leu Gly
 28                  33                  38                  43

ggc gac ttc ggc ggc ggc gac ttc ggc ggc ggc gac ttc ggc ggc ggc      196
Gly Asp Phe Gly Gly Gly Asp Phe Gly Gly Gly Asp Phe Gly Gly Gly
 44                  49                  54                  59

gac ttc ggc ggc ggc gac ttc ggc ggt ggc ggc agc ttc ggt ggg cat      244
Asp Phe Gly Gly Gly Asp Phe Gly Gly Gly Gly Ser Phe Gly Gly His
 60                  65                  70                  75

tgc ttg gac tat tgc gaa agc cct acg gcg cac tgc aat gtg ctg aac      292
Cys Leu Asp Tyr Cys Glu Ser Pro Thr Ala His Cys Asn Val Leu Asn
 76                  81                  86                  91

tgg gag caa gtg cag cgg ctg gac ggc atc ctg agc gag acc att ccg      340
Trp Glu Gln Val Gln Arg Leu Asp Gly Ile Leu Ser Glu Thr Ile Pro
 92                  97                 102                 107

att cac ggg cgc ggc aac ttc ccc acg ctc gag ctg cag ccg agc ctg      388
Ile His Gly Arg Gly Asn Phe Pro Thr Leu Glu Leu Gln Pro Ser Leu
108                 113                 118                 123

atc gtg aag gtg gtg cgg cgg cgc ctg gcc gag aag cgc att ggc gtc      436
Ile Val Lys Val Val Arg Arg Arg Leu Ala Glu Lys Arg Ile Gly Val
124                 129                 134                 139

cgc gac gtg cgc ctc aac ggc tcg gca gcc agc cat gtc ctg cac cag      484
Arg Asp Val Arg Leu Asn Gly Ser Ala Ala Ser His Val Leu His Gln
140                 145                 150                 155

gac agc ggc ctg ggc tac aag gac ctg gac ctc atc ttc tgc gcc gac      532
Asp Ser Gly Leu Gly Tyr Lys Asp Leu Asp Leu Ile Phe Cys Ala Asp
156                 161                 166                 171

ctg cgc ggg gaa ggg gag ttt cag act gtg aag gac gtc gtg ctg gac      580
Leu Arg Gly Glu Gly Glu Phe Gln Thr Val Lys Asp Val Val Leu Asp
172                 177                 182                 187

tgc ctg ttg gac ttc tta ccc gag ggg gtg aac aaa gag aag atc aca      628
Cys Leu Leu Asp Phe Leu Pro Glu Gly Val Asn Lys Glu Lys Ile Thr
188                 193                 198                 203

cca ctc acg ctc aag gaa gct tat gtg cag aaa atg gtt aaa gtg tgc      676
Pro Leu Thr Leu Lys Glu Ala Tyr Val Gln Lys Met Val Lys Val Cys
204                 209                 214                 219

aat gac tct gac cga tgg agt ctt ata tcc ctg tca aac aac agt ggc      724
```

```
Asn Asp Ser Asp Arg Trp Ser Leu Ile Ser Leu Ser Asn Asn Ser Gly
220                 225                 230                 235

aaa aat gtg gaa ctg aaa ttt gtg gat tcc ctc cgg agg cag ttt gaa      772
Lys Asn Val Glu Leu Lys Phe Val Asp Ser Leu Arg Arg Gln Phe Glu
236                 241                 246                 251

ttc agt gta gat tct ttt caa atc aaa tta gac tct ctt ctg ctc ttt      820
Phe Ser Val Asp Ser Phe Gln Ile Lys Leu Asp Ser Leu Leu Leu Phe
252                 257                 262                 267

tat gaa tgt tca gag aac cca atg act gag aca ttt cac ccc aca ata      868
Tyr Glu Cys Ser Glu Asn Pro Met Thr Glu Thr Phe His Pro Thr Ile
268                 273                 278                 283

atc ggg gag agc gtc tat ggc gat ttc cag gaa gcc ttt gat cac ctt      916
Ile Gly Glu Ser Val Tyr Gly Asp Phe Gln Glu Ala Phe Asp His Leu
284                 289                 294                 299

tgt aac aag atc att gcc acc agg aac cca gag gaa atc cga ggg gga      964
Cys Asn Lys Ile Ile Ala Thr Arg Asn Pro Glu Glu Ile Arg Gly Gly
300                 305                 310                 315

ggc ctg ctt aag tac tgc aac ctc ttg gtg agg ggc ttt agg ccc gcc     1012
Gly Leu Leu Lys Tyr Cys Asn Leu Leu Val Arg Gly Phe Arg Pro Ala
316                 321                 326                 331

tct gat gaa atc aag acc ctt caa agg tat atg tgt tcc agg ttt ttc     1060
Ser Asp Glu Ile Lys Thr Leu Gln Arg Tyr Met Cys Ser Arg Phe Phe
332                 337                 342                 347

atc gac ttc tca gac att gga gag cag cag aga aaa ctg gag tcc tat     1108
Ile Asp Phe Ser Asp Ile Gly Glu Gln Gln Arg Lys Leu Glu Ser Tyr
348                 353                 358                 363

ttg cag aac cac ttt gtg gga ttg gaa gac cgc aag tat gag tat ctc     1156
Leu Gln Asn His Phe Val Gly Leu Glu Asp Arg Lys Tyr Glu Tyr Leu
364                 369                 374                 379

atg acc ctt cat gga gtg gta aat gag agc aca gtg tgc ctg atg gga     1204
Met Thr Leu His Gly Val Val Asn Glu Ser Thr Val Cys Leu Met Gly
380                 385                 390                 395

cat gaa aga aga cag act tta aac ctt atc acc atg ctg gct atc cgg     1252
His Glu Arg Arg Gln Thr Leu Asn Leu Ile Thr Met Leu Ala Ile Arg
396                 401                 406                 411

gtg tta gct gac caa aat gtc att cct aat gtg gct aat gtc act tgc     1300
Val Leu Ala Asp Gln Asn Val Ile Pro Asn Val Ala Asn Val Thr Cys
412                 417                 422                 427

tat tac cag cca gcc ccc tat gta gca gat gcc aac ttt agc aat tac     1348
Tyr Tyr Gln Pro Ala Pro Tyr Val Ala Asp Ala Asn Phe Ser Asn Tyr
428                 433                 438                 443

tac att gca cag gtt cag cca gta ttc acg tgc cag caa cag acc tac     1396
Tyr Ile Ala Gln Val Gln Pro Val Phe Thr Cys Gln Gln Gln Thr Tyr
```

```
444                 449                 454                 459

tcc act tgg gct acc ctg caa tta aga atc att taa aaat gtcctgtggg     1446
Ser Thr Trp Ala Thr Leu Gln Leu Arg Ile Ile  *
460                 465                 470

gaagccattt cagacaagac aggagagaaa aaaaaataaa gaaaaaaaaa anggcggccc   1506

cttcaatttt aagggcccct ttaaaacccg ttggaaaccc ccaaggggcc tttttattgc   1566

cacc                                                                1570
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<210> 250
<211> 2191
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (167)..(1822)

<400> 250

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ctcgttagtg ccccctgtgt ttggggcccc gtgatctcaa cggtcctgcc ctcggtctcc     60

ctcttccccc gccccgccct gggccaggtg ttcgaatccc gactccagaa ctggcggcgt    120

cccagtcccg cgggcgtgga gcgccggagg acccgccctc gggctc   atg gcg gcc     175
                                                     Met Ala Ala
                                                       1

ccg gtc cgc ctg ggc cgg aag cgc ccg ctg cct gcc tgt ccc aac ccg      223
Pro Val Arg Leu Gly Arg Lys Arg Pro Leu Pro Ala Cys Pro Asn Pro
  4                   9                  14                  19

ctc ttc gtt cgc tgg ctg acc gag tgg cgg gac gag gcg acc cgc agc      271
Leu Phe Val Arg Trp Leu Thr Glu Trp Arg Asp Glu Ala Thr Arg Ser
 20                  25                  30                  35

agg cac cgc acg cgc ttc gta ttt cag aag gcg ctg cgt tcc ctc cga      319
Arg His Arg Thr Arg Phe Val Phe Gln Lys Ala Leu Arg Ser Leu Arg
 36                  41                  46                  51

cgg tac cca ctg ccg ctg cgc agc ggg aag gaa gct aag atc cta cag      367
Arg Tyr Pro Leu Pro Leu Arg Ser Gly Lys Glu Ala Lys Ile Leu Gln
 52                  57                  62                  67

cac ttc gga gac ggg ctc tgc cgg atg ctg gac gag cgg ctg cag cgg      415
His Phe Gly Asp Gly Leu Cys Arg Met Leu Asp Glu Arg Leu Gln Arg
 68                  73                  78                  83

cac cga aca tcg ggc ggt gac cat gcc ccg gac tca cca tct gga gag      463
His Arg Thr Ser Gly Gly Asp His Ala Pro Asp Ser Pro Ser Gly Glu
 84                  89                  94                  99
```

```
aac agt cca gcc ccg cag ggg cga ctt gcg gaa gtc cag gac tct tcc      511
Asn Ser Pro Ala Pro Gln Gly Arg Leu Ala Glu Val Gln Asp Ser Ser
100                 105                 110                 115

atg cca gtt cct gcc cag ccc aaa gcg gga ggc tct ggc agc tac tgg      559
Met Pro Val Pro Ala Gln Pro Lys Ala Gly Gly Ser Gly Ser Tyr Trp
116                 121                 126                 131

cca gct cgg cac tca gga gcc cga gtg ata ctg ctg gtg ctc tac cgg      607
Pro Ala Arg His Ser Gly Ala Arg Val Ile Leu Leu Val Leu Tyr Arg
132                 137                 142                 147

gag cac ctg aat cct aat ggt cac cac ttc tta acc aag gag gag ctg      655
Glu His Leu Asn Pro Asn Gly His His Phe Leu Thr Lys Glu Glu Leu
148                 153                 158                 163

ctg cag agg tgt gct cag aag tcc ccc agg gta gcc cct ggg agt gcc      703
Leu Gln Arg Cys Ala Gln Lys Ser Pro Arg Val Ala Pro Gly Ser Ala
164                 169                 174                 179

cca ccc tgg cca gcc ctc cgc tcc ctc ctt cac agg aac ctg gtc ctc      751
Pro Pro Trp Pro Ala Leu Arg Ser Leu Leu His Arg Asn Leu Val Leu
180                 185                 190                 195

agg aca cac cag cca gcc agg tac tca ttg acc cca gag ggc ctg gag      799
Arg Thr His Gln Pro Ala Arg Tyr Ser Leu Thr Pro Glu Gly Leu Glu
196                 201                 206                 211

ctg gcc cag aag ttg gcc gag tca gaa ggc ctg agc ttg ctg aat gtg      847
Leu Ala Gln Lys Leu Ala Glu Ser Glu Gly Leu Ser Leu Leu Asn Val
212                 217                 222                 227

ggc atc ggg ccc aag gag ccc cct ggg gag gag aca gca gtg cca gga      895
Gly Ile Gly Pro Lys Glu Pro Pro Gly Glu Glu Thr Ala Val Pro Gly
228                 233                 238                 243

gca gct tca gca gag ctt gcc agt gaa gca ggg gtc cag cag cag cca      943
Ala Ala Ser Ala Glu Leu Ala Ser Glu Ala Gly Val Gln Gln Gln Pro
244                 249                 254                 259

ctg gag ctg agg cct gga gag tac agg gtg ctg ttg tgt gtg gac att      991
Leu Glu Leu Arg Pro Gly Glu Tyr Arg Val Leu Leu Cys Val Asp Ile
260                 265                 270                 275

ggc gag acc cgg ggg ggc ggg cac agg ccg gag ctg ctc cga gag cta     1039
Gly Glu Thr Arg Gly Gly Gly His Arg Pro Glu Leu Leu Arg Glu Leu
276                 281                 286                 291

cag cgg ctg cac gtg acc cac acg gtg cgc aag ctg cac gtt gga gat     1087
Gln Arg Leu His Val Thr His Thr Val Arg Lys Leu His Val Gly Asp
292                 297                 302                 307

ttt gtg tgg gtg gct cag gag acc aat cct aga gac cca gca aac cct     1135
Phe Val Trp Val Ala Gln Glu Thr Asn Pro Arg Asp Pro Ala Asn Pro
308                 313                 318                 323

ggg gag ttg gta ctg gat cac att gtg gag cgc aag cga ctg gat gac     1183
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Gly Glu Leu Val Leu Asp His Ile Val Glu Arg Lys Arg Leu Asp Asp
324                 329                 334                 339

ctt tgc agc agc atc atc gac ggc cgc ttc cgg gag cag aag ttc cga     1231
Leu Cys Ser Ser Ile Ile Asp Gly Arg Phe Arg Glu Gln Lys Phe Arg
340                 345                 350                 355

ctg aag cgc tgt ggt ctg gag cgc cgg gta tac ctg gtg gaa gag cat     1279
Leu Lys Arg Cys Gly Leu Glu Arg Arg Val Tyr Leu Val Glu Glu His
356                 361                 366                 371

ggt tcc gtc cac aac ctc agc ctt cct gag agc aca ctg ctg cag gct     1327
Gly Ser Val His Asn Leu Ser Leu Pro Glu Ser Thr Leu Leu Gln Ala
372                 377                 382                 387

gtc acc aac act cag gtc att gat ggc ttt ttt gtg aag cgc aca gca     1375
Val Thr Asn Thr Gln Val Ile Asp Gly Phe Phe Val Lys Arg Thr Ala
388                 393                 398                 403

gac att aag gag tca gcc gcc tac ctg gcc ctc ttg act cgg ggc ctg     1423
Asp Ile Lys Glu Ser Ala Ala Tyr Leu Ala Leu Leu Thr Arg Gly Leu
404                 409                 414                 419

cag aga ctc tac cag ggc cac acc cta cgc agc cgc ccc tgg gga acc     1471
Gln Arg Leu Tyr Gln Gly His Thr Leu Arg Ser Arg Pro Trp Gly Thr
420                 425                 430                 435

cct ggg aac cct gaa tca ggg gcc atg acc tct cca aac cct ctc tgc     1519
Pro Gly Asn Pro Glu Ser Gly Ala Met Thr Ser Pro Asn Pro Leu Cys
436                 441                 446                 451

tca ctc ctc acc ttc agt gac ttc aac gca gga gcc atc aag aat aag     1567
Ser Leu Leu Thr Phe Ser Asp Phe Asn Ala Gly Ala Ile Lys Asn Lys
452                 457                 462                 467

gcc cag tcg gtg cga gaa gtg ttt gcc cgg cag ctg atg cag gtg cgc     1615
Ala Gln Ser Val Arg Glu Val Phe Ala Arg Gln Leu Met Gln Val Arg
468                 473                 478                 483

gga gtg agt ggg gag aag gca gca gcc ctg gtg gat cga tac agc acc     1663
Gly Val Ser Gly Glu Lys Ala Ala Ala Leu Val Asp Arg Tyr Ser Thr
484                 489                 494                 499

cct gcc agc ctc ctg gcc gcc tat gat gcc tgt gcc acc ccc aag gaa     1711
Pro Ala Ser Leu Leu Ala Ala Tyr Asp Ala Cys Ala Thr Pro Lys Glu
500                 505                 510                 515

caa gag aca ctg ctg agc acc att aag tgt ggg cgt cta cag agg aat     1759
Gln Glu Thr Leu Leu Ser Thr Ile Lys Cys Gly Arg Leu Gln Arg Asn
516                 521                 526                 531

ctg ggg cct gct ctg agc agg acc tta tcc cag ctc tac tgc agc tac     1807
Leu Gly Pro Ala Leu Ser Arg Thr Leu Ser Gln Leu Tyr Cys Ser Tyr
532                 537                 542                 547

ggc ccc ttg acc tga gcttatgccg tgaaacagcc cccagccccc gtctgtcctc     1862
Gly Pro Leu Thr  *
```

548

caacccaagg ctagccagcc ttttagaatc taagtcgttt gcagccatat gtgtcatgta 1922

gaagatgcct agccctgggg accgttgtga aatacgcagg aaccagggat accatctcgg 1982

tccacgtggt ttttaaacaa agctgcttag cacctggaac ttccctggtc gagggagatg 2042

gagtcagtgg ggcattgcag cttggaatct attttatgtc accagttggt cctcatcaaa 2102

taaaatttcc ttaggagtgc agagggctca ttgggaaaat aaaaataata aaaataaata 2162

aaacttccta aaagaaaaga ttgaaaacc 2191

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Met Ser Pro Arg
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tcg tgc ctg cgt tcg ctg cgc ctc ctc gtc ttc gcc gtc ttc tca gcc 104
Ser Cys Leu Arg Ser Leu Arg Leu Leu Val Phe Ala Val Phe Ser Ala
5 10 15 20

gcc gcg agc aac tgg ctg tac ctg gcc aag ctg tcg tcg gtg ggg agc 152
Ala Ala Ser Asn Trp Leu Tyr Leu Ala Lys Leu Ser Ser Val Gly Ser
21 26 31 36

atc tca gag gag gag acg tgc gag aaa ctc aag ggc ctg atc cag agg 200
Ile Ser Glu Glu Glu Thr Cys Glu Lys Leu Lys Gly Leu Ile Gln Arg
37 42 47 52

cag gtg cag atg tgc aag cgg aac ctg gaa gtc atg gac tcg gtg cgc 248
Gln Val Gln Met Cys Lys Arg Asn Leu Glu Val Met Asp Ser Val Arg
53 58 63 68

cgc ggt gcc cag ctg gcc att gag gag tgc cag tac cag ttc cgg aac 296
Arg Gly Ala Gln Leu Ala Ile Glu Glu Cys Gln Tyr Gln Phe Arg Asn
69 74 79 84

cgg cgc tgg aac tgc tcc aca ctc gac tcc ttg ccc gtc ttc ggc aag 344
Arg Arg Trp Asn Cys Ser Thr Leu Asp Ser Leu Pro Val Phe Gly Lys
85 90 95 100

gtg gtg acg caa ggg act cgg gag gcg gcc ttc gtg tac gcc atc tct 392
Val Val Thr Gln Gly Thr Arg Glu Ala Ala Phe Val Tyr Ala Ile Ser

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101                 106                 111                 116

tcg gca ggt gtg gcc ttt gca gtg acg cgg gcg tgc agc agt ggg gag      440
Ser Ala Gly Val Ala Phe Ala Val Thr Arg Ala Cys Ser Ser Gly Glu
117                 122                 127                 132

ctg gag aag tgc ggc tgt gac agg aca gtg cat ggg gtc agc cca cag      488
Leu Glu Lys Cys Gly Cys Asp Arg Thr Val His Gly Val Ser Pro Gln
133                 138                 143                 148

ggc ttc cag tgg tca gga tgc tct gac aac atc gcc tac ggt gtg gcc      536
Gly Phe Gln Trp Ser Gly Cys Ser Asp Asn Ile Ala Tyr Gly Val Ala
149                 154                 159                 164

ttc tca cag tcg ttt gtg gat gtg cgg gag aga agc aag ggg gcc tcg      584
Phe Ser Gln Ser Phe Val Asp Val Arg Glu Arg Ser Lys Gly Ala Ser
165                 170                 175                 180

tcc agc aga gcc ctc atg aac ctc cac aac aat gag gcc ggc agg aag      632
Ser Ser Arg Ala Leu Met Asn Leu His Asn Asn Glu Ala Gly Arg Lys
181                 186                 191                 196

gcc atc ctg aca cac atg cgg gtg gaa tgc aag tgc cac ggg gtg tca      680
Ala Ile Leu Thr His Met Arg Val Glu Cys Lys Cys His Gly Val Ser
197                 202                 207                 212

ggc tcc tgt gag gta aag acg tgc tgg cga gcc gtg ccg ccc ttc cgc      728
Gly Ser Cys Glu Val Lys Thr Cys Trp Arg Ala Val Pro Pro Phe Arg
213                 218                 223                 228

cag gtg ggt cac gca ctg aag gag aag ttt gat ggt gcc act gag gtg      776
Gln Val Gly His Ala Leu Lys Glu Lys Phe Asp Gly Ala Thr Glu Val
229                 234                 239                 244

gag cca cgc cgc gtg ggc tcc tcc agg gca ctg gtg cca cgc aac gca      824
Glu Pro Arg Arg Val Gly Ser Ser Arg Ala Leu Val Pro Arg Asn Ala
245                 250                 255                 260

cag ttc aag ccg cac aca gat gag gac ctg gtg tac ttg gag cct agc      872
Gln Phe Lys Pro His Thr Asp Glu Asp Leu Val Tyr Leu Glu Pro Ser
261                 266                 271                 276

ccc gac ttc tgt gag cag gac atg cgc agc ggc gtg ctg ggc acg agg      920
Pro Asp Phe Cys Glu Gln Asp Met Arg Ser Gly Val Leu Gly Thr Arg
277                 282                 287                 292

ggc cgc aca tgc aac aag acg tcc aag gcc atc gac ggc tgt gag ctg      968
Gly Arg Thr Cys Asn Lys Thr Ser Lys Ala Ile Asp Gly Cys Glu Leu
293                 298                 303                 308

ctg tgc tgt ggc cgc ggc ttc cac acg gcg cag gtg gag ctg gct gaa     1016
Leu Cys Cys Gly Arg Gly Phe His Thr Ala Gln Val Glu Leu Ala Glu
309                 314                 319                 324

cgc tgc agc tgc aaa ttc cac tgg tgc tgc ttc gtc aag tgc cgg cag     1064
Arg Cys Ser Cys Lys Phe His Trp Cys Cys Phe Val Lys Cys Arg Gln
325                 330                 335                 340
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tgc cag cgg ctc gtg gag ttg cac acg tgc cga tga ccgc ctgcctagcc     1114
Cys Gln Arg Leu Val Glu Leu His Thr Cys Arg  *
341                 346                 351

ctgcgccggc aaccacctag tggcccaggg aaggccgata atttaaacag tctcccacca   1174

cctaccccaa gagatactgg ttgtattttt tgttctggtt tggtttttgg gtcctcatgt   1234

tatttattgc cgaaaccagg caggcaaccc caagggcacc aaccagggcc tccccaaagc   1294

ctgggccttt gtggctgcca ctgaccaaag ggaccttgct cgtgccgctg gctgcccgca   1354

tgtggctgcc actgaccact cagttgttat ctgtgtccgt ttttctactt gcagacctaa   1414

ggtggagtaa caaggagtat taccaccaca tggctactga ccgtgtcatc ggggaagagg   1474

gggccttatg gcagggaaaa taggtaccga cttgatggaa gtcacaccct ctggaaaaaa   1534

agaactctta actctccagc acacatacac atggactcct ggcagcttga gcctaaaagc   1594

catg                                                               1598
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caccactccg ccaggactgc agcccacctg tctgcaaccc agctgaggcc   atg ccc     116
                                                         Met Pro
                                                           1

tcc cca ggg acc gtc tgc agc ctc ctg ctc ctc ggc atg ctc tgg ctg      164
Ser Pro Gly Thr Val Cys Ser Leu Leu Leu Leu Gly Met Leu Trp Leu
  3                   8                  13                  18

gac ttg gcc atg gca ggc tcc agc ttc ctg agc cct gaa cac cag aga      212
Asp Leu Ala Met Ala Gly Ser Ser Phe Leu Ser Pro Glu His Gln Arg
 19                  24                  29                  34

gtc cag cag aga aag gag tcg aag aag cca cca gcc aag ctg cag ccc      260
Val Gln Gln Arg Lys Glu Ser Lys Lys Pro Pro Ala Lys Leu Gln Pro
 35                  40                  45                  50

cga gct cta gca ggc tgg ctc cgc ccg gaa gat gga ggt caa gca gaa      308
Arg Ala Leu Ala Gly Trp Leu Arg Pro Glu Asp Gly Gly Gln Ala Glu
 51                  56                  61                  66
```

```
ggg gca gag gat gaa ctg gaa gtc cgg ttc aac gcc ccc ttt gat gtt      356
Gly Ala Glu Asp Glu Leu Glu Val Arg Phe Asn Ala Pro Phe Asp Val
 67                  72                  77                  82

gga atc aag ctg tca ggg gtt cag tac cag cag cac agc cag gcc ctg      404
Gly Ile Lys Leu Ser Gly Val Gln Tyr Gln Gln His Ser Gln Ala Leu
 83                  88                  93                  98

ggg aag ttt ctt cag gac atc ctc tgg gaa gag gcc aaa gag gcc cca      452
Gly Lys Phe Leu Gln Asp Ile Leu Trp Glu Glu Ala Lys Glu Ala Pro
 99                 104                 109                 114

gcc gac aag tga tcg cccacaagcc ttactcacct ctctctaagt ttagaagcgc      507
Ala Asp Lys  *
115

tcatctggct tttcgcttgc ttctgcagca actcccacga ctgttgtaca agctcaggag    567

gcgaataaat gttcaaactg taaaaaaaa                                      596
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20050176050

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<220>
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<222> (106)..(1032)

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cctctcaggc aggcagaccc agggcctccc cgccacacct tgttc    atg gat ttt     114
                                                     Met Asp Phe
                                                       1

gtc gct gga gcc atc gga ggc gtc tgc ggt gtt gct gtg ggc tac ccc      162
Val Ala Gly Ala Ile Gly Gly Val Cys Gly Val Ala Val Gly Tyr Pro
  4                   9                  14                  19

ctg gac acg gtg aag gtc agg atc cag acg gag cca aag tac aca ggc      210
Leu Asp Thr Val Lys Val Arg Ile Gln Thr Glu Pro Lys Tyr Thr Gly
 20                  25                  30                  35

atc tgg cac tgc gtc cgg gat acg tat cac cga gag cgc gtg tgg ggc      258
Ile Trp His Cys Val Arg Asp Thr Tyr His Arg Glu Arg Val Trp Gly
 36                  41                  46                  51

ttc tac cgg ggc ctc tcg ctg ccc gtg tgc acg gtg tcc ctg gta tct      306
Phe Tyr Arg Gly Leu Ser Leu Pro Val Cys Thr Val Ser Leu Val Ser
 52                  57                  62                  67

tcc gtg tct ttt ggc acc tac cgc cac tgc ctg gcg cac atc tgc cgg      354
```

```
Ser Val Ser Phe Gly Thr Tyr Arg His Cys Leu Ala His Ile Cys Arg
 68                  73                  78                  83

ctc cgg tac ggt aac cct gac gcc aag ccc acc aag gcc gac atc acg      402
Leu Arg Tyr Gly Asn Pro Asp Ala Lys Pro Thr Lys Ala Asp Ile Thr
 84                  89                  94                  99

ctc tcg gga tgc gcc tcc ggc ctc gtc cgc gtg ttc ctg acg tcg ccc      450
Leu Ser Gly Cys Ala Ser Gly Leu Val Arg Val Phe Leu Thr Ser Pro
100                 105                 110                 115

act gag gtg gcc aaa gtc cgc ttg cag acg cag aca cag gcg cag aag      498
Thr Glu Val Ala Lys Val Arg Leu Gln Thr Gln Thr Gln Ala Gln Lys
116                 121                 126                 131

cag cag cgg cgg ctt tcg gcc tcg ggg ccg ttg gct gtg ccc ccc atg      546
Gln Gln Arg Arg Leu Ser Ala Ser Gly Pro Leu Ala Val Pro Pro Met
132                 137                 142                 147

tgt cct gtg ccc cca gcc tgc cca gag ccc aag tac cgc ggg cca ctg      594
Cys Pro Val Pro Pro Ala Cys Pro Glu Pro Lys Tyr Arg Gly Pro Leu
148                 153                 158                 163

cac tgc ctg gcc acg gta gcc cgt gag gag ggg ctg tgc ggc ctc tac      642
His Cys Leu Ala Thr Val Ala Arg Glu Glu Gly Leu Cys Gly Leu Tyr
164                 169                 174                 179

aag ggc agc tcg gcc ctg gtc tta cgg gac ggc cac tcc ttt gcc acc      690
Lys Gly Ser Ser Ala Leu Val Leu Arg Asp Gly His Ser Phe Ala Thr
180                 185                 190                 195

tac ttc ctt tcc tac gcg gtc ctc tgc gag tgg ctc agc ccc gct ggc      738
Tyr Phe Leu Ser Tyr Ala Val Leu Cys Glu Trp Leu Ser Pro Ala Gly
196                 201                 206                 211

cac agc cgg cca gat gtc ccg ggc gtg ctg gtg gcc ggg ggc tgt gca      786
His Ser Arg Pro Asp Val Pro Gly Val Leu Val Ala Gly Gly Cys Ala
212                 217                 222                 227

gga gtc ctg gcc tgg gct gtg gcc acc ccc atg gac gtg atc aag tcg      834
Gly Val Leu Ala Trp Ala Val Ala Thr Pro Met Asp Val Ile Lys Ser
228                 233                 238                 243

aga ctg cag gca gac ggg cag ggc cag agg cgc tac cgg ggt ctc ctg      882
Arg Leu Gln Ala Asp Gly Gln Gly Gln Arg Arg Tyr Arg Gly Leu Leu
244                 249                 254                 259

cac tgt atg gtg acc atc gtt cga gag gag gga ccc cgg gtc ctt ttc      930
His Cys Met Val Thr Ile Val Arg Glu Glu Gly Pro Arg Val Leu Phe
260                 265                 270                 275

aag ggg ctg gta ctc aat tgc tgc cgc gcc ttc cct gtc aac atg gtg      978
Lys Gly Leu Val Leu Asn Cys Cys Arg Ala Phe Pro Val Asn Met Val
276                 281                 286                 291

gtc ttc gtc gcc tat gag gca gtg ctg agg ctc gcc cgg ggt ctg ctc     1026
Val Phe Val Ala Tyr Glu Ala Val Leu Arg Leu Ala Arg Gly Leu Leu
```

```
292                 297                 302                 307

aca tag ccggtcccca cgcccagcgg cccacccacc agcagctgct ggaggtcgta      1082
Thr  *
308

gtggctggag gaggcaaggg gtagtgtggc tgggttcggg accccacagg gccattgccc   1142

aggagaatga ggagcctccc tgcagtgttg tcggccgagg cctgagctcg ccctgcccag   1202

ctactgacct caggtcgagg ggcccgccag ccatcagcca gggttggcct agggtggcag   1262

gagccaggga ggagtgggcc tctttgatga gagcgttgag ttgcatggag tcggttgttc   1322

atcccagcct ccccatggcc ctcgcctccc atgtctttga agc                     1365
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<400> 254

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ggaaggcgac tttaaaggcg ccgggactga gcgaagggcg tttgggtact gccgtcgccg    120

ccgcccaggc cggggagggg tgcgttagtg tcaggaagcg ggctgcgccg aggtcgtagc    180

ggaaccagct ggcgaccccg caga   atg aac cac aag agc aag aag cgc atc      231
                             Met Asn His Lys Ser Lys Lys Arg Ile
                               1               5

cgc gag gcc aag cgg agt gcg cgg ccg gag ctc aag gac tcg ctg gat      279
Arg Glu Ala Lys Arg Ser Ala Arg Pro Glu Leu Lys Asp Ser Leu Asp
 10                  15                  20                  25

tgg acc cgg cac aac tac tac gag agc ttc tcg ctg agc ccg gcg gcc      327
Trp Thr Arg His Asn Tyr Tyr Glu Ser Phe Ser Leu Ser Pro Ala Ala
 26                  31                  36                  41

gtg gcg gat aac gtg gaa agg gca gat gct tta cag ctg tct gtg gaa      375
Val Ala Asp Asn Val Glu Arg Ala Asp Ala Leu Gln Leu Ser Val Glu
 42                  47                  52                  57

gaa ttt gtg gag cgg tat gaa aga cct tac aag ccc gtg gtt ttg ttg      423
Glu Phe Val Glu Arg Tyr Glu Arg Pro Tyr Lys Pro Val Val Leu Leu
 58                  63                  68                  73

aat gcg caa gag ggc tgg tct gcg cag gag aaa tgg act ctg gag cgc      471
Asn Ala Gln Glu Gly Trp Ser Ala Gln Glu Lys Trp Thr Leu Glu Arg
```

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 74                  79                  84                  89

cta aaa agg aaa tat cgg aac cag aag ttc aag tgt ggt gag gat aac      519
Leu Lys Arg Lys Tyr Arg Asn Gln Lys Phe Lys Cys Gly Glu Asp Asn
 90                  95                 100                 105

gat ggc tac tca gtg aag atg aag atg aaa tac tac atc gag tac atg      567
Asp Gly Tyr Ser Val Lys Met Lys Met Lys Tyr Tyr Ile Glu Tyr Met
106                 111                 116                 121

gag agc act cga gat gat agt ccc ctt tac atc ttt gac agc agc tat      615
Glu Ser Thr Arg Asp Asp Ser Pro Leu Tyr Ile Phe Asp Ser Ser Tyr
122                 127                 132                 137

ggt gaa cac cct aaa aga agg aaa ctt ttg gaa gac tac aag gtg cca      663
Gly Glu His Pro Lys Arg Arg Lys Leu Leu Glu Asp Tyr Lys Val Pro
138                 143                 148                 153

aag ttt ttc act gat gac ctt ttc cag tat gct ggg gag aag cgc agg      711
Lys Phe Phe Thr Asp Asp Leu Phe Gln Tyr Ala Gly Glu Lys Arg Arg
154                 159                 164                 169

ccc cct tac agg tgg ttt gtg atg ggg cca cca cgc tcc gga act ggg      759
Pro Pro Tyr Arg Trp Phe Val Met Gly Pro Pro Arg Ser Gly Thr Gly
170                 175                 180                 185

att cac atc gac cct ctg gga acc agt gcc tgg aat gcc tta gtt cag      807
Ile His Ile Asp Pro Leu Gly Thr Ser Ala Trp Asn Ala Leu Val Gln
186                 191                 196                 201

ggc cac aag cgc tgg tgc ctg ttt cct acc agc act ccc agg gaa ctc      855
Gly His Lys Arg Trp Cys Leu Phe Pro Thr Ser Thr Pro Arg Glu Leu
202                 207                 212                 217

atc aaa gtg acc cga gac gaa gga ggg aac cag caa gac gaa gct att      903
Ile Lys Val Thr Arg Asp Glu Gly Gly Asn Gln Gln Asp Glu Ala Ile
218                 223                 228                 233

acc tgg ttt aat gtt att tat ccc cgg aca cag ctt cca acc tgg cca      951
Thr Trp Phe Asn Val Ile Tyr Pro Arg Thr Gln Leu Pro Thr Trp Pro
234                 239                 244                 249

cct gaa ttc aaa ccc ctg gaa atc tta caa aaa cca gga gag act gtc      999
Pro Glu Phe Lys Pro Leu Glu Ile Leu Gln Lys Pro Gly Glu Thr Val
250                 255                 260                 265

ttt gta cca gga ggc tgg tgg cat gtt gtc ctc aat ctc gac act act     1047
Phe Val Pro Gly Gly Trp Trp His Val Val Leu Asn Leu Asp Thr Thr
266                 271                 276                 281

atc gcc atc acc caa aat ttt gcc agc agc acc aac ttc cct gtg gta     1095
Ile Ala Ile Thr Gln Asn Phe Ala Ser Ser Thr Asn Phe Pro Val Val
282                 287                 292                 297

tgg cac aag acg gta aga ggg aga cca aag tta tca agg aaa tgg tat     1143
Trp His Lys Thr Val Arg Gly Arg Pro Lys Leu Ser Arg Lys Trp Tyr
298                 303                 308                 313
```

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agg att ttg aag caa gag cac ccc gag ttg gca gtc ctc gca gac tcg     1191
Arg Ile Leu Lys Gln Glu His Pro Glu Leu Ala Val Leu Ala Asp Ser
314                 319                 324                 329

gtt gac ctt cag gag tcc aca ggg ata gct tcc gac agc tcc agc gac     1239
Val Asp Leu Gln Glu Ser Thr Gly Ile Ala Ser Asp Ser Ser Ser Asp
330                 335                 340                 345

tct tcc agc tcc tcc agc tcc agt tcg tca gac tcc gac tca gag tgc     1287
Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Asp Ser Asp Ser Glu Cys
346                 351                 356                 361

gag tct gga tcc gag ggc gat ggg aca gtg cac cgc agg aag aag agg     1335
Glu Ser Gly Ser Glu Gly Asp Gly Thr Val His Arg Arg Lys Lys Arg
362                 367                 372                 377

agg acg tgc agc atg gtg gga aac ggg gac acc acc tcc cag gac gac     1383
Arg Thr Cys Ser Met Val Gly Asn Gly Asp Thr Thr Ser Gln Asp Asp
378                 383                 388                 393

tgt gtc agc aaa gag cgc agc tcc tcc agg att agg gac act tgt gga     1431
Cys Val Ser Lys Glu Arg Ser Ser Ser Arg Ile Arg Asp Thr Cys Gly
394                 399                 404                 409

ggc cgg gct cac ccc tga gcagat aaagagactc tccctgaggt gctttcagcg     1485
Gly Arg Ala His Pro  *
410                 415

taagcttttg gcagccaccc aactcagttc tcgcatcttc tgctcctacc ttctcctctg   1545

tcttctttga atttggatat tccttccctg gtccaagctc ctatcttcgg tcaaatgctg   1605

tttttactgc ttcctaagga tagattatca agaaatttaa cagctcggcc agctcagtga   1665

aacactgaag ctaatgggat gttgggtaag aaggttctgt gctgtctcat tgaaaaccga   1725

gccagtcaac cacaaggctg gcagggtgtg atccttgtaa cgtcttgtgt ctgttacctc   1785

acggatgtcg gtaaggagtt tccacagagc cagctgtgta ccacagagac tgagagtggt   1845

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atgtcatcat cagcccacaa atgcattcag tggcagtgac ccagcaccat caccatcacc   1965

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         Met Ala Trp Thr Lys Tyr Gln Leu Phe Leu Ala Gly Leu Met
           1               5                  10

ctt gtt acc ggc tcc atc aac acg ctc tcg gca aaa tgg gcg gac aat      217
Leu Val Thr Gly Ser Ile Asn Thr Leu Ser Ala Lys Trp Ala Asp Asn
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ttc atg gcc gag ggc tgt gga ggg agc aag gag cac agc ttc cag cat      265
Phe Met Ala Glu Gly Cys Gly Gly Ser Lys Glu His Ser Phe Gln His
 31                  36                  41                  46

ccc ttc ctc cag gca gtg ggc atg ttc ctg gga gaa ttc tcc tgc ctg      313
Pro Phe Leu Gln Ala Val Gly Met Phe Leu Gly Glu Phe Ser Cys Leu
 47                  52                  57                  62

gct gcc ttc tac ctc ctc cga tgc aga gct gca ggg caa tca gac tcc      361
Ala Ala Phe Tyr Leu Leu Arg Cys Arg Ala Ala Gly Gln Ser Asp Ser
 63                  68                  73                  78

agc gta gac ccc cag cag ccc ttc aac cct ctt ctt ttc ctg ccc cca      409
Ser Val Asp Pro Gln Gln Pro Phe Asn Pro Leu Leu Phe Leu Pro Pro
 79                  84                  89                  94

gcg ctc tgt gac atg aca ggg acc agc ctc atg tat gtg gct ctg aac      457
Ala Leu Cys Asp Met Thr Gly Thr Ser Leu Met Tyr Val Ala Leu Asn
 95                 100                 105                 110

atg acc agt gcc tcc agc ttc cag atg ctg cgg ggt gca gtg atc ata      505
Met Thr Ser Ala Ser Ser Phe Gln Met Leu Arg Gly Ala Val Ile Ile
111                 116                 121                 126

ttc act ggc ctg ttc tcg gtg gcc ttc ctg ggc cgg agg ctg gtg ctg      553
Phe Thr Gly Leu Phe Ser Val Ala Phe Leu Gly Arg Arg Leu Val Leu
127                 132                 137                 142

agc cag tgg ctg ggc atc cta gcc acc atc gcg ggg ctg gtg gtc gtg      601
Ser Gln Trp Leu Gly Ile Leu Ala Thr Ile Ala Gly Leu Val Val Val
143                 148                 153                 158

ggc ctg gct gac ctc ctg agc aag cac gac agt cag cac aag ctc agc      649
Gly Leu Ala Asp Leu Leu Ser Lys His Asp Ser Gln His Lys Leu Ser
159                 164                 169                 174

gaa gtg atc aca ggg gac ctg ttg atc atc atg gcc cag atc atc gtt      697
Glu Val Ile Thr Gly Asp Leu Leu Ile Ile Met Ala Gln Ile Ile Val
175                 180                 185                 190

gcc atc cag atg gtg cta gag gag aag ttc gtc tac aaa cac aat gtg      745
Ala Ile Gln Met Val Leu Glu Glu Lys Phe Val Tyr Lys His Asn Val
191                 196                 201                 206

cac cca ctg cgg gca gtt ggc act gag ggc ctc ttt ggc ttt gtg atc      793
His Pro Leu Arg Ala Val Gly Thr Glu Gly Leu Phe Gly Phe Val Ile
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223                 228                 233                 238

agc gga aac cct cgt ggg aca ctg gag gat gca ttg gac gcc ttc tgc      889
Ser Gly Asn Pro Arg Gly Thr Leu Glu Asp Ala Leu Asp Ala Phe Cys
239                 244                 249                 254

cag gtg ggc cag cag ccg ctc att gcc gtg gca ctg ctg ggc aac atc      937
Gln Val Gly Gln Gln Pro Leu Ile Ala Val Ala Leu Leu Gly Asn Ile
255                 260                 265                 270

agc agc att gcc ttc ttc aac ttc gca ggc atc agc gtc acc aag gaa      985
Ser Ser Ile Ala Phe Phe Asn Phe Ala Gly Ile Ser Val Thr Lys Glu
271                 276                 281                 286

ctg agc gcc acc acc cgc atg gtg ttg gac agc ttg cgc acc gtt gtc     1033
Leu Ser Ala Thr Thr Arg Met Val Leu Asp Ser Leu Arg Thr Val Val
287                 292                 297                 302

atc tgg gca ctg agc ctg gca ctg ggc tgg gag gcc ttc cat gca ctg     1081
Ile Trp Ala Leu Ser Leu Ala Leu Gly Trp Glu Ala Phe His Ala Leu
303                 308                 313                 318

cag atc ctt ggc ttc ctc ata ctc ctt ata ggc act gcc ctc tac aat     1129
Gln Ile Leu Gly Phe Leu Ile Leu Leu Ile Gly Thr Ala Leu Tyr Asn
319                 324                 329                 334

ggg cta cac cgt ccg ctg ctg ggc cgc ctg tcc agg ggc cgg ccc ctg     1177
Gly Leu His Arg Pro Leu Leu Gly Arg Leu Ser Arg Gly Arg Pro Leu
335                 340                 345                 350

gca gag gag agc gag cag gag aga ctg ctg ggt ggc acc cgc act ccc     1225
Ala Glu Glu Ser Glu Gln Glu Arg Leu Leu Gly Gly Thr Arg Thr Pro
351                 356                 361                 366

atc aat gat gcc agc tga ggttcc ctggaggctt ctactgccac ccgggtgctc     1279
Ile Asn Asp Ala Ser  *
367                 372

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Document 5 of 5 - Date Saved: 2/6/2006

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Ser Gly Glu Leu Ser Asn Arg Phe Gln Gly Gly Lys Ala Phe Gly Leu
2 7 12 17

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Leu Lys Ala Arg Gln Glu Arg Arg Leu Ala Glu Ile Asn Arg Glu Phe
18 23 28 33

ctg tgt gac cag aag tac agt gat gaa gag aac ctt cca gaa aag ctc 259
Leu Cys Asp Gln Lys Tyr Ser Asp Glu Glu Asn Leu Pro Glu Lys Leu
34 39 44 49

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Thr Ala Phe Lys Glu Lys Tyr Met Glu Phe Asp Leu Asn Asn Glu Gly
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Glu Ile Asp Leu Met Ser Leu Lys Arg Met Met Glu Lys Leu Gly Val
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Pro Lys Thr His Leu Glu Met Lys Lys Met Ile Ser Glu Val Thr Gly
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ggg gtc agt gac act ata tcc tac cga gac ttt gtg aac atg atg ctg 451
Gly Val Ser Asp Thr Ile Ser Tyr Arg Asp Phe Val Asn Met Met Leu
98 103 108 113

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Gly Lys Arg Ser Ala Val Leu Lys Leu Val Met Met Phe Glu Gly Lys
114 119 124 129

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Ala Asn Glu Ser Ser Pro Lys Pro Val Gly Pro Pro Pro Glu Arg Asp
130 135 140 145

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Ile Ala Ser Leu Pro *
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 32                  37                  42                  47

tta aat gag ttt tcc tat acg gcc acc gaa gcc aga agg ctt tat ctg      251
Leu Asn Glu Phe Ser Tyr Thr Ala Thr Glu Ala Arg Arg Leu Tyr Leu
 48                  53                  58                  63

caa agg aag aca gtt ccc agc gcg ctg ctc gtc cag ctg att cag gaa      299
Gln Arg Lys Thr Val Pro Ser Ala Leu Leu Val Gln Leu Ile Gln Glu
 64                  69                  74                  79

cgc ctg gct gaa gag gat tgc atc aag cag ggc tgg att ctg gat ggc      347
Arg Leu Ala Glu Glu Asp Cys Ile Lys Gln Gly Trp Ile Leu Asp Gly
 80                  85                  90                  95

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Ile Pro Glu Thr Arg Glu Gln Ala Leu Arg Ile Gln Thr Leu Gly Ile
 96                 101                 106                 111

aca ccc aga cac gtc att gtg ctg agt gct cca gac acg gtc ctg atc      443
Thr Pro Arg His Val Ile Val Leu Ser Ala Pro Asp Thr Val Leu Ile
112                 117                 122                 127

gag aga aac ttg ggg aag aga atc gac cct caa act gga gag att tat      491
Glu Arg Asn Leu Gly Lys Arg Ile Asp Pro Gln Thr Gly Glu Ile Tyr
128                 133                 138                 143

cac acc acc ttt gac tgg cca ccc gaa tct gaa atc cag aac cgt ctc      539
His Thr Thr Phe Asp Trp Pro Pro Glu Ser Glu Ile Gln Asn Arg Leu
144                 149                 154                 159

atg gtg cca gag gac atc tca gag ctg gag acg gct cag aaa ctg ctg      587
Met Val Pro Glu Asp Ile Ser Glu Leu Glu Thr Ala Gln Lys Leu Leu
160                 165                 170                 175

gag tat cat agg aac atc gtc agg gtc att ccc tcc tac ccc aaa atc      635
Glu Tyr His Arg Asn Ile Val Arg Val Ile Pro Ser Tyr Pro Lys Ile
176                 181                 186                 191

ctc aaa gtc atc agt gct gac cag cca tgt gtg gac gtc ttc tac cag      683
Leu Lys Val Ile Ser Ala Asp Gln Pro Cys Val Asp Val Phe Tyr Gln
192                 197                 202                 207

gct ctg acc tat gtc caa agc aac cat cgt act aat gcc ccg ttc acc      731
Ala Leu Thr Tyr Val Gln Ser Asn His Arg Thr Asn Ala Pro Phe Thr
208                 213                 218                 223

ccg agg gtg ctg ctg ctc ggg cct gtg ggc agt ggg aaa agt ctg cag      779
Pro Arg Val Leu Leu Leu Gly Pro Val Gly Ser Gly Lys Ser Leu Gln
224                 229                 234                 239

gcc gcc ctc ctg gcc cag aaa tac agg ctt gtc aat gtc tgc tgt ggg      827
Ala Ala Leu Leu Ala Gln Lys Tyr Arg Leu Val Asn Val Cys Cys Gly
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atc cag ccc ttc ttt gaa aag gag atg gca gag gga ggc cac agg gtg      923
Ile Gln Pro Phe Phe Glu Lys Glu Met Ala Glu Gly Gly His Arg Val
272                 277                 282                 287

aag gga aca gtg gaa ttc agc ttc cga aca ctg ccc tgc aac cag aag      971
Lys Gly Thr Val Glu Phe Ser Phe Arg Thr Leu Pro Cys Asn Gln Lys
288                 293                 298                 303

gac ctg ccc tgc ctc ctg aaa ctg gag gac atg ctg ctg tat ccc ctg     1019
Asp Leu Pro Cys Leu Leu Lys Leu Glu Asp Met Leu Leu Tyr Pro Leu
304                 309                 314                 319

agg ctt tca gaa ctt cca gaa gag gag ctg ctg gtt ggt gct ctc cca     1067
Arg Leu Ser Glu Leu Pro Glu Glu Glu Leu Leu Val Gly Ala Leu Pro
320                 325                 330                 335

tat acc ttt ggg gag tca ttg gag aca tcc cag att ccc ctt ttc aat     1115
Tyr Thr Phe Gly Glu Ser Leu Glu Thr Ser Gln Ile Pro Leu Phe Asn
336                 341                 346                 351

cct aga ccc ccc aac ggc agg tgc agc ttg aag cct ctt tcc ctc tgg     1163
Pro Arg Pro Pro Asn Gly Arg Cys Ser Leu Lys Pro Leu Ser Leu Trp
352                 357                 362                 367

gaa cat cct cgc ctg acg gga gct gac acg ggt tct ttc tca ttg ggc     1211
Glu His Pro Arg Leu Thr Gly Ala Asp Thr Gly Ser Phe Ser Leu Gly
368                 373                 378                 383

tgt gag cgg ggc ctg cag agg cag ggg cag gac atg agg ggt gag gaa     1259
Cys Glu Arg Gly Leu Gln Arg Gln Gly Gln Asp Met Arg Gly Glu Glu
384                 389                 394                 399

gag gtg gcc cca gtg acc ctc tgc agc ctc tac act tat gat cag gga     1307
Glu Val Ala Pro Val Thr Leu Cys Ser Leu Tyr Thr Tyr Asp Gln Gly
400                 405                 410                 415

gat tcc ctg gac ctc ctg ggt cct att ggg atc ctt cag gag ggg cgg     1355
Asp Ser Leu Asp Leu Leu Gly Pro Ile Gly Ile Leu Gln Glu Gly Arg
416                 421                 426                 431

gac cca ggg acc cag gga cca cag gag aaa gag aag caa atg cca gcc     1403
Asp Pro Gly Thr Gln Gly Pro Gln Glu Lys Glu Lys Gln Met Pro Ala
432                 437                 442                 447

tcc ccc atg aac act gat gct cat ctt gac atc aat ttc aag gag ggc     1451
Ser Pro Met Asn Thr Asp Ala His Leu Asp Ile Asn Phe Lys Glu Gly
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ttg aag aag gaa aga agt tac acc ggg cag ttt gaa gcg aat gtg agg     1499
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atg aag gtg ctg agc cag cgc ctg gac cag cag gac tgc atc cag aaa     1595
Met Lys Val Leu Ser Gln Arg Leu Asp Gln Gln Asp Cys Ile Gln Lys
496                 501                 506                 511

ggc tgg gtg cta cac ggc gtc ccg cgg gac ctc gac cag gca cac ctg     1643
Gly Trp Val Leu His Gly Val Pro Arg Asp Leu Asp Gln Ala His Leu
512                 517                 522                 527

ctg aac cgc ctg ggc tac aat ccc aac agg gct cag ctg aag ggg tcc     1691
Leu Asn Arg Leu Gly Tyr Asn Pro Asn Arg Ala Gln Leu Lys Gly Ser
528                 533                 538                 543

agg tta cac aag cct tca cgt gtt cct gaa gtg gaa tgt ctc ctg gtc     1739
Arg Leu His Lys Pro Ser Arg Val Pro Glu Val Glu Cys Leu Leu Val
544                 549                 554                 559

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cggcccttcg ccgggcagag aag    atg ttg ccc ctg tcc atc aaa gac gat     230
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gaa tac aaa cca ccc aag ttc aat ttg ttc ggc aag atc tcg ggc tgg      278
Glu Tyr Lys Pro Pro Lys Phe Asn Leu Phe Gly Lys Ile Ser Gly Trp
 10                  15                  20                  25

ttt agg tct ata ctg tcc gac aag act tcc cgg aac ctg ttt ttc ttc      326
Phe Arg Ser Ile Leu Ser Asp Lys Thr Ser Arg Asn Leu Phe Phe Phe
 26                  31                  36                  41
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ctg tgc ctg aac ctc tct ttc gct ttt gtg gaa cta ctc tac ggc atc      374
Leu Cys Leu Asn Leu Ser Phe Ala Phe Val Glu Leu Leu Tyr Gly Ile
 42                  47                  52                  57

tgg agc aac tgc tta ggc ttg att tcc gac tct ttt cac atg ttt ttc      422
Trp Ser Asn Cys Leu Gly Leu Ile Ser Asp Ser Phe His Met Phe Phe
 58                  63                  68                  73

gat agc act gcc att ttg gct gga ctg gca gct tct gtt att tca aaa      470
Asp Ser Thr Ala Ile Leu Ala Gly Leu Ala Ala Ser Val Ile Ser Lys
 74                  79                  84                  89

tgg aga gat aat gat gct ttc tcc tat ggg tat gtt aga gcg gaa gtt      518
Trp Arg Asp Asn Asp Ala Phe Ser Tyr Gly Tyr Val Arg Ala Glu Val
 90                  95                 100                 105

ctg gct ggc ttt gtc aat ggc cta ttt ttg atc ttc act gct ttt ttt      566
Leu Ala Gly Phe Val Asn Gly Leu Phe Leu Ile Phe Thr Ala Phe Phe
106                 111                 116                 121

att ttc tca gaa gga gtt gag aga gca tta gcc cct cca gat gtc cac      614
Ile Phe Ser Glu Gly Val Glu Arg Ala Leu Ala Pro Pro Asp Val His
122                 127                 132                 137

cat gag aga ctg ctt ctt gtt tcc att ctt ggg ttt gtg gta aac cta      662
His Glu Arg Leu Leu Leu Val Ser Ile Leu Gly Phe Val Val Asn Leu
138                 143                 148                 153

ata gga ata ttt gtt ttc aaa cat gga ggt cat gga cat tct cat ggc      710
Ile Gly Ile Phe Val Phe Lys His Gly Gly His Gly His Ser His Gly
154                 159                 164                 169

tct ggc cac gga cac agt cat tcc ctc ttt aat ggt gct cta gat cag      758
Ser Gly His Gly His Ser His Ser Leu Phe Asn Gly Ala Leu Asp Gln
170                 175                 180                 185

gca cat ggc cat gtc gat cat tgc cat agc cat gaa gtg aaa cat ggt      806
Ala His Gly His Val Asp His Cys His Ser His Glu Val Lys His Gly
186                 191                 196                 201

gct gca cat agc cat gat cat gct cat gga cat gga cac ttt cat tct      854
Ala Ala His Ser His Asp His Ala His Gly His Gly His Phe His Ser
202                 207                 212                 217

cat gat ggc ccg tcc tta aaa gaa aca aca gga ccc agc aga cag att      902
His Asp Gly Pro Ser Leu Lys Glu Thr Thr Gly Pro Ser Arg Gln Ile
218                 223                 228                 233

tta caa ggt gta ttt tta cat atc cta gca gat aca ctt gga agt att      950
Leu Gln Gly Val Phe Leu His Ile Leu Ala Asp Thr Leu Gly Ser Ile
234                 239                 244                 249

ggt gta att gct tct gcc atc atg atg caa aat ttt ggt ctg atg ata      998
Gly Val Ile Ala Ser Ala Ile Met Met Gln Asn Phe Gly Leu Met Ile
250                 255                 260                 265

gca gat cct atc tgt tca att ctt ata gcc att ctt ata gtt gta agt     1046
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Ala Asp Pro Ile Cys Ser Ile Leu Ile Ala Ile Leu Ile Val Val Ser
266                 271                 276                 281

gtt att cct ctt tta aga gaa tct gtt gga ata tta atg cag aga act     1094
Val Ile Pro Leu Leu Arg Glu Ser Val Gly Ile Leu Met Gln Arg Thr
282                 287                 292                 297

cct ccc cta tta gaa aat agt ctg cct cag tgc tat cag agg gta cag     1142
Pro Pro Leu Leu Glu Asn Ser Leu Pro Gln Cys Tyr Gln Arg Val Gln
298                 303                 308                 313

cag ttg caa gga gtt tac agt tta cag gaa cag cac ttc tgg act tta     1190
Gln Leu Gln Gly Val Tyr Ser Leu Gln Glu Gln His Phe Trp Thr Leu
314                 319                 324                 329

tgt tct gac gtt tat gtt ggg acc ttg aaa tta ata gta gca cct gat     1238
Cys Ser Asp Val Tyr Val Gly Thr Leu Lys Leu Ile Val Ala Pro Asp
330                 335                 340                 345

gct gat gct agg tgg att tta agc caa aca cat aat att ttt act cag     1286
Ala Asp Ala Arg Trp Ile Leu Ser Gln Thr His Asn Ile Phe Thr Gln
346                 351                 356                 361

gct gga gtg aga cag ctc tac gta cag att gac ttt gca gcc atg tag     1334
Ala Gly Val Arg Gln Leu Tyr Val Gln Ile Asp Phe Ala Ala Met  *
362                 367                 372                 377

tgaatggaaa gaaattatgc acctttttatg gaccaaattt ttctggtact gtacgatcca   1394

aaacattgta cccagctttt taaaagagag aaattatcac tacaactccc gagcactaag   1454

tagacggggt agagtcagcc gttcatgctt tgtggggagt tcacagctaa gggatcagat   1514

ttaagaggat atctcctgga cttttggtct tttcttttgt gctctttcct ccaaatcttt   1574

ttgacttctg aggtttttag cttaggatgt taatttgtcc ttttgtcttt ctttttttgt   1634

ttttgttttc tgtttgtttg ttttcatgtt gaatgcccac accaccatcc tctcatccca   1694

gccagtaaga atttcagttg tgggcctcca gtcttctgga atgtcttcac tgcagctgct   1754

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atg ggc ccc tgg ctt ttc cct ttc tct ggg cag ggg act gac ttc ctc      106
Met Gly Pro Trp Leu Phe Pro Phe Ser Gly Gln Gly Thr Asp Phe Leu
  1               5                  10                  15

ttg tcc cgg aat gag cat gcc tgc cct ttg caa gca ggt ttg ggt ctc      154
Leu Ser Arg Asn Glu His Ala Cys Pro Leu Gln Ala Gly Leu Gly Leu
 17                  22                  27                  32

acg cag agg aaa cca aaa gca ata aga ggg agg gaa ggc aga gca acc      202
Thr Gln Arg Lys Pro Lys Ala Ile Arg Gly Arg Glu Gly Arg Ala Thr
 33                  38                  43                  48

aat caa ggg cag ggt gag act caa aac gag cgg gct ccc tgg gga gcc      250
Asn Gln Gly Gln Gly Glu Thr Gln Asn Glu Arg Ala Pro Trp Gly Ala
 49                  54                  59                  64

aga cag agg ctg ggg gtg atg gcg gag cta cag cag ctg cag gag ttt      298
Arg Gln Arg Leu Gly Val Met Ala Glu Leu Gln Gln Leu Gln Glu Phe
 65                  70                  75                  80

gag atc ccc act ggc cgg gag gct ctg agg ggc aac cac agt gcc ctg      346
Glu Ile Pro Thr Gly Arg Glu Ala Leu Arg Gly Asn His Ser Ala Leu
 81                  86                  91                  96

ctg cgg gtc gct gac tac tgc gag gac aac tat gtg cag gcc aca gac      394
Leu Arg Val Ala Asp Tyr Cys Glu Asp Asn Tyr Val Gln Ala Thr Asp
 97                 102                 107                 112

aag cgg aag gcg ctg gag gag acc atg gcc ttc act acc cag gca ctg      442
Lys Arg Lys Ala Leu Glu Glu Thr Met Ala Phe Thr Thr Gln Ala Leu
113                 118                 123                 128

gcc agc gtg gcc tac cag gtg ggc aac ctg gcc ggg cac act ctg cgc      490
Ala Ser Val Ala Tyr Gln Val Gly Asn Leu Ala Gly His Thr Leu Arg
129                 134                 139                 144

atg ttg gac ctg cag ggg gcc gcc ctg cgg cag gtg gaa gcc cgt gta      538
Met Leu Asp Leu Gln Gly Ala Ala Leu Arg Gln Val Glu Ala Arg Val
145                 150                 155                 160

agc acg ctg ggc cag atg gtg aac atg cat atg gag aag gtg gcc cga      586
Ser Thr Leu Gly Gln Met Val Asn Met His Met Glu Lys Val Ala Arg
161                 166                 171                 176

agg gag atc ggc acc tta gcc act gtc cag cgg ctg ccc ccc ggc cag      634
Arg Glu Ile Gly Thr Leu Ala Thr Val Gln Arg Leu Pro Pro Gly Gln
177                 182                 187                 192

aag gtc atc gcc cca gag aac cta ccc cct ctc acg ccc tac tgc agg      682
Lys Val Ile Ala Pro Glu Asn Leu Pro Pro Leu Thr Pro Tyr Cys Arg
193                 198                 203                 208

aga ccc ctc aac ttt ggc tgc ctg gac gac att ggc cat ggg atc aag      730
Arg Pro Leu Asn Phe Gly Cys Leu Asp Asp Ile Gly His Gly Ile Lys
209                 214                 219                 224
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gac ctc agc acg cag ctg tca aga aca ggc acc ctg tct cga aag agc      778
Asp Leu Ser Thr Gln Leu Ser Arg Thr Gly Thr Leu Ser Arg Lys Ser
225                 230                 235                 240

atc aag gcc cct gcc aca ccc gcc tcc gcc acc ttg ggg aga cca ccc      826
Ile Lys Ala Pro Ala Thr Pro Ala Ser Ala Thr Leu Gly Arg Pro Pro
241                 246                 251                 256

cgg att ccc gag cca gtg cac ctg ccg gtg gtg ccc gac ggc aga ctc      874
Arg Ile Pro Glu Pro Val His Leu Pro Val Val Pro Asp Gly Arg Leu
257                 262                 267                 272

tcc gcc gcc tcc tct gcg tct tcc ctg gcc tcg gcc ggc agc gcc gaa      922
Ser Ala Ala Ser Ser Ala Ser Ser Leu Ala Ser Ala Gly Ser Ala Glu
273                 278                 283                 288

ggt gtc ggt ggg gcc ccc acg ccc aag ggg cag gca gca cct cca gcc      970
Gly Val Gly Gly Ala Pro Thr Pro Lys Gly Gln Ala Ala Pro Pro Ala
289                 294                 299                 304

cca cct ctc ccc agc tcc ttg gac cca cct cct cca cca gca gcc gtc     1018
Pro Pro Leu Pro Ser Ser Leu Asp Pro Pro Pro Pro Pro Ala Ala Val
305                 310                 315                 320

gag gtg ttc cag cgg cct ccc acg ctg gag gag ttg tcc cca ccc cca     1066
Glu Val Phe Gln Arg Pro Pro Thr Leu Glu Glu Leu Ser Pro Pro Pro
321                 326                 331                 336

ccg gac gaa gag ctg ccc ctg cca ctg gac ctg cct cct cct cca ccc     1114
Pro Asp Glu Glu Leu Pro Leu Pro Leu Asp Leu Pro Pro Pro Pro Pro
337                 342                 347                 352

ctg gat gga gat gaa ttg ggg ctg cct cca ccc cca cca gga ttt ggg     1162
Leu Asp Gly Asp Glu Leu Gly Leu Pro Pro Pro Pro Pro Gly Phe Gly
353                 358                 363                 368

cct gat gag ccc agc tgg gtg cct gcc tca tac ttg gag aaa gtg gtg     1210
Pro Asp Glu Pro Ser Trp Val Pro Ala Ser Tyr Leu Glu Lys Val Val
369                 374                 379                 384

aca ctg tac cca tac acc agc cag aag gac aat gag ctc tcc ttc tct     1258
Thr Leu Tyr Pro Tyr Thr Ser Gln Lys Asp Asn Glu Leu Ser Phe Ser
385                 390                 395                 400

gag ggc act gtc atc tgt gtc act cgc cgc tac tcc gat ggc tgg tgc     1306
Glu Gly Thr Val Ile Cys Val Thr Arg Arg Tyr Ser Asp Gly Trp Cys
401                 406                 411                 416

gag ggc gtc agc tca gag ggg act gga ttc ttc cct ggg aac tat gtg     1354
Glu Gly Val Ser Ser Glu Gly Thr Gly Phe Phe Pro Gly Asn Tyr Val
417                 422                 427                 432

gag ccc agc tgc tga cagcccaggg ctctctgggc agctgatgtc tgcactgagt     1409
Glu Pro Ser Cys  *
433

gggtttcatg agccccaagc caaaaccagc tccagtcaca gctggactgg gtctgcccac   1469
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ctcttgggct gtgagctgtg ttctgtcctt cctcccatcg gagggagaag gggtcctggg   1529

gagagagaat ttatccagag gcctgctgca gatggggaag agctggaaac caagaagttt   1589

gtcaacagag gacccctact ccatgcagga cagggtctcc tgctgcaagt cccaactttg   1649

aataaaacag atgatgtcct gtgactgccc cacagagata aggggccagg agggattgaa   1709

aggcatccca gttctaaggc tgctgctaat tacagccccc aacctccaac ccaccagctg   1769

acctagaagc agcatcttcc catttcctca gtacccacaa agtgcagccc acattggacc   1829

ccagacaccc ctctgcagcc attgactgca acttgttctt ttgcccattg aaaaaaaaaa   1889

a                                                                   1890
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<400> 260

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                                                 Met Glu Ala Ala
                                                   1

gcg acg ccg gcg gct gcc ggg gcg gcg agg cgc gag gag cta gat atg      104
Ala Thr Pro Ala Ala Ala Gly Ala Ala Arg Arg Glu Glu Leu Asp Met
  5                  10                  15                  20

gat gta atg agg ccc ttg ata aat gag cag aat ttt gat ggg aca tca      152
Asp Val Met Arg Pro Leu Ile Asn Glu Gln Asn Phe Asp Gly Thr Ser
 21                  26                  31                  36

gat gaa gaa cat gag caa gag ctt ctg cct gtt cag aag cat tac caa      200
Asp Glu Glu His Glu Gln Glu Leu Leu Pro Val Gln Lys His Tyr Gln
 37                  42                  47                  52

ctt gat gat caa gag ggc att tca ttt gta caa act ctt atg cac ctt      248
Leu Asp Asp Gln Glu Gly Ile Ser Phe Val Gln Thr Leu Met His Leu
 53                  58                  63                  68

ctt aaa gga aat att gga act ggc ctt tta gga ctt cca ttg gca ata      296
Leu Lys Gly Asn Ile Gly Thr Gly Leu Leu Gly Leu Pro Leu Ala Ile
 69                  74                  79                  84

aaa aat gca ggc ata gtg ctt gga cca atc agc ctt gtg ttt ata gga      344
Lys Asn Ala Gly Ile Val Leu Gly Pro Ile Ser Leu Val Phe Ile Gly
 85                  90                  95                 100
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att att tct gtt cac tgt atg cac ata ttg gta cgt tgc agt cac ttt      392
Ile Ile Ser Val His Cys Met His Ile Leu Val Arg Cys Ser His Phe
101                 106                 111                 116

cta tgt ctg agg ttt aaa aag tca aca tta ggt tat agt gac act gtg      440
Leu Cys Leu Arg Phe Lys Lys Ser Thr Leu Gly Tyr Ser Asp Thr Val
117                 122                 127                 132

agc ttt gct atg gaa gtg agt cct tgg agt tgt ctt cag aag caa gca      488
Ser Phe Ala Met Glu Val Ser Pro Trp Ser Cys Leu Gln Lys Gln Ala
133                 138                 143                 148

gca tgg ggg cgg agt gtg gtt gac ttt ttt ctg gtg ata aca cag ctg      536
Ala Trp Gly Arg Ser Val Val Asp Phe Phe Leu Val Ile Thr Gln Leu
149                 154                 159                 164

gga ttc tgt agt gtt tat att gtc ttc tta gct gaa aat gtg aaa caa      584
Gly Phe Cys Ser Val Tyr Ile Val Phe Leu Ala Glu Asn Val Lys Gln
165                 170                 175                 180

gtt cat gaa gga ttc ctg gag agt aaa gtg ttt att tca aat agt acc      632
Val His Glu Gly Phe Leu Glu Ser Lys Val Phe Ile Ser Asn Ser Thr
181                 186                 191                 196

aat tca tca aac cct tgt gag aga aga agt gtt gac cta agg ata tat      680
Asn Ser Ser Asn Pro Cys Glu Arg Arg Ser Val Asp Leu Arg Ile Tyr
197                 202                 207                 212

atg ctt tgc ttt ctt cca ttt ata att ctt ttg gtc ttc att cgt gaa      728
Met Leu Cys Phe Leu Pro Phe Ile Ile Leu Leu Val Phe Ile Arg Glu
213                 218                 223                 228

cta aag aat cta ttt gta ctt tca ttc ctt gcc aac gtt tcc atg gct      776
Leu Lys Asn Leu Phe Val Leu Ser Phe Leu Ala Asn Val Ser Met Ala
229                 234                 239                 244

gtc agt ctt gtg ata att tac cag tat gtt gtc agg aac atg cca gat      824
Val Ser Leu Val Ile Ile Tyr Gln Tyr Val Val Arg Asn Met Pro Asp
245                 250                 255                 260

ccc cac aac ctt cca ata gtg gct ggt tgg aag aaa tac cca ctc ttt      872
Pro His Asn Leu Pro Ile Val Ala Gly Trp Lys Lys Tyr Pro Leu Phe
261                 266                 271                 276

ttt ggt act gct gta ttt gct ttt gaa ggc ata gga gtg gtc ctt cca      920
Phe Gly Thr Ala Val Phe Ala Phe Glu Gly Ile Gly Val Val Leu Pro
277                 282                 287                 292

ctg gaa aac caa atg aaa gaa tca aag cgt ttc cct caa gcg ttg aat      968
Leu Glu Asn Gln Met Lys Glu Ser Lys Arg Phe Pro Gln Ala Leu Asn
293                 298                 303                 308

att ggc atg ggg att gtt aca act ttg tat gta aca tta gct act tta     1016
Ile Gly Met Gly Ile Val Thr Thr Leu Tyr Val Thr Leu Ala Thr Leu
309                 314                 319                 324
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gga tat atg tgt ttc cat gat gaa atc aaa ggc agc ata act tta aat     1064
Gly Tyr Met Cys Phe His Asp Glu Ile Lys Gly Ser Ile Thr Leu Asn
325                 330                 335                 340

ctt ccc caa gat gta tgg tta tat caa tca gtg aaa att cta tat tcc     1112
Leu Pro Gln Asp Val Trp Leu Tyr Gln Ser Val Lys Ile Leu Tyr Ser
341                 346                 351                 356

ttt ggc att ttt gtg aca tat tca att cag ttc tat gtt cca gca gag     1160
Phe Gly Ile Phe Val Thr Tyr Ser Ile Gln Phe Tyr Val Pro Ala Glu
357                 362                 367                 372

atc att atc cct ggg atc aca tcc aaa ttt cat act aaa tgg aag caa     1208
Ile Ile Ile Pro Gly Ile Thr Ser Lys Phe His Thr Lys Trp Lys Gln
373                 378                 383                 388

atc tgt gaa ttt ggg ata aga tcc ttc ttg gtt agt att act tgt gcc     1256
Ile Cys Glu Phe Gly Ile Arg Ser Phe Leu Val Ser Ile Thr Cys Ala
389                 394                 399                 404

gga gca att ctt att cct cgt tta gac att gtg att tcc ttc gtt gga     1304
Gly Ala Ile Leu Ile Pro Arg Leu Asp Ile Val Ile Ser Phe Val Gly
405                 410                 415                 420

gct gtg agc agc agc aca ttg gcc cta atc ctg cca cct ttg gtt gaa     1352
Ala Val Ser Ser Ser Thr Leu Ala Leu Ile Leu Pro Pro Leu Val Glu
421                 426                 431                 436

att ctt aca ttt tcg aag gaa cat tat aat ata tgg atg gtc ctg aaa     1400
Ile Leu Thr Phe Ser Lys Glu His Tyr Asn Ile Trp Met Val Leu Lys
437                 442                 447                 452

aat att tct ata gca ttc act gga gtt gtt ggc ttc tta tta ggt aca     1448
Asn Ile Ser Ile Ala Phe Thr Gly Val Val Gly Phe Leu Leu Gly Thr
453                 458                 463                 468

tat ata act gtt gaa gaa att att tat cct act ccc aaa gtt gta gct     1496
Tyr Ile Thr Val Glu Glu Ile Ile Tyr Pro Thr Pro Lys Val Val Ala
469                 474                 479                 484

ggc act cca cag agt cct ttt cta aat ttg aat tca aca tgc tta aca     1544
Gly Thr Pro Gln Ser Pro Phe Leu Asn Leu Asn Ser Thr Cys Leu Thr
485                 490                 495                 500

tct ggt ttg aaa tag taaaagcaga atcatgagtc ttctattttt gtcccatttc     1599
Ser Gly Leu Lys  *
501

tgaaaattat caagataact agtaaaatac attgctatat acataaaaat ggtaacaaac   1659

tctgttttct ttggcacgat attaatattt tggaagtaat cataactctt taccagtagt   1719

ggtaaaccta tgaaaaatcc ttgcttttaa gtgttagcaa tagttcaaaa aattaagttc   1779

tgaaaattga aaaaattaaa atgtaaaaaa attaaagaat aaaaatactt ctattattct   1839

tttatctcag taagaaatac cttaaccaag atatctctct tttatgctac tcttttgcca   1899
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ctcacttgag aacagaatag gatttcaaca ataagagaat aaaataagaa catgtataac   1959

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aaaaaaaaat ctcagttatg tttttattag ccaaattcta atgattggct cctggaagta   2079

tagaaaactc ccattaacat aatataagca tcagaaaatt gcaaacacta gaattaattt   2139

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tgtttcaatg aaatttgaaa agggacttta aaacttatcc agtgcaactc ccttgttttt   2259

cgtcagagga aaaggaggcc tagaaaggtt aagtaacttg gtcgagacca ctcagccttg   2319

agatcaagaa aacctaatct tctgactccc aggccaggga tgttttattt ctcacatcat   2379

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US 2005/0059024 A1

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                                         Met Gly Ala Ser Ala Arg
                                           1

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Leu Leu Arg Ala Val Ile Met Gly Ala Pro Gly Ser Gly Lys Gly Thr
  7                  12                  17                  22

gtg tcg tcg cgc atc act aca cac ttc gag ctg aag cac ctc tcc agc      150
Val Ser Ser Arg Ile Thr Thr His Phe Glu Leu Lys His Leu Ser Ser
 23                  28                  33                  38

ggg gac ctg ctc cgg gac aac atg ctg cgg ggc aca gaa att ggc gtg      198
Gly Asp Leu Leu Arg Asp Asn Met Leu Arg Gly Thr Glu Ile Gly Val
 39                  44                  49                  54

tta gcc aag gct ttc att gac caa ggg aaa ctc atc cca gat gat gtc      246
Leu Ala Lys Ala Phe Ile Asp Gln Gly Lys Leu Ile Pro Asp Asp Val
 55                  60                  65                  70

atg act cgg ctg gcc ctt cat gag ctg aaa aat ctc acc cag tat agc      294
Met Thr Arg Leu Ala Leu His Glu Leu Lys Asn Leu Thr Gln Tyr Ser
 71                  76                  81                  86

tgg ctg ttg gat ggt ttt cca agg aca ctt cca cag gca gaa gcc cta      342
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Trp Leu Leu Asp Gly Phe Pro Arg Thr Leu Pro Gln Ala Glu Ala Leu
 87                  92                  97                  102

gat aga gct tat cag atc gac aca gtg att aac ctg aat gtg ccc ttt      390
Asp Arg Ala Tyr Gln Ile Asp Thr Val Ile Asn Leu Asn Val Pro Phe
103                 108                 113                 118

gag gtc att aaa caa cgc ctt act gct cgc tgg att cat ccc gcc agt      438
Glu Val Ile Lys Gln Arg Leu Thr Ala Arg Trp Ile His Pro Ala Ser
119                 124                 129                 134

ggc cga gtc tat aac att gaa ttc aac cct ccc aaa act gtg ggc att      486
Gly Arg Val Tyr Asn Ile Glu Phe Asn Pro Pro Lys Thr Val Gly Ile
135                 140                 145                 150

gat gac ctg act ggg gag cct ctc att cag cgt gag gat gat aaa cca      534
Asp Asp Leu Thr Gly Glu Pro Leu Ile Gln Arg Glu Asp Asp Lys Pro
151                 156                 161                 166

gag acg gtt atc aag aga cta aag gct tat gaa gac caa aca aag cca      582
Glu Thr Val Ile Lys Arg Leu Lys Ala Tyr Glu Asp Gln Thr Lys Pro
167                 172                 177                 182

gtc ctg gaa tat tac cag aaa aaa ggg gtg ctg gaa aca ttc tcc gga      630
Val Leu Glu Tyr Tyr Gln Lys Lys Gly Val Leu Glu Thr Phe Ser Gly
183                 188                 193                 198

aca gaa acc aac aag att tgg ccc tat gta tat gct ttc cta caa act      678
Thr Glu Thr Asn Lys Ile Trp Pro Tyr Val Tyr Ala Phe Leu Gln Thr
199                 204                 209                 214

aaa gtt cca caa aga agc cag aaa gct tca gtt act cca tga ggagaaa      727
Lys Val Pro Gln Arg Ser Gln Lys Ala Ser Val Thr Pro  *
215                 220                 225

tgtgtgtaac tattaatagt aagatgggca aacctcctag tccttgcatt tagaagctgc    787

ttttcctaag acttctagta tgtatgaatt ctttgaaaat tatattactt ttatttctac    847

tgattttatt ttggatacta aggatgtgcc aaatgattcg gatactaaga tgcatcgttt    907

gaaatcatct agtgtgttgt atgcagttat cctcaaaaac atcagcgatg tctgaacctt    967

taaaacatct gttagagcaa aattaaaaga gcatttggta gtaatctaac tttttgttca   1027

gttaataagt ggttgataag tttccatatt ttctggaaag ttaaaaaagt tacatgtcat   1087

ttggagaaaa tacgtaatca gaaatttgtg catagattga tgccaaaaaa gacatttcca   1147

gcattgtgga acatggtgag acactatata aaattccaga aagaaagcaa ctggatttac   1207

agatttattg tgagacacaa attcactgct gcctttacac taagaaatgt atatgttaac   1267

catatatgct gtatttattt tgtcgttaag catactttca gtttactcag aattttcaat   1327

ttgctataaa gatgtatcaa ttagcatata gaaaaatatt actttaagat gacttgtttc   1387
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09750-5050-US

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taatgcctta tttgaatgtt aatcttatgt gctttctaaa aaatgttgtg aaataccaaa 2347

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ttcataaaaa aaaa 2421

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gaggtgcggg acgcggagac tgcgcgggcc cggtagccct ggagaggccg aggctctagg    180

ccgcgagggg cgggtgca  atg gcg gag gaa cag gtg aac cgc agc gcc ggc     231
                     Met Ala Glu Glu Gln Val Asn Arg Ser Ala Gly
                       1               5

ctg gcc ccc gac tgt gag gcc tcg gcg act gca gaa act acg gtt tcc      279
Leu Ala Pro Asp Cys Glu Ala Ser Ala Thr Ala Glu Thr Thr Val Ser
 12                  17                  22                  27

tca gtg ggg acc tgt gaa gcc gct ggc aag tca cca gag ccc aag gac      327
Ser Val Gly Thr Cys Glu Ala Ala Gly Lys Ser Pro Glu Pro Lys Asp
 28                  33                  38                  43

tac gac agc acc tgc gtg ttc tgc cgg atc gcg ggg cgg cag gac ccg      375
Tyr Asp Ser Thr Cys Val Phe Cys Arg Ile Ala Gly Arg Gln Asp Pro
 44                  49                  54                  59

ggc acc gaa ctc ctg cac tgc gag aat gag gac cta att tgc ttc aaa      423
Gly Thr Glu Leu Leu His Cys Glu Asn Glu Asp Leu Ile Cys Phe Lys
 60                  65                  70                  75

gat atc aaa cca gca gca act cat cat tat ctt gtg gtg cca aag aag      471
Asp Ile Lys Pro Ala Ala Thr His His Tyr Leu Val Val Pro Lys Lys
 76                  81                  86                  91

cat att gga aac tgc aga act cta agg aaa gat caa gta gaa ctg gtt      519
His Ile Gly Asn Cys Arg Thr Leu Arg Lys Asp Gln Val Glu Leu Val
 92                  97                 102                 107

gag aac atg gta act gtt gga aaa acc att ctt gaa aga aat aat ttc      567
Glu Asn Met Val Thr Val Gly Lys Thr Ile Leu Glu Arg Asn Asn Phe
108                 113                 118                 123

act gac ttc acg aat gtg agg atg ggt ttt cat atg cca cca ttc tgt      615
Thr Asp Phe Thr Asn Val Arg Met Gly Phe His Met Pro Pro Phe Cys
124                 129                 134                 139

tcc att tcc cac ttg cac ctt cat gtt ctg gca cca gtg gat cag ctt      663
Ser Ile Ser His Leu His Leu His Val Leu Ala Pro Val Asp Gln Leu
140                 145                 150                 155

ggc ttc tta tcc aag ttg gtt tat aga gtc aat tcc tat tgg ttt atc      711
Gly Phe Leu Ser Lys Leu Val Tyr Arg Val Asn Ser Tyr Trp Phe Ile
156                 161                 166                 171

aca gct gat cac ttg att gaa aaa cta aga aca tga aaat gtcaagagtg      761
Thr Ala Asp His Leu Ile Glu Lys Leu Arg Thr  *
172                 177                 182

gaagattttt ctaatcttgg ttcagcatga agtggtattt aggtcccttt taagtctaat    821

tgcaatttta agatttgttg ggttttatga gaggctgtta cttagtggcc ttaaatcttt    881

tctgaatgtc tgtttcctaa gatctgtgat acagttatgt gaatattttg ttactgactt    941
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taatttatat caatgaattt acaataacta tcaaattggc tatcagaatt cactgtaatg 1421

gaattttgcc tctaataaca taaaggggga agaaacataa agtggttctc ttaataaaac 1481

tagcagaaaa tgttgcttta tggcatgttt ttgtatcaaa gagaaatcag aggttaaact 1541

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tgataacgca atgttaatac tattgatatt tcataggtat attttgttag aaattggttt 1661

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gcatgatatt aaagatagtt ttaagtaaca aattacttat tacaaagtta caacatgtgg 1901

aatcaatact gttttatttg ttcattaatt tattcattca gcaaacattt gttgaacatt 1961

taatgtgtac cagatattgc caggatcagg aaataaagaa ctaaaaatgg acattcagac 2021

tgcaattgct agtacagggg tcaaacaaaa tcagtgatta gaatttagtg cgttaagttc 2081

cctgatgcct tcacagccag aagaggctgt gaaggggata aacacttctg agagtggggt 2141

ggtagtagaa ctgagtattc aagactgaat gttagggcag gtaggacagt gactggttta 2201

ngcctgagga accttccang ttttttccgtt nagtcctgnc ttccnctatt atttnctttc 2261

ccatgggttt tgnaagttcc a 2282

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<400> 263

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taaagtccat ccggctcctc agtgagattg aaaaacttgt tggtacatca gtacctgggc    180

ttctggaaat tattctcagc agttccattt tagagattta taatcacatc cttcaaacag    240

tggttccaga tgaagatgtg acattcagga agagttgtgc cacaaaaagg aaactcagca    300

acattaatca agaggaagcc agtggaacat ctttacatca gaaagccatc   atg act     356
                                                          Met Thr
                                                            1

ttc act tgc cac aat gag att aat gct ttt gtt gta ctg agc aga ggg      404
Phe Thr Cys His Asn Glu Ile Asn Ala Phe Val Val Leu Ser Arg Gly
  3                   8                  13                  18

agt caa att ttg tct ctg aat tcc act agg ttt tta aca aag tta gga      452
Ser Gln Ile Leu Ser Leu Asn Ser Thr Arg Phe Leu Thr Lys Leu Gly
 19                  24                  29                  34

cat tgc tct tca gcc tgt cct tct gac tca gtt tca cag acc aac att      500
His Cys Ser Ser Ala Cys Pro Ser Asp Ser Val Ser Gln Thr Asn Ile
 35                  40                  45                  50

caa aat ttg aaa ggc tta aat tct cca gtt ctt att ggg aag tca aaa      548
Gln Asn Leu Lys Gly Leu Asn Ser Pro Val Leu Ile Gly Lys Ser Lys
 51                  56                  61                  66

gat cca tcc tgt gtt gca aaa gtt tct gaa gag ggg aaa cct gcg ata      596
Asp Pro Ser Cys Val Ala Lys Val Ser Glu Glu Gly Lys Pro Ala Ile
 67                  72                  77                  82

ggg act cag aaa atg gag tta cat gtg agg tgg agg tca gac aca ggc      644
Gly Thr Gln Lys Met Glu Leu His Val Arg Trp Arg Ser Asp Thr Gly
 83                  88                  93                  98

aaa tgt gta gat gct tca ccg ctg gtt gta ata ccc act ttt gat aag      692
Lys Cys Val Asp Ala Ser Pro Leu Val Val Ile Pro Thr Phe Asp Lys
 99                 104                 109                 114

tca tct aca act gtg tac att ggt tcc cat tct cat aga atg aag gca      740
Ser Ser Thr Thr Val Tyr Ile Gly Ser His Ser His Arg Met Lys Ala
115                 120                 125                 130

gtt gac ttt tac tct ggg aag gta aaa tgg gaa cag att ttg gga gat      788
Val Asp Phe Tyr Ser Gly Lys Val Lys Trp Glu Gln Ile Leu Gly Asp
131                 136                 141                 146

cga att gaa tcc tca gca tgt gta tct aag tgt gga aac ttt att gtg      836
Arg Ile Glu Ser Ser Ala Cys Val Ser Lys Cys Gly Asn Phe Ile Val
147                 152                 157                 162

gtg ggc tgt tat aat gga tta gtt tat gtt ctg aaa agt aat agt gga      884
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Val Gly Cys Tyr Asn Gly Leu Val Tyr Val Leu Lys Ser Asn Ser Gly
163                 168                 173                 178

gaa aaa tac tgg atg ttt act act gaa gat gct gtc aaa agc tcg gca      932
Glu Lys Tyr Trp Met Phe Thr Thr Glu Asp Ala Val Lys Ser Ser Ala
179                 184                 189                 194

acc atg gat cca acc aca gga ctc att tac att gga tct cat gac cag      980
Thr Met Asp Pro Thr Thr Gly Leu Ile Tyr Ile Gly Ser His Asp Gln
195                 200                 205                 210

cac gca tat gct tta gat att tat aga aag aag tgt gtt tgg aag tca     1028
His Ala Tyr Ala Leu Asp Ile Tyr Arg Lys Lys Cys Val Trp Lys Ser
211                 216                 221                 226

aaa tgt gga gga act gtc ttt tcc tct ccg tgt ttg aac ctg att cca     1076
Lys Cys Gly Gly Thr Val Phe Ser Ser Pro Cys Leu Asn Leu Ile Pro
227                 232                 237                 242

cat cat ttg tat ttt gct aca ttg gga gga ctt tta ctg gct gta aat     1124
His His Leu Tyr Phe Ala Thr Leu Gly Gly Leu Leu Leu Ala Val Asn
243                 248                 253                 258

cct gct act ggg aac gtt att tgg aaa cat tcc tgt gga aaa cca ctc     1172
Pro Ala Thr Gly Asn Val Ile Trp Lys His Ser Cys Gly Lys Pro Leu
259                 264                 269                 274

ttc tct tcc cca caa tgt tgc tca cag tat att tgt att ggc tgt gta     1220
Phe Ser Ser Pro Gln Cys Cys Ser Gln Tyr Ile Cys Ile Gly Cys Val
275                 280                 285                 290

gat ggg aat tta ctc tgc ttt act cac ttt gga gaa cag gtt tgg cag     1268
Asp Gly Asn Leu Leu Cys Phe Thr His Phe Gly Glu Gln Val Trp Gln
291                 296                 301                 306

ttc tct acc agt gga cca atc ttt tca tcc ccg tgt acc tca cca tca     1316
Phe Ser Thr Ser Gly Pro Ile Phe Ser Ser Pro Cys Thr Ser Pro Ser
307                 312                 317                 322

gag caa aaa ata ttt ttt ggt tcc cat gat tgc ttt atc tac tgt tgt     1364
Glu Gln Lys Ile Phe Phe Gly Ser His Asp Cys Phe Ile Tyr Cys Cys
323                 328                 333                 338

aac atg aaa ggt cac ctg cag tgg aaa ttt gaa act act tca agg gtc     1412
Asn Met Lys Gly His Leu Gln Trp Lys Phe Glu Thr Thr Ser Arg Val
339                 344                 349                 354

tat gca aca ccg ttt gct ttc cat aac tac aat ggc agc aat gaa atg     1460
Tyr Ala Thr Pro Phe Ala Phe His Asn Tyr Asn Gly Ser Asn Glu Met
355                 360                 365                 370

ttg ctg gca gca gca tct act gat ggg aaa gtg tgg atc ttg gaa tct     1508
Leu Leu Ala Ala Ala Ser Thr Asp Gly Lys Val Trp Ile Leu Glu Ser
371                 376                 381                 386

cag agt gga caa ttg caa agt gtt tat gaa ctt cct gga gaa gtc ttc     1556
Gln Ser Gly Gln Leu Gln Ser Val Tyr Glu Leu Pro Gly Glu Val Phe
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387                 392                 397                 402

tct tct cct gtg gtc ctg gaa tca atg ctc att att ggg tgt aga gat     1604
Ser Ser Pro Val Val Leu Glu Ser Met Leu Ile Ile Gly Cys Arg Asp
403                 408                 413                 418

aat tat gtt tat tgt ctg gat tta ttg ggt ggc aat caa aaa taa tca     1652
Asn Tyr Val Tyr Cys Leu Asp Leu Leu Gly Gly Asn Gln Lys  *
419                 424                 429

aatacagtcc ttatttgtat aacaaatgtg agatatttga aaatatttta ccattataca   1712

tcatgtggac ttattttata ttaaagaaga ttatattttg gctaagaaaa aaaaaaaa     1770
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<213> Homo sapiens

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<222> (376)..(708)

<400> 264

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cccccaggtg caggtcgtgg ctgcccctgc cccgctcagt ccctgcacag ccaccagctg    180

gctgcctggg acccccttgaa gccaagcctg aggagctacc caccacacct gcttcagcac   240

cctcagctcc gctccctcac agccagctca ggccacctgg ggaggcgctc ttgccccccag   300

ccccgccctc tggaagagct actgcgtgca ggctccagca cccggcccca gcccctcacc    360

agcagctgct gcggg atg agc tgc atg tac agc ttc ctt ggc cac tgc tcg      411
                Met Ser Cys Met Tyr Ser Phe Leu Gly His Cys Ser
                  1               5                  10

gtc ctc ctg tgg ggc aca aag gga cga ggg tca gga agc ccc agc tcc      459
Val Leu Leu Trp Gly Thr Lys Gly Arg Gly Ser Gly Ser Pro Ser Ser
 13                  18                  23                  28

cct gga tgc tgc ctc cac ccc cca gcc cag cac tca cag gat ctc ccc      507
Pro Gly Cys Cys Leu His Pro Pro Ala Gln His Ser Gln Asp Leu Pro
 29                  34                  39                  44

ctg gtt cac gta gac gtg gga tgg cag cca cct ctt gga ccg act gtt      555
Leu Val His Val Asp Val Gly Trp Gln Pro Pro Leu Gly Pro Thr Val
 45                  50                  55                  60

ggg ctc agg cct ggg ctt ttg ggg gag agg caa aga gga gcc ctc agg      603
Gly Leu Arg Pro Gly Leu Leu Gly Glu Arg Gln Arg Gly Ala Leu Arg
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 61                  66                  71                  76

gct gga gac ccc caa tgc cag tgt ccc ctc cca gcc aca gtc cgt gag      651
Ala Gly Asp Pro Gln Cys Gln Cys Pro Leu Pro Ala Thr Val Arg Glu
 77                  82                  87                  92

gat ctg ggg gtc cca agt ccc tgg gct gcc gag tgc tca cct cct gcc      699
Asp Leu Gly Val Pro Ser Pro Trp Ala Ala Glu Cys Ser Pro Pro Ala
 93                  98                 103                 108

act cca tga caccact ccatgccaga aacttgttgt tgacgatctg gactgggcct      755
Thr Pro  *
109

gagttgacac caccaggtcc cactgcctgt tggaagggaa cggggtggga agaggggccc    815

aggctcctgg gaaacctgtc tgtctgtcct ggggcctgcc atccctccct ccgagccttg    875

gcctgttagc cccagctggg tccattctct agtcccaggg gaacaggccc tgcccctcat    935

ctgctcacag ccccccatgg ctccccagtg gcctgagaca ggtcccggcc ctcacctggt    995

gcacaggacc tgcagagtct gcctcaactg gcaaggcatg accaggacac gtggttacca   1055

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ttccatggag ccctgggtgg gaacccgccc ggcatcctcc gggctcccct gcagctcctt   1235

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cttctgggcc tccatcatct gtaaaaccgg gtaatagtgc acacagttgg tgccacataa   1955

aggctcaaca gataaagtgc tggtgcctct tgaggatggc gcatgggaga actaagcctg   2015

acagatgtgc ctggctgtgg tgtctagatg aagtggtgtg accgtcccaa aaccccatgt   2075
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US 9,550,842 B2

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tccctcccca caccgggcca ccccccacag tgctggcccc tccacgctgc cggcctaact   2135

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<400> 265

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atg ttt ctt acc cgg tct gag tac gac agg ggc gtg aat act ttt tct      168
Met Phe Leu Thr Arg Ser Glu Tyr Asp Arg Gly Val Asn Thr Phe Ser
  1               5                  10                  15

ccc gaa gga aga tta ttt caa gtg gaa tat gcc att gag gct atc aag      216
Pro Glu Gly Arg Leu Phe Gln Val Glu Tyr Ala Ile Glu Ala Ile Lys
 17                  22                  27                  32

ctt ggt tct aca gcc att ggg atc cag aca tca gag ggt gtg tgc cta      264
Leu Gly Ser Thr Ala Ile Gly Ile Gln Thr Ser Glu Gly Val Cys Leu
 33                  38                  43                  48

gct gtg gag aag aga att act tcc cca ctg atg gag ccc agc agc att      312
Ala Val Glu Lys Arg Ile Thr Ser Pro Leu Met Glu Pro Ser Ser Ile
 49                  54                  59                  64

gag aaa att gta gag att gat gct cac ata ggt tgt gcc atg agt ggg      360
Glu Lys Ile Val Glu Ile Asp Ala His Ile Gly Cys Ala Met Ser Gly
 65                  70                  75                  80

cta att gct gat gct aag act tta att gat aaa gcc aga gtg gag aca      408
Leu Ile Ala Asp Ala Lys Thr Leu Ile Asp Lys Ala Arg Val Glu Thr
 81                  86                  91                  96

cag aac cac tgg ttc acc tac aat gag aca atg aca gtg gag agt gtg      456
Gln Asn His Trp Phe Thr Tyr Asn Glu Thr Met Thr Val Glu Ser Val
 97                 102                 107                 112

acc caa gct gtg tcc aat ctg gct ttg cag ttt gga gaa gaa gat gca      504
Thr Gln Ala Val Ser Asn Leu Ala Leu Gln Phe Gly Glu Glu Asp Ala
113                 118                 123                 128

gat cca ggt gcc atg tct cgt ccc ttt gga gta gca tta tta ttt gga      552
Asp Pro Gly Ala Met Ser Arg Pro Phe Gly Val Ala Leu Leu Phe Gly
129                 134                 139                 144
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gga gtt gat gag aaa gga ccc cag ctg ttt cat atg gac cca tct ggg      600
Gly Val Asp Glu Lys Gly Pro Gln Leu Phe His Met Asp Pro Ser Gly
145                 150                 155                 160

acc ttt gta cag tgt gat gct cga gca att ggc tct gct tca gag ggt      648
Thr Phe Val Gln Cys Asp Ala Arg Ala Ile Gly Ser Ala Ser Glu Gly
161                 166                 171                 176

gcc cag agc tcc ttg caa gaa gtt tac cac aag tct atg act ttg aaa      696
Ala Gln Ser Ser Leu Gln Glu Val Tyr His Lys Ser Met Thr Leu Lys
177                 182                 187                 192

gaa gcc atc aag tct tca ctc atc atc ctc aaa caa gta atg gag gag      744
Glu Ala Ile Lys Ser Ser Leu Ile Ile Leu Lys Gln Val Met Glu Glu
193                 198                 203                 208

aag ctg aat gca aca aac att gag cta gcc aca gtg cag cct ggc cag      792
Lys Leu Asn Ala Thr Asn Ile Glu Leu Ala Thr Val Gln Pro Gly Gln
209                 214                 219                 224

aat ttc cac atg ttc aca aag gaa gaa ctt gaa gag gtt atc aag gac      840
Asn Phe His Met Phe Thr Lys Glu Glu Leu Glu Glu Val Ile Lys Asp
225                 230                 235                 240

att taa ggaatcctga tcctcagaac ttctctggga caatttcagt tctaataatg      896
Ile  *
241

tccttaaatt ttatttccag ctcctgttcc ttggaaaatc tccattgtat gtgcattttt    956

taaatgatgt ctgtacataa aggcagttct gaaataaaga aaattttaaa atattaaaaa   1016

aaaaaaa                                                            1023
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US 2006/0275782 A1

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<220>
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<222> (200)..(655)

<400> 266

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aataggtatg ttggattatt ttaaatgatc tatatttatt aaataataaa attaataaaa    180

tttttaattt ttctctttt atg cag agt tac ctt cct aat gac act gta gaa     232
                    Met Gln Ser Tyr Leu Pro Asn Asp Thr Val Glu
                      1               5
```

```
tct ggc atc cat cca gta tat ttt tgc agc acc cat tat att gaa atg      280
Ser Gly Ile His Pro Val Tyr Phe Cys Ser Thr His Tyr Ile Glu Met
 12                  17                  22                  27

cta ctg aag gct gag ttg cct ctt gtg ttt tca gct ttt cac atg tct      328
Leu Leu Lys Ala Glu Leu Pro Leu Val Phe Ser Ala Phe His Met Ser
 28                  33                  38                  43

ggt ttt gca cca tca cag att tgc ctg caa tgg ata acc cag tgt ttt      376
Gly Phe Ala Pro Ser Gln Ile Cys Leu Gln Trp Ile Thr Gln Cys Phe
 44                  49                  54                  59

tgg aat tac tta gat tgg ata gaa atc tgc cat tat att gct act tgt      424
Trp Asn Tyr Leu Asp Trp Ile Glu Ile Cys His Tyr Ile Ala Thr Cys
 60                  65                  70                  75

gtt ttc ctt ggt cct gat tat caa gtg tat atc tgt ata gct gta ttc      472
Val Phe Leu Gly Pro Asp Tyr Gln Val Tyr Ile Cys Ile Ala Val Phe
 76                  81                  86                  91

aaa cat tta cag caa gac att cta cag cac act cag act caa gat ctg      520
Lys His Leu Gln Gln Asp Ile Leu Gln His Thr Gln Thr Gln Asp Leu
 92                  97                 102                 107

caa gtt ttc cta aaa gaa gaa gca ctg cat ggg ttt cga gtg agt gat      568
Gln Val Phe Leu Lys Glu Glu Ala Leu His Gly Phe Arg Val Ser Asp
108                 113                 118                 123

tat ttt gaa tac atg gaa att ttg gaa caa aac tac cga aca gtg ctg      616
Tyr Phe Glu Tyr Met Glu Ile Leu Glu Gln Asn Tyr Arg Thr Val Leu
124                 129                 134                 139

ctg aga gac atg cgg aac att aga ctg cag agc aca tag atcatgagac      665
Leu Arg Asp Met Arg Asn Ile Arg Leu Gln Ser Thr  *
140                 145                 150

acacggttta aatttaggtt ttatttattt ttaaacacag cagggggct tgatgttttt    725

ctgtgtctgt aacaacattt actttgtgaa tatacatatt gtaaatactg agaagtataa    785

cgatatattt aagtaggtat gagctcaatt tgtgaattca tttttgtaaa tttgttgttt    845

tgtaaggtta ttatagaatc agatctagct tacttttagt tcttattcat gtttaagagt    905

tagtcctggc caggcgcggt ggctcactgc ctgtaatccc agcactttgg gagtctgagg    965

tgggcggatc acgaggtcaa gagatcgaga ccatcctggc caaaatggtg aaacctcgtc   1025

tctgctaaca atactgaaat tagctgggtg cagtgatgcg cctgtagtcc ctgctacttg   1085

ggaggctgag gcaggagaat cgcttgaacc cgggaggcgg aggttgcagt gagccaagat   1145

tgtgccactg tactccagcc aggccacaga gtgagactcg tctgggccgg gtgctgaggc   1205

gaggctggag acgccggagc acggcgcggc ggaacaggat atacacccag gggtccagga   1265
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tctggttcca ggtggccacg cgcaagtaga tgagcagctc cttctccgtg gtgcgggaca 1325

gctgcccggc ggggctcatg gcaggcgggt ttcgcagcac tgtctgggca atgaagacca 1385

gaaggggcag ccaacacacg ctggccacca ccatgatccc caggagctga gccatcatct 1445

ccacctcgga gtcccgggga cgctgctggg ccgcctcctg cccgtggtag acgtggcaca 1505

gggtggccac gctgaccgtg ttcagcagga aggacagccc gaccgagagg ccgcccagca 1565

tggagaagag cagcccgaag gccacgtccc cggactcggc gcccagcgtc aggaagcacc 1625

aggaccccgg gtattgcacg gtgtagcgac ccacgcccag caggggcagc aggcccagcg 1685

ccagcgcggc cgcccacacc agccccacgg tggcccaggc gcggcgctgc gaggcgaccg 1745

ccgggcgcga gaagggccgg gtgataccca ggtagcgctc tgaggccatg gcggccccca 1805

gcagcagcgg ggacaggccg aagaagatca tgacgacgcc catgaagcga cagagacggc 1865

agccagggtc cacggcgtgc cactcgaaga gcgcggcgtg ctgggacacc acgatggtac 1925

cggtcaccag cagccccagg aagtcggtga ggacgaggcc gcagaggaag gtgaggaagg 1985

aggagcgcgt gtgcgaaccc ccctgccgcg cgcccgccag cacgctcagg gccagcaggt 2045

tggaggccag gcccaccacg cagaaggagg cggcgaacca gggcgaggcg atcagccgtc 2105

tctcctccag ggtaatgttt gtgggccgga aacagggccc cagggaactg ccgttgggcc 2165

acat 2169

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<400> 267
tgtactggcc cgaattcccg ggncgacgat ttcgtctggt caaccttctg tgatctcctg 60

gagatttcca gggcacggta gtggttggca tgagtatgtg ttatcctgtt gggagtcttg 120

gttactaaac ttttcttctt ttttccaggc aggtaagggg gacgtgctgg ggtggaggtt 180

gggagcaggg catcacattt ccttacgtgg caaaggatca cgtctgaaga gtgacttttc 240

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tgtttccaca atatgtgcta ttgacttctt tctc    atg ggt ctt gct gtg act     292
                                         Met Gly Leu Ala Val Thr
                                           1

ttt ctt tct gag act ttt ctg tcc tcg gcc cag aag aga ggt aga ggt     340
Phe Leu Ser Glu Thr Phe Leu Ser Ser Ala Gln Lys Arg Gly Arg Gly
  7                  12                  17                  22

ggg gag tct gac ctg gag ccc ata gac agc tgg ctt ata acc cca gga     388
Gly Glu Ser Asp Leu Glu Pro Ile Asp Ser Trp Leu Ile Thr Pro Gly
 23                  28                  33                  38

atg atc ccc gtt gcg cag cca tct gtc atg gac gac att gag gtg tgg     436
Met Ile Pro Val Ala Gln Pro Ser Val Met Asp Asp Ile Glu Val Trp
 39                  44                  49                  54

ctc agg acc gac ctg aag ggt gat gat ctg gag gag ggt gtc aca agt     484
Leu Arg Thr Asp Leu Lys Gly Asp Asp Leu Glu Glu Gly Val Thr Ser
 55                  60                  65                  70

gaa gag ttt gat aaa ttc ctt gaa gaa aga gcc aaa gct gct gaa atg     532
Glu Glu Phe Asp Lys Phe Leu Glu Glu Arg Ala Lys Ala Ala Glu Met
 71                  76                  81                  86

gtt ccc gac ctc ccc tcg ccc ccc atg gag gct cct gcc cca gcc tca     580
Val Pro Asp Leu Pro Ser Pro Pro Met Glu Ala Pro Ala Pro Ala Ser
 87                  92                  97                 102

aac cct tct ggc cgg aag aag cca gag cgg tca gag gat gcc ctc ttc     628
Asn Pro Ser Gly Arg Lys Lys Pro Glu Arg Ser Glu Asp Ala Leu Phe
103                 108                 113                 118

gcc ctg tga gcagctc tgtggtttgc ctccccagat ggcgggtccc cgcttgcacc     684
Ala Leu  *
119

ccgtggacac cgggcactgg ccactcctac atccccagca ctgtattgcg gccgctctag    744

aggatccaag cttacgtacg cgggcattca cgtct                              779
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<212> DNA
<213> Homo sapiens

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<222> (128)..(700)

<400> 268

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caggaagaga agccacagcg cttcagaaaa gagtgggaca gggacaagca tatctaagag    120
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gctgaac  atg aat cca cag atc aga aac ccg atg aag gca atg tat cca     169
         Met Asn Pro Gln Ile Arg Asn Pro Met Lys Ala Met Tyr Pro
           1               5                  10

ggc aca ttc tac ttc caa ttt aaa aac cta tgg gaa gcc aac gat cgg     217
Gly Thr Phe Tyr Phe Gln Phe Lys Asn Leu Trp Glu Ala Asn Asp Arg
 15                  20                  25                  30

aac gaa act tgg ctg tgc ttc acc gtg gaa ggt ata aag cgc cgc tca     265
Asn Glu Thr Trp Leu Cys Phe Thr Val Glu Gly Ile Lys Arg Arg Ser
 31                  36                  41                  46

gtt gtc tcc tgg aag acg ggc gtc ttc cga aac cag gtg gat tct gag     313
Val Val Ser Trp Lys Thr Gly Val Phe Arg Asn Gln Val Asp Ser Glu
 47                  52                  57                  62

acc cat tgt cat gca gaa agg tgc ttc ctc tct tgg ttc tgc gac gac     361
Thr His Cys His Ala Glu Arg Cys Phe Leu Ser Trp Phe Cys Asp Asp
 63                  68                  73                  78

ata ctg tct cct aac aca aag tac cag gtc acc tgg tac aca tct tgg     409
Ile Leu Ser Pro Asn Thr Lys Tyr Gln Val Thr Trp Tyr Thr Ser Trp
 79                  84                  89                  94

agc cct tgc cca gac tgt gca ggg gag gtg gcc gag ttc ctg gcc agg     457
Ser Pro Cys Pro Asp Cys Ala Gly Glu Val Ala Glu Phe Leu Ala Arg
 95                 100                 105                 110

cac agc aac gtg aat ctc acc atc ttc acc gcc cgc ctc tac tac ttc     505
His Ser Asn Val Asn Leu Thr Ile Phe Thr Ala Arg Leu Tyr Tyr Phe
111                 116                 121                 126

cag tat cca tgt tac cag gag ggg ctc cgc agc ctg agt cag gaa ggg     553
Gln Tyr Pro Cys Tyr Gln Glu Gly Leu Arg Ser Leu Ser Gln Glu Gly
127                 132                 137                 142

gtc gct gtg gag atc atg gac tat gaa gat ttt aaa tat tgt tgg gaa     601
Val Ala Val Glu Ile Met Asp Tyr Glu Asp Phe Lys Tyr Cys Trp Glu
143                 148                 153                 158

aac ttt gtg tac aat gat aat gag cca ttc aag cct tgg aag gga tta     649
Asn Phe Val Tyr Asn Asp Asn Glu Pro Phe Lys Pro Trp Lys Gly Leu
159                 164                 169                 174

aaa acc aac ttt cga ctt ctg aaa aga agg cta cgg gag agt ctc cag     697
Lys Thr Asn Phe Arg Leu Leu Lys Arg Arg Leu Arg Glu Ser Leu Gln
175                 180                 185                 190

tga gggg tctccctggg cctcatggtc tgtctcctct agcctcctgc tcatgctgca     754
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191

cgggcctccc ctccaccctg gacccgctct gtttctgcct ggtcatcctg agcccctcct    814

ggcctcaggg ccattccaca gtgctccccc gcctcaccgc ttcctcctcg ctcttccaga    874
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ctcttcctgc agaggctcct ttctgcctcc atggctatcc atccaccccc acagaccccg    934

ttcctccagc ctgcgtgccc ctaacctggc ttttcccatc tccccagcat aaccaaatct    994

tactaaactc atcctaggct gggcatggtg actcacgcct gtaatccccc agcaatttgg   1054

gaggcaaagg tgggagaatc gcgtgagccc aggagttcca gaccaggctg ggtcacatga   1114

caaagcccca tctctacaaa aaaaaaaaa                                     1143
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<210> 269
<211> 2512
<212> DNA
<213> Homo sapiens

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<400> 269

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ggatccacta gtccagtgtg gtggaattca tttcctcccg ttctttatca gagcccccaa    120

aataagtagg aatgggcagt ggctattcac attcactaca ccttttccat ttgctaataa    180

ggccctgcca ggctgggagg gaattgtccc tgcctgcttc tggagaaaga agatattgac    240

accatctacg ggcacc    atg gaa ctg ctt caa gtg acc att ctt ttt ctt     289
                     Met Glu Leu Leu Gln Val Thr Ile Leu Phe Leu
                       1               5

ctg ccc agt att tgc agc agt aac agc aca ggt gtt tta gag gca gct      337
Leu Pro Ser Ile Cys Ser Ser Asn Ser Thr Gly Val Leu Glu Ala Ala
 12                  17                  22                  27

aat aat tca ctt gtt gtt act aca aca aaa cca tct ata aca aca cca      385
Asn Asn Ser Leu Val Val Thr Thr Thr Lys Pro Ser Ile Thr Thr Pro
 28                  33                  38                  43

aac aca gaa tca tta cag aaa aat gtt gtc aca cca aca act gga aca      433
Asn Thr Glu Ser Leu Gln Lys Asn Val Val Thr Pro Thr Thr Gly Thr
 44                  49                  54                  59

act cct aaa gga aca atc acc aat gaa tta ctt aaa atg tct ctg atg      481
Thr Pro Lys Gly Thr Ile Thr Asn Glu Leu Leu Lys Met Ser Leu Met
 60                  65                  70                  75

tca aca gct act ttt tta aca agt aaa gat gaa gga ttg aaa gcc aca      529
Ser Thr Ala Thr Phe Leu Thr Ser Lys Asp Glu Gly Leu Lys Ala Thr
 76                  81                  86                  91

acc act gat gtc agg aag aat gac tcc atc att tca aac gta aca gta      577
Thr Thr Asp Val Arg Lys Asn Asp Ser Ile Ile Ser Asn Val Thr Val
```

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 92                  97                  102                 107

aca agt gtt aca ctt cca aat gct gtt tca aca tta caa agt tcc aaa      625
Thr Ser Val Thr Leu Pro Asn Ala Val Ser Thr Leu Gln Ser Ser Lys
108                 113                 118                 123

ccc aag act gaa act cag agt tca att aaa aca aca gaa ata cca ggt      673
Pro Lys Thr Glu Thr Gln Ser Ser Ile Lys Thr Thr Glu Ile Pro Gly
124                 129                 134                 139

agt gtt cta caa cca gat gca tca cct tct aaa act ggt aca tta acc      721
Ser Val Leu Gln Pro Asp Ala Ser Pro Ser Lys Thr Gly Thr Leu Thr
140                 145                 150                 155

tca ata cca gtt aca att cca gaa aac acc tca cag tct caa gta ata      769
Ser Ile Pro Val Thr Ile Pro Glu Asn Thr Ser Gln Ser Gln Val Ile
156                 161                 166                 171

ggc act gag ggt gga aaa aat gca agc act tca gca acc agc cgg tct      817
Gly Thr Glu Gly Gly Lys Asn Ala Ser Thr Ser Ala Thr Ser Arg Ser
172                 177                 182                 187

tat tcc agt att att ttg ccg gtg gtt att gct ttg att gta ata aca      865
Tyr Ser Ser Ile Ile Leu Pro Val Val Ile Ala Leu Ile Val Ile Thr
188                 193                 198                 203

ctt tca gta ttt gtt ctg gtg ggt ttg tac cga atg tgc tgg aag gca      913
Leu Ser Val Phe Val Leu Val Gly Leu Tyr Arg Met Cys Trp Lys Ala
204                 209                 214                 219

gat ccg ggc aca cca gaa aat gga aat gat caa cct cag tct gat aaa      961
Asp Pro Gly Thr Pro Glu Asn Gly Asn Asp Gln Pro Gln Ser Asp Lys
220                 225                 230                 235

gag agc gtg aag ctt ctt acc gtt aag aca att tct cat gag tct ggt     1009
Glu Ser Val Lys Leu Leu Thr Val Lys Thr Ile Ser His Glu Ser Gly
236                 241                 246                 251

gag cac tct gca caa gga aaa acc aag aac tga cagcttga ggaattctct     1060
Glu His Ser Ala Gln Gly Lys Thr Lys Asn  *
252                 257                 262

ccacacctag gcaataatta cgcttaatct tcagcttcta tgcaccaagc gtggaaaagg   1120

agaaagtcct gcagaatcaa tcccgacttc catacctgct gctggactgt accagacgtc   1180

tgtcccagta aagtgatgtc cagctgacat gcaataattt gatggaatca aaaagaaccc   1240

cggggctctc ctgttctctc acatttaaaa attccattac tccatttaca ggagcgttcc   1300

taggaaaagg aattttagga ggagaatttg tgagcagtga atctgacagc ccaggaggtg   1360

ggctcgctga taggcatgac tttccttaat gtttaaagtt ttccgggcca agaattttta   1420

tccatgaaga ctttcctact tttctcggtg ttcttatatt acctactgtt agtatttatt   1480

gtttaccact atgttaatgc agggaaaagt tgcacgtgta ttattaaata ttaggtagaa   1540
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atcataccat gctactttgt acatataagt attttattcc tgctttcgtg ttacttttaa 1600

taaataacta ctgtactcaa tactctaaaa atactataac atgactgtga aaatggcaat 1660

gttattgtct tcctataatt atgaatattt ttggatggat tattagaata catgaactca 1720

ctaatgaaag gcatttgtaa taagtcagaa agggacatac gattcacata tcagactgtt 1780

agggggagag taatttatca gttctttggt ctttctattt gtcattcata ctatgtgatg 1840

aagatgtaag tgcaagggca tttataacac tatactgcat tcattaagat aataggatca 1900

tgatttttca ttaactcatt tgattgatat tatctccatg catttttttat ttcttttaga 1960

aatgtaatta tttgctctag caatcattgc taacctctag tttgtagaaa atcaacactt 2020

tataaataca taattatgat attatttttc attgtatcac tgttctaaaa ataccatatg 2080

attatagctg ccactccatc aggagcaaat tcttctgtta aaagctaact gatcaacctt 2140

gaccactttt ttgacatgtg agatcaaagt gtcaagttgg ctgaggtttt ttggaaagct 2200

ttagaactaa taagctgctg gtggcagctt tgtaacgtat gattatctaa gctgattttg 2260

atgctaaatt atcttagtga tctaaggggc agtttagtga agatggaatc ttgtatttaa 2320

aatagccttt taaaatttgt tttgtgatga tgtattttga caacttccat ctttaggagt 2380

tatataatca ccttgatttt agtttcctga tgtttggact atttataatc aaggacacca 2440

agcaagcata agcatatcta tatttctgac tggtgtctct ttgagaagga tgggaagtag 2500

aaaaaaaaaa aa 2512

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<213> Homo sapiens

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<222> (417)..(899)

<400> 270
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gtaacagtag cttctttggt ctccctgtgt ccaatttctt ccatttcaaa acatcctggt 120

tattgatgca agactaatct tcaaaatgtc atttttgacc gggcgtcgcc gctgccgccg 180

gcgcccttcc ccagtaccac ggcccggcgc ctgcactcgt ttcctgcagg agagagctaa 240

gcttgtctgc tggatccctg cagctggagc gcaaaaggag agatttcacc tcttctggga 300

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gcaggaaact ctacttcgac actcatgcct tagtgtgctt actggaagac aatgggtttg    360

ctactcaaca agcagaaatc attgtgtctg cattggtcaa gatcctggag gccaac   416

atg gac atc gtc tac aaa gat atg gtc acc aag atg cag cag gaa atc      464
Met Asp Ile Val Tyr Lys Asp Met Val Thr Lys Met Gln Gln Glu Ile
  1               5                  10                  15

act ttt cag caa gta atg tct cag att gcg aat gtg aaa aag gat atg      512
Thr Phe Gln Gln Val Met Ser Gln Ile Ala Asn Val Lys Lys Asp Met
 17                  22                  27                  32

att att ttg gag aag agt gaa ttt tca gcc ctc aga gca gaa aat gag      560
Ile Ile Leu Glu Lys Ser Glu Phe Ser Ala Leu Arg Ala Glu Asn Glu
 33                  38                  43                  48

aaa ata aaa ctc gaa cta cat cag tta aaa caa caa gta atg gat gaa      608
Lys Ile Lys Leu Glu Leu His Gln Leu Lys Gln Gln Val Met Asp Glu
 49                  54                  59                  64

gtg atc aaa gtc cga aca gat acc aaa tta gac ttc aac cta gaa aag      656
Val Ile Lys Val Arg Thr Asp Thr Lys Leu Asp Phe Asn Leu Glu Lys
 65                  70                  75                  80

agc aga gta aaa gaa ttg tat tca ttg aac gaa aag aag ctg ctg gaa      704
Ser Arg Val Lys Glu Leu Tyr Ser Leu Asn Glu Lys Lys Leu Leu Glu
 81                  86                  91                  96

ttg aga aca gaa ata gtg gca ttg cat gcc cag caa gat cgg gcc ctt      752
Leu Arg Thr Glu Ile Val Ala Leu His Ala Gln Gln Asp Arg Ala Leu
 97                 102                 107                 112

acc cag aca gac agg aag atc gaa act gag gtt gct ggc ctc aaa acc      800
Thr Gln Thr Asp Arg Lys Ile Glu Thr Glu Val Ala Gly Leu Lys Thr
113                 118                 123                 128

atg ctt gag tca cac aag ctt gat aat att aaa tat tta gca ggg tct      848
Met Leu Glu Ser His Lys Leu Asp Asn Ile Lys Tyr Leu Ala Gly Ser
129                 134                 139                 144

ata ttt acg tgc cta aca gta gct ctg gga ttt tat cgc ctg tgg atc      896
Ile Phe Thr Cys Leu Thr Val Ala Leu Gly Phe Tyr Arg Leu Trp Ile
145                 150                 155                 160

taa taaa gtgtctattt aaagtgaaaa aaaaagggcg gccgctctag agtatccctc      953
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161

gaggggccca agcttacgcg tacccagctt tcttgtacaa agtgg                   998
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<210> 271
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<212> DNA

<213> Homo sapiens

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<222> (139)..(1215)

<400> 271
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cgggccggcc cacctgctgg tgccctggag gctctgagcc ccggcggcgc ccgggcccac    120

gcggaacgac ggggcgag  atg cga gcc acc cct ctg gct gct cct gcg ggt      171
                     Met Arg Ala Thr Pro Leu Ala Ala Pro Ala Gly
                       1               5

tcc ctg tcc agg aag aag cgg ttg gag ttg gat gac aac tta gat acc      219
Ser Leu Ser Arg Lys Lys Arg Leu Glu Leu Asp Asp Asn Leu Asp Thr
 12                  17                  22                  27

gag cgt ccc gtc cag aaa cga gct cga agt ggg ccc cag ccc aga ctg      267
Glu Arg Pro Val Gln Lys Arg Ala Arg Ser Gly Pro Gln Pro Arg Leu
 28                  33                  38                  43

ccc ccc tgc ctg ttg ccc ctg agc cca cct act gct cca gat cgt gca      315
Pro Pro Cys Leu Leu Pro Leu Ser Pro Pro Thr Ala Pro Asp Arg Ala
 44                  49                  54                  59

act gct gtg gcc act gcc tcc cgt ctt ggg ccc tat gtc ctc ctg gag      363
Thr Ala Val Ala Thr Ala Ser Arg Leu Gly Pro Tyr Val Leu Leu Glu
 60                  65                  70                  75

ccc gag gag ggc ggg cgg gcc tac cag gcc ctg cac tgc cct aca ggc      411
Pro Glu Glu Gly Gly Arg Ala Tyr Gln Ala Leu His Cys Pro Thr Gly
 76                  81                  86                  91

act gag tat acc tgc agg gtg tac ccc gtc cag gaa gcc ctg gcc gtg      459
Thr Glu Tyr Thr Cys Arg Val Tyr Pro Val Gln Glu Ala Leu Ala Val
 92                  97                 102                 107

ctg gag ccc tat gcg cgg ctg ccc ccg cac aag cat gtg gct cgg ccc      507
Leu Glu Pro Tyr Ala Arg Leu Pro Pro His Lys His Val Ala Arg Pro
108                 113                 118                 123

act gag gtc ctg gct ggt acc cag ctc ctc tac gcc ttt ttc act cgg      555
Thr Glu Val Leu Ala Gly Thr Gln Leu Leu Tyr Ala Phe Phe Thr Arg
124                 129                 134                 139

acc cat ggg gac atg cac agc ctg gtg cga agc cgc cac cgt atc cct      603
Thr His Gly Asp Met His Ser Leu Val Arg Ser Arg His Arg Ile Pro
140                 145                 150                 155

gag cct gag gct gcc gtg ctc ttc cgc cag atg gcc acc gcc ctg gcg      651
Glu Pro Glu Ala Ala Val Leu Phe Arg Gln Met Ala Thr Ala Leu Ala
156                 161                 166                 171

cac tgt cac cag cac ggt ctg gtc ctg cgt gat ctc aag ctg tgt cgc      699
His Cys His Gln His Gly Leu Val Leu Arg Asp Leu Lys Leu Cys Arg
```

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172                 177                 182                 187

ttt gtc ttc gct gac cgt gag agg aag aag ctg gtg ctg gag aac ctg      747
Phe Val Phe Ala Asp Arg Glu Arg Lys Lys Leu Val Leu Glu Asn Leu
188                 193                 198                 203

gag gac tcc tgc gtg ctg act ggg cca gat gat tcc ctg tgg gac aag      795
Glu Asp Ser Cys Val Leu Thr Gly Pro Asp Asp Ser Leu Trp Asp Lys
204                 209                 214                 219

cac gcg tgc cca gcc tac gtg gga cct gag ata ctc agc tca cgg gcc      843
His Ala Cys Pro Ala Tyr Val Gly Pro Glu Ile Leu Ser Ser Arg Ala
220                 225                 230                 235

tca tac tcg ggc aag gca gcc gat gtc tgg agc ctg ggc gtg gcg ctc      891
Ser Tyr Ser Gly Lys Ala Ala Asp Val Trp Ser Leu Gly Val Ala Leu
236                 241                 246                 251

ttc acc atg ctg gcc ggc cac tac ccc ttc cag gac tcg gag cct gtc      939
Phe Thr Met Leu Ala Gly His Tyr Pro Phe Gln Asp Ser Glu Pro Val
252                 257                 262                 267

ctg ctc ttc ggc aag atc cgc cgc ggg gcc tac gcc ttg cct gca ggc      987
Leu Leu Phe Gly Lys Ile Arg Arg Gly Ala Tyr Ala Leu Pro Ala Gly
268                 273                 278                 283

ctc tcg gcc cct gcc cgc tgt ctg gtt cgc tgc ctc ctt cgt cgg gag     1035
Leu Ser Ala Pro Ala Arg Cys Leu Val Arg Cys Leu Leu Arg Arg Glu
284                 289                 294                 299

cca gct gaa cgg ctc aca gcc aca ggc atc ctc ctg cac ccc tgg ctg     1083
Pro Ala Glu Arg Leu Thr Ala Thr Gly Ile Leu Leu His Pro Trp Leu
300                 305                 310                 315

cga cag gac ccg atg ccc tta gcc cca acc cga tcc cat ctc tgg gag     1131
Arg Gln Asp Pro Met Pro Leu Ala Pro Thr Arg Ser His Leu Trp Glu
316                 321                 326                 331

gct gcc cag gtg gtc cct gat gga ctg ggg ctg gac gaa gcc agg gaa     1179
Ala Ala Gln Val Val Pro Asp Gly Leu Gly Leu Asp Glu Ala Arg Glu
332                 337                 342                 347

gag gag gga gac aga gaa gtg gtt ctg tat ggc tag gacc accctactac     1229
Glu Glu Gly Asp Arg Glu Val Val Leu Tyr Gly  *
348                 353                 358

acgctcagct gccaacagtg gattgagttt gggggtagct ccaagccttc tcctgcctct   1289

gaactgagcc aaaccttcag tgccttccag aagggagaaa ggcagaagcc tgtgtggagt   1349

gtgctgtgta cacatctgct ttgttccaca cacatgcagt tcctgcttgg gtgcttatca   1409

ggtgccaagc cctgttctcg gtgctgggag tacagcagtg agcaaaggag acaatattcc   1469

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Met Glu Asn
1

cag gtg ttg acg ccg cat gtc tac tgg gct cag cga cac cgc gag cta 225
Gln Val Leu Thr Pro His Val Tyr Trp Ala Gln Arg His Arg Glu Leu
4 9 14 19

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Tyr Leu Arg Val Glu Leu Ser Asp Val Gln Asn Pro Ala Ile Ser Ile
20 25 30 35

act gaa aac gtg ctg cat ttc aaa gct caa gga cat ggt gcc aaa gga 321
Thr Glu Asn Val Leu His Phe Lys Ala Gln Gly His Gly Ala Lys Gly
36 41 46 51

gac aat gtc tat gaa ttt cac ctg gag ttc tta gac ctt gtg aaa cca 369
Asp Asn Val Tyr Glu Phe His Leu Glu Phe Leu Asp Leu Val Lys Pro
52 57 62 67

gag cct gtt tac aaa ctg acc cag agg cag gta aac att aca gta cag 417

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Glu Pro Val Tyr Lys Leu Thr Gln Arg Gln Val Asn Ile Thr Val Gln
 68                  73                  78                  83

aag aaa gtg agt cag tgg tgg gag aga ctc aca aag cag gaa aag cga      465
Lys Lys Val Ser Gln Trp Trp Glu Arg Leu Thr Lys Gln Glu Lys Arg
 84                  89                  94                  99

cca ctg ttt ttg gct cct gac ttt gat cgt tgg ctg gat gaa tct gat      513
Pro Leu Phe Leu Ala Pro Asp Phe Asp Arg Trp Leu Asp Glu Ser Asp
100                 105                 110                 115

gcg gaa atg gag ctc aga gct aag gaa gaa gag cgc cta aat aaa ctc      561
Ala Glu Met Glu Leu Arg Ala Lys Glu Glu Glu Arg Leu Asn Lys Leu
116                 121                 126                 131

cga ctg gaa agc gaa ggc tct cct gaa act ctt aca aac tta agg aaa      609
Arg Leu Glu Ser Glu Gly Ser Pro Glu Thr Leu Thr Asn Leu Arg Lys
132                 137                 142                 147

gga tac ctg ttt atg tat aat ctt gtg caa ttc ttg gga ttc tcc tgg      657
Gly Tyr Leu Phe Met Tyr Asn Leu Val Gln Phe Leu Gly Phe Ser Trp
148                 153                 158                 163

atc ttt gtc aac ctg act gtg cga ttc tgt atc ttg gga aaa gag tcc      705
Ile Phe Val Asn Leu Thr Val Arg Phe Cys Ile Leu Gly Lys Glu Ser
164                 169                 174                 179

ttt tat gac aca ttc cat act gtg gct gac atg atg tat ttc tgc cag      753
Phe Tyr Asp Thr Phe His Thr Val Ala Asp Met Met Tyr Phe Cys Gln
180                 185                 190                 195

atg ctg gca gtt gtg gaa act atc aat gca gca att gga gtc act acg      801
Met Leu Ala Val Val Glu Thr Ile Asn Ala Ala Ile Gly Val Thr Thr
196                 201                 206                 211

tca ccg gtg ctg cct tct ctg atc cag ctt ctt gga aga aat ttt att      849
Ser Pro Val Leu Pro Ser Leu Ile Gln Leu Leu Gly Arg Asn Phe Ile
212                 217                 222                 227

ttg ttt atc atc ttt ggc acc atg gaa gaa atg cag aac aaa gct gtg      897
Leu Phe Ile Ile Phe Gly Thr Met Glu Glu Met Gln Asn Lys Ala Val
228                 233                 238                 243

gtt ttc ttt gtg ttt tat ttg tgg agt gca att gaa att ttc agg tac      945
Val Phe Phe Val Phe Tyr Leu Trp Ser Ala Ile Glu Ile Phe Arg Tyr
244                 249                 254                 259

tct ttc tac atg ctg acg tgc att gac atg gat tgg aag gtg ctc aca      993
Ser Phe Tyr Met Leu Thr Cys Ile Asp Met Asp Trp Lys Val Leu Thr
260                 265                 270                 275

tgg ctt cgt tac act ctg tgg att ccc tta tat cca ctg gga tgt ttg     1041
Trp Leu Arg Tyr Thr Leu Trp Ile Pro Leu Tyr Pro Leu Gly Cys Leu
276                 281                 286                 291

gcg gaa gct gtc tca gtg att cag tcc att cca ata ttc aat gag acc     1089
Ala Glu Ala Val Ser Val Ile Gln Ser Ile Pro Ile Phe Asn Glu Thr
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292                 297                 302                 307

gga cga ttc agt ttc aca ttg cca tat cca gtg aaa atc aaa gtt aga     1137
Gly Arg Phe Ser Phe Thr Leu Pro Tyr Pro Val Lys Ile Lys Val Arg
308                 313                 318                 323

ttt tcc ttt ttt ctt cag att tat ctt ata atg ata ttt tta ggt tta     1185
Phe Ser Phe Phe Leu Gln Ile Tyr Leu Ile Met Ile Phe Leu Gly Leu
324                 329                 334                 339

tac ata aat ttt cgt cac ctt tat aaa cag cgc aga cgg cgc tat gga     1233
Tyr Ile Asn Phe Arg His Leu Tyr Lys Gln Arg Arg Arg Arg Tyr Gly
340                 345                 350                 355

caa aaa aag aaa aag atc cac taa aaagaaagat ttagatggct tcttgccagt    1287
Gln Lys Lys Lys Lys Ile His  *
356                 361

ttgagcctaa tctgattctt acagttttac cttcttgaac caatgtaaaa gttttttaa    1347

tgttaaatga ttaaattctc agtgaggcta tcttcctttt ccccagtaac attcctgaat    1407

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cattcttgtg tattcagtta atgacaccaa aaggctcagc ccaccccaac cctatctcat    1527

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caagactatg tcactctata gaaggctgtt aaagtgactc aggcaggaat taattattct    1707

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gagtcattga taaaacattt ctaagagtgg ggctagagaa catactttac atctgacatc    1827

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gcagggatcc aaagggaaca cagtatgtag gtcaaactgg cagtaacagt gtacagcctt    2427

tgacaaacta gaaatattag agtaggccaa acacacctcc aaactgtaag gctgtgcaca    2487
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agcgaggcgc agcgagccta gcctccccgc gccctgggca gtgtggcc atg gag aat     177
                                                      Met Glu Asn
                                                        1

cag gtg ttg acg ccg cat gtc tac tgg gct cag cga cac cgc gag cta      225
Gln Val Leu Thr Pro His Val Tyr Trp Ala Gln Arg His Arg Glu Leu
  4                   9                  14                  19

tat ctg cgc gtg gag ctg agt gac gta cag aac cct gcc atc agc atc      273
Tyr Leu Arg Val Glu Leu Ser Asp Val Gln Asn Pro Ala Ile Ser Ile
 20                  25                  30                  35

act gaa aac gtg ctg cat ttc aaa gct caa gga cat ggt gcc aaa gga      321
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Thr Glu Asn Val Leu His Phe Lys Ala Gln Gly His Gly Ala Lys Gly
 36                  41                  46                  51

gac aat gtc tat gaa ttt cac ctg gag ttc tta gac ctt gtg aaa cca      369
Asp Asn Val Tyr Glu Phe His Leu Glu Phe Leu Asp Leu Val Lys Pro
 52                  57                  62                  67

gag gaa gaa gag cgc cta aat aaa ctc cga ctg gaa agc gaa ggc tct      417
Glu Glu Glu Glu Arg Leu Asn Lys Leu Arg Leu Glu Ser Glu Gly Ser
 68                  73                  78                  83

cct gaa act ctt aca aac tta agg aaa gga tac ctg ttt atg tat aat      465
Pro Glu Thr Leu Thr Asn Leu Arg Lys Gly Tyr Leu Phe Met Tyr Asn
 84                  89                  94                  99

ctt gtg caa ttc ttg gga ttc tcc tgg atc ttt gtc aac ctg act gtg      513
Leu Val Gln Phe Leu Gly Phe Ser Trp Ile Phe Val Asn Leu Thr Val
100                 105                 110                 115

cga ttc tgt atc ttg gga aaa gag tcc ttt tat gac aca ttc cat act      561
Arg Phe Cys Ile Leu Gly Lys Glu Ser Phe Tyr Asp Thr Phe His Thr
116                 121                 126                 131

gtg gct gac atg atg tat ttc tgc cag atg ctg gca gtt gtg gaa act      609
Val Ala Asp Met Met Tyr Phe Cys Gln Met Leu Ala Val Val Glu Thr
132                 137                 142                 147

atc aat gca gca att gga gtc act acg tca ccg gtg ctg cct tct ctg      657
Ile Asn Ala Ala Ile Gly Val Thr Thr Ser Pro Val Leu Pro Ser Leu
148                 153                 158                 163

atc cag ctt ctt gga aga aat ttt att ttg ttt atc atc ttt ggc acc      705
Ile Gln Leu Leu Gly Arg Asn Phe Ile Leu Phe Ile Ile Phe Gly Thr
164                 169                 174                 179

atg gaa gaa atg cag aac aaa gct gtg gtt ttc ttt gtg ttt tat ttg      753
Met Glu Glu Met Gln Asn Lys Ala Val Val Phe Phe Val Phe Tyr Leu
180                 185                 190                 195

tgg agt gca att gaa att ttc agg tac tct ttc tac atg ctg acg tgc      801
Trp Ser Ala Ile Glu Ile Phe Arg Tyr Ser Phe Tyr Met Leu Thr Cys
196                 201                 206                 211

att gac atg gat tgg aag gtg ctc aca tgg ctt cgt tac act ctg tgg      849
Ile Asp Met Asp Trp Lys Val Leu Thr Trp Leu Arg Tyr Thr Leu Trp
212                 217                 222                 227

att ccc tta tat cca ctg gga tgt ttg gcg gaa gct gtc tca gtg att      897
Ile Pro Leu Tyr Pro Leu Gly Cys Leu Ala Glu Ala Val Ser Val Ile
228                 233                 238                 243

cag tcc att cca ata ttc aat gag acc gga cga ttc agt ttc aca ttg      945
Gln Ser Ile Pro Ile Phe Asn Glu Thr Gly Arg Phe Ser Phe Thr Leu
244                 249                 254                 259

cca tat cca gtg aaa atc aaa gtt aga ttt tcc ttt ttt ctt cag att      993
Pro Tyr Pro Val Lys Ile Lys Val Arg Phe Ser Phe Phe Leu Gln Ile
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tat ctt ata atg ata ttt tta ggt tta tac ata aat ttt cgt cac ctt     1041
Tyr Leu Ile Met Ile Phe Leu Gly Leu Tyr Ile Asn Phe Arg His Leu
276                 281                 286                 291

tat aaa cag cgc aga cgg cgc tat gga caa aaa aag aaa aag atc cac     1089
Tyr Lys Gln Arg Arg Arg Arg Tyr Gly Gln Lys Lys Lys Lys Ile His
292                 297                 302                 307

taa aaag aaagatttag atggcttctt gccagtttga gcctaatctg attcttacag     1146
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308

ttttaccttc ttgaaccaat gtaaaagttt ttttaatgtt aaatgattaa attctcagtg   1206

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caccaaaagg ctcagcccac cccaacccta tctcatgttc agtctgtcta atacatgcca   1386

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cacatacaca cacacacaca cgaggtccaa atggtagcag ggatccaaag ggaacacagt   2226

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US 10,059,758 B2

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Met Ala Ser Lys Cys Leu Lys Ala Gly
1 5

ttc tct tct ggg tct ctc aag agc cca gga ggg gcc agt ggg ggc tcc 161
Phe Ser Ser Gly Ser Leu Lys Ser Pro Gly Gly Ala Ser Gly Gly Ser
10 15 20 25

act cgt gtg tcc gca atg tac tcc agc agc cct tgc aag ctt cca agt 209
Thr Arg Val Ser Ala Met Tyr Ser Ser Ser Pro Cys Lys Leu Pro Ser
26 31 36 41

ctc tcc cct gtg gcc aga agt ttc tct gcc tgc tca gtg ggt ctg ggc 257
Leu Ser Pro Val Ala Arg Ser Phe Ser Ala Cys Ser Val Gly Leu Gly
42 47 52 57

aga agc agc tac agg gcc acc agc tgc ctc cct gct ctc tgc ctc cct 305

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Arg Ser Ser Tyr Arg Ala Thr Ser Cys Leu Pro Ala Leu Cys Leu Pro
 58                  63                  68                  73

gct gga ggc ttc gct acc agc tac agt ggg ggt ggg ggc tgg ttt ggg      353
Ala Gly Gly Phe Ala Thr Ser Tyr Ser Gly Gly Gly Gly Trp Phe Gly
 74                  79                  84                  89

gag ggc atc ctc act ggc aat gag aag gag acc atg caa tcc ctg aac      401
Glu Gly Ile Leu Thr Gly Asn Glu Lys Glu Thr Met Gln Ser Leu Asn
 90                  95                 100                 105

gac cgc ctg gcc ggc tac ctg gag aag gtg cgt cag ctg gag cag gag      449
Asp Arg Leu Ala Gly Tyr Leu Glu Lys Val Arg Gln Leu Glu Gln Glu
106                 111                 116                 121

aac gcc agc ctg gag agc cgc atc cgt gag tgg tgt gag cag cag gtc      497
Asn Ala Ser Leu Glu Ser Arg Ile Arg Glu Trp Cys Glu Gln Gln Val
122                 127                 132                 137

ccc tac atg tgc cct gac tac cag tcc tac ttc cgg acc atc gag gag      545
Pro Tyr Met Cys Pro Asp Tyr Gln Ser Tyr Phe Arg Thr Ile Glu Glu
138                 143                 148                 153

ctc cag aag aag act cta tgc agc aag gct gag aat gcc agg ctg gtg      593
Leu Gln Lys Lys Thr Leu Cys Ser Lys Ala Glu Asn Ala Arg Leu Val
154                 159                 164                 169

gtg gag att gac aat gcc aaa ttg gct gca gat gac ttc agg acc aag      641
Val Glu Ile Asp Asn Ala Lys Leu Ala Ala Asp Asp Phe Arg Thr Lys
170                 175                 180                 185

tat gag acg gag gtg tcc ctg cgg cag ctg gtg gag tca gac atc aac      689
Tyr Glu Thr Glu Val Ser Leu Arg Gln Leu Val Glu Ser Asp Ile Asn
186                 191                 196                 201

ggc ctg cgc agg atc ctg gat gac ctg acc ctg tgc aag tct gac ctg      737
Gly Leu Arg Arg Ile Leu Asp Asp Leu Thr Leu Cys Lys Ser Asp Leu
202                 207                 212                 217

gag gcc cag gtg gag tcc ctg aag gag gag ctg ctc tgc ctg aag aag      785
Glu Ala Gln Val Glu Ser Leu Lys Glu Glu Leu Leu Cys Leu Lys Lys
218                 223                 228                 233

aac cat gag gag gaa gtg aac tca ctg cgc tgc caa ctt ggt gac cgc      833
Asn His Glu Glu Glu Val Asn Ser Leu Arg Cys Gln Leu Gly Asp Arg
234                 239                 244                 249

ctc aat gtt gag gtg gac gct gcc cca cct gtt gac ctg aac cga gtt      881
Leu Asn Val Glu Val Asp Ala Ala Pro Pro Val Asp Leu Asn Arg Val
250                 255                 260                 265

ctg gag gag atg agg tgc cag tat gaa acc ctg gtg gag aat aac cgc      929
Leu Glu Glu Met Arg Cys Gln Tyr Glu Thr Leu Val Glu Asn Asn Arg
266                 271                 276                 281

cgg gat gct gaa gac tgg ttg gac acc cag agt gag gag ctg aac cag      977
Arg Asp Ala Glu Asp Trp Leu Asp Thr Gln Ser Glu Glu Leu Asn Gln
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282                 287                 292                 297

cag gtg gtg tcc agc tca gag cag ttg cag tcc tgc cag gca gag atc     1025
Gln Val Val Ser Ser Ser Glu Gln Leu Gln Ser Cys Gln Ala Glu Ile
298                 303                 308                 313

atc gag ctg aga cgc acg gtc aac gcc ctg gag att gag ctg cag gct     1073
Ile Glu Leu Arg Arg Thr Val Asn Ala Leu Glu Ile Glu Leu Gln Ala
314                 319                 324                 329

cag cac agc atg aga gat gct ttg gaa tcc acc ctg gca gag acg gag     1121
Gln His Ser Met Arg Asp Ala Leu Glu Ser Thr Leu Ala Glu Thr Glu
330                 335                 340                 345

gcc cgc tat agc tcc cag ctg gcc cag atg cag tgc atg atc acc aac     1169
Ala Arg Tyr Ser Ser Gln Leu Ala Gln Met Gln Cys Met Ile Thr Asn
346                 351                 356                 361

gtg gag gcc cag ctg gcc gag atc cgg gct gac ctg gag cgg cag aac     1217
Val Glu Ala Gln Leu Ala Glu Ile Arg Ala Asp Leu Glu Arg Gln Asn
362                 367                 372                 377

cag gag tac cag gtg ctg ctg gac gtc cgg gcc cgg ctg gag tgt gag     1265
Gln Glu Tyr Gln Val Leu Leu Asp Val Arg Ala Arg Leu Glu Cys Glu
378                 383                 388                 393

atc aac acg tac cgg ggc ctg ctg gag agt gag gac agc aag ctc ccc     1313
Ile Asn Thr Tyr Arg Gly Leu Leu Glu Ser Glu Asp Ser Lys Leu Pro
394                 399                 404                 409

tgt aac cca tgt gca cct gac tac tca ccc tcc aag tca tgc ctt ccc     1361
Cys Asn Pro Cys Ala Pro Asp Tyr Ser Pro Ser Lys Ser Cys Leu Pro
410                 415                 420                 425

tgt ctt cct gcg gcc tcc tgc ggt cct agt gca gcc cgc aca aac tgc     1409
Cys Leu Pro Ala Ala Ser Cys Gly Pro Ser Ala Ala Arg Thr Asn Cys
426                 431                 436                 441

agc ccc cgc ccc att tgt gtg ccc tgc cca ggg ggt cgg ttc tga gag     1457
Ser Pro Arg Pro Ile Cys Val Pro Cys Pro Gly Gly Arg Phe  *
442                 447                 452

cgggtgaccc agatggccat ggctattgtc tccagggctt gaacttggcc tctacccaaa   1517

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gcccccaaag gtctcaactc ctcatcattt caatgggtgc cagggtctct gttctcaggc   1697

tgcctcctgg gtcaggtttt ccttctaggt gctgttccgg tggattctga aatgcagtag   1757

agggcttttg ttggcagaac aataaagtgc atttgctcag gccaaaaaaa aaaaa        1812
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<210> 275
<211> 2285
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (260)..(1351)

<400> 275
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cggccgcccg cgatccagct ccgacaacag gaattttctc cgagagcggg ccgggctcag     60

ttcagctgct gtccagaccc ggatcggcaa cagtgccgcc tccagacgtt ctcctgccgc    120

tcgcccgccc gtcccagcgc ccccagccct cccgcgaggg cgccccggga cggaaggatc    180

caccagtctg tcggcgcccg ccgttctcgt ggtcgccgtc gccgtcgtcg tggtggtagt    240

ctccgccgtc gcctgggcc atg gcc aat tac atc cac gtc cct ccc ggc tcc     292
                    Met Ala Asn Tyr Ile His Val Pro Pro Gly Ser
                      1               5

ccg gag gtg ccc aag ctg aac gtc acc gtt cag gat cag gag gag cat      340
Pro Glu Val Pro Lys Leu Asn Val Thr Val Gln Asp Gln Glu Glu His
 12                  17                  22                  27

cgc tgc cgg gag ggg gcc ctg agc ctc ctg caa cac ctg cgg cct cac      388
Arg Cys Arg Glu Gly Ala Leu Ser Leu Leu Gln His Leu Arg Pro His
 28                  33                  38                  43

tgg gac ccc cag gag gtg acc ctg cag ctc ttc aca gat gga atc aca      436
Trp Asp Pro Gln Glu Val Thr Leu Gln Leu Phe Thr Asp Gly Ile Thr
 44                  49                  54                  59

aat aaa ctt att ggc tgt tac gtg gga aac acc atg gag gat gta gtc      484
Asn Lys Leu Ile Gly Cys Tyr Val Gly Asn Thr Met Glu Asp Val Val
 60                  65                  70                  75

ctg gtg aga att tat ggc aat aag act gag tta tta gtc gat cga gat      532
Leu Val Arg Ile Tyr Gly Asn Lys Thr Glu Leu Leu Val Asp Arg Asp
 76                  81                  86                  91

gag gaa gta aag agt ttt cga gtg ttg cag gct cat ggg tgt gca cca      580
Glu Glu Val Lys Ser Phe Arg Val Leu Gln Ala His Gly Cys Ala Pro
 92                  97                 102                 107

caa ctc tac tgt acc ttc aat aat gga cta tgc tat gaa ttt ata caa      628
Gln Leu Tyr Cys Thr Phe Asn Asn Gly Leu Cys Tyr Glu Phe Ile Gln
108                 113                 118                 123

gga gaa gca ctg gat cca aag cat gtc tgc aac cca gcc att ttc agg      676
Gly Glu Ala Leu Asp Pro Lys His Val Cys Asn Pro Ala Ile Phe Arg
124                 129                 134                 139

cta ata gct cgt cag ctt gct aaa atc cat gct att cat gca cac aat      724
Leu Ile Ala Arg Gln Leu Ala Lys Ile His Ala Ile His Ala His Asn
140                 145                 150                 155
```

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ggc tgg atc ccc aaa tct aat ctt tgg cta aag atg gga aag tat ttc      772
Gly Trp Ile Pro Lys Ser Asn Leu Trp Leu Lys Met Gly Lys Tyr Phe
156                 161                 166                 171

tct ctc att ccc aca gga ttt gca gat gaa gac att aat aaa agg ttc      820
Ser Leu Ile Pro Thr Gly Phe Ala Asp Glu Asp Ile Asn Lys Arg Phe
172                 177                 182                 187

cta agt gat atc cca agc tct cag att ctc cag gaa gag atg act tgg      868
Leu Ser Asp Ile Pro Ser Ser Gln Ile Leu Gln Glu Glu Met Thr Trp
188                 193                 198                 203

atg aag gag att ctt tcc aac ctg ggc tca cct gtt gtg ctt tgc cat      916
Met Lys Glu Ile Leu Ser Asn Leu Gly Ser Pro Val Val Leu Cys His
204                 209                 214                 219

aat gac cta ttg tgt aag aat ata atc tac aat gag aaa caa ggt gat      964
Asn Asp Leu Leu Cys Lys Asn Ile Ile Tyr Asn Glu Lys Gln Gly Asp
220                 225                 230                 235

gta cag ttc att gat tat gaa tat tct gga tac aac tac ctg gca tat     1012
Val Gln Phe Ile Asp Tyr Glu Tyr Ser Gly Tyr Asn Tyr Leu Ala Tyr
236                 241                 246                 251

gat att gga aat cat ttc aat gaa ttt gca ggt gtg agt gat gta gac     1060
Asp Ile Gly Asn His Phe Asn Glu Phe Ala Gly Val Ser Asp Val Asp
252                 257                 262                 267

tat agt ctg tat cca gat aga gaa cta cag agt cag tgg ctg cgt gct     1108
Tyr Ser Leu Tyr Pro Asp Arg Glu Leu Gln Ser Gln Trp Leu Arg Ala
268                 273                 278                 283

tac ctt gaa gcc tac aaa gaa ttt aag ggc ttt ggg act gaa gtt act     1156
Tyr Leu Glu Ala Tyr Lys Glu Phe Lys Gly Phe Gly Thr Glu Val Thr
284                 289                 294                 299

gaa aag gag gta gaa ata ctc ttc att caa gtc aat cag ttt gca ttg     1204
Glu Lys Glu Val Glu Ile Leu Phe Ile Gln Val Asn Gln Phe Ala Leu
300                 305                 310                 315

gct tct cat ttc ttt tgg gga ttg tgg gct ttg att caa gcc aaa tac     1252
Ala Ser His Phe Phe Trp Gly Leu Trp Ala Leu Ile Gln Ala Lys Tyr
316                 321                 326                 331

tcc act att gag ttt gat ttc ctt ggg tat gca att gtt cgt ttt aac     1300
Ser Thr Ile Glu Phe Asp Phe Leu Gly Tyr Ala Ile Val Arg Phe Asn
332                 337                 342                 347

cag tac ttt aaa atg aag cct gag gtt act gca tta aaa gtg cct gag     1348
Gln Tyr Phe Lys Met Lys Pro Glu Val Thr Ala Leu Lys Val Pro Glu
348                 353                 358                 363

taa agaa gagatttaat tattctccag tagctgagca atgcttgtga atcttttctt     1405
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364
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aagaaatccc aaaaagccaa tattagttaa aattctgttg tttaatttgg ttatcttgct 1465

ttataaatta tgcctctaaa caatcaaatc tatttttgaa atagactgaa tgatgtcaag 1525

aaatatacct actgctatcc gtatgtggtg gattagaaat gtgttaaatc tgcaaaaggt 1585

ataaagatgt cagtttaatt tctttgataa tttaacctat gttgtatgtg aattatttat 1645

tataaactta gcacgattct gtgactgttt ttctctgttt cacgttcgtt gagtgtaagc 1705

aatgaaaatg tcccaaataa gtttttaag ttttacttta ataagattaa tttcagtaaa 1765

cattctagtt gttcagtgta acctttttat cttgatgcat tgtaagtaaa atgaatcatt 1825

tactcttgaa atgccagtca ttgactgatg tagataattt aggattttca tataaaaata 1885

gctgtttagg aaggtgaaat acattcactg tctctgttgg tggtacatct tgttgaattc 1945

aatattagaa agtatttctt tttggggtaa tataacttag aattaaatcc ctgtttctct 2005

atgtagtctg gcagtataaa tataaatatt taccatataa tcttggaata agtattagtt 2065

aatgttacca aaatctgtat taaataatgt tttcaaatgc taaatatggt cgttactatt 2125

ttcagtttta aaaattttat agtatcaaat tgtttctaac caaaaatttc cttttacttc 2185

tagagatgct ttatgttttt gattattaaa tagtcactag tattgctaat ttttgaaaca 2245

aatacccaaa atttatcata tgtagaaata agaaaaaaaa 2285

<210> 276
<211> 1276
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (286)..(1113)

<400> 276
taccgctccg gaattcccgg gtcgacccac gcgtccgggg aggactgggt tatgccctgc 60

ttatcagcag cttcccagct tcctctgcct ggattcttag aggcctgggg tcctagaacg 120

agctggtgca cgtggcttcc caaagatctc tcagataatg agaggaaatg cagtcatcag 180

tttgcagaag gctagggatt ctgggccata gctcagacct gcgcccacca tctccctcca 240

ggcagccctt ggctggtccc tgcgagcccg tggagactgc cagag atg tcc tct 294
Met Ser Ser
1

ttc ggt tac agg acc ctg act gtg gcc ctc ttc acc ctg atc tgc tgt 342
Phe Gly Tyr Arg Thr Leu Thr Val Ala Leu Phe Thr Leu Ile Cys Cys

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  4                   9                  14                  19

cca gga tcg gat gag aag gta ttc gag gta cac gtg agg cca aag aag      390
Pro Gly Ser Asp Glu Lys Val Phe Glu Val His Val Arg Pro Lys Lys
 20                  25                  30                  35

ctg gcg gtt gag ccc aaa ggg tcc ctc gag gtc aac tgc agc acc acc      438
Leu Ala Val Glu Pro Lys Gly Ser Leu Glu Val Asn Cys Ser Thr Thr
 36                  41                  46                  51

tgt aac cag cct gaa gtg ggt ggt ctg gag acc tct cta gat aag att      486
Cys Asn Gln Pro Glu Val Gly Gly Leu Glu Thr Ser Leu Asp Lys Ile
 52                  57                  62                  67

ctg ctg gac gaa cag gct cag tgg aaa cat tac ttg gtc tca aac atc      534
Leu Leu Asp Glu Gln Ala Gln Trp Lys His Tyr Leu Val Ser Asn Ile
 68                  73                  78                  83

tcc cat gac acg gtc ctc caa tgc cac ttc acc tgc tcc ggg aag cag      582
Ser His Asp Thr Val Leu Gln Cys His Phe Thr Cys Ser Gly Lys Gln
 84                  89                  94                  99

gag tca atg aat tcc aac gtc agc gtg tac cag cct cca agg cag gtc      630
Glu Ser Met Asn Ser Asn Val Ser Val Tyr Gln Pro Pro Arg Gln Val
100                 105                 110                 115

atc ctg aca ctg caa ccc act ttg gtg gct gtg ggc aag tcc ttc acc      678
Ile Leu Thr Leu Gln Pro Thr Leu Val Ala Val Gly Lys Ser Phe Thr
116                 121                 126                 131

att gag tgc agg gtg ccc acc gtg gag ccc ctg gac agc ctc acc ctc      726
Ile Glu Cys Arg Val Pro Thr Val Glu Pro Leu Asp Ser Leu Thr Leu
132                 137                 142                 147

ttc ctg ttc cgt ggc aat gag act ctg cac tat gag acc ttc ggg aag      774
Phe Leu Phe Arg Gly Asn Glu Thr Leu His Tyr Glu Thr Phe Gly Lys
148                 153                 158                 163

gca gcc cct gct ccg cag gag gcc aca gcc aca ttc aac agc acg gct      822
Ala Ala Pro Ala Pro Gln Glu Ala Thr Ala Thr Phe Asn Ser Thr Ala
164                 169                 174                 179

gac aga gag gat ggc cac cgc aac ttc tcc tgc ctg gct gtg ctg gac      870
Asp Arg Glu Asp Gly His Arg Asn Phe Ser Cys Leu Ala Val Leu Asp
180                 185                 190                 195

ttg atg tct cgc ggt ggc aac atc ttt cac aaa cac tca gcc ccg aag      918
Leu Met Ser Arg Gly Gly Asn Ile Phe His Lys His Ser Ala Pro Lys
196                 201                 206                 211

atg ttg gag atc tat gag cct gtg tcg gac agc cag atg gtc atc ata      966
Met Leu Glu Ile Tyr Glu Pro Val Ser Asp Ser Gln Met Val Ile Ile
212                 217                 222                 227

gtc acg gtg gtg tcg gtg ttg ctg tcc ctg ttc gtg aca tct gtc ctg     1014
Val Thr Val Val Ser Val Leu Leu Ser Leu Phe Val Thr Ser Val Leu
228                 233                 238                 243
```

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ctc tgc ttc atc ttc ggc cag cac ttg cgc cag cag cgg atg ggc acc     1062
Leu Cys Phe Ile Phe Gly Gln His Leu Arg Gln Gln Arg Met Gly Thr
244                 249                 254                 259

tac ggg gtg cga gcg gct tgg agg agg ctg ccc cag gcc ttc cgg cca     1110
Tyr Gly Val Arg Ala Ala Trp Arg Arg Leu Pro Gln Ala Phe Arg Pro
260                 265                 270                 275

tag caac catgagtggc atggccacca ccacggtggt cactggaact cagtgtgact     1167
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276

cctcagggtt gaggtccagc cctggctgaa ggactgtgac aggcagcaga gacttgggac   1227

attgcctttt ctagcccgaa tacaaacacc tggacttaaa aaaaaaaaa               1276
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<210> 277
<211> 1048
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (92)..(766)

<400> 277

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ttcccgggtc gacgatttcg tccgacccga gccgagccga gccgagccga gccggagcgg     60

gcggcgaagg ccggcgcggc gagcagcaac c   atg tcg gtg ttc ggg aag ctg     112
                                    Met Ser Val Phe Gly Lys Leu
                                      1               5

ttc ggg gct gga ggg ggt aag gcc ggc aag ggc ggc ccg acc ccc cag     160
Phe Gly Ala Gly Gly Gly Lys Ala Gly Lys Gly Gly Pro Thr Pro Gln
  8                  13                  18                  23

gag gcc atc cag cgg ctg cgg gac acg gaa gag atg tta agc aag aaa     208
Glu Ala Ile Gln Arg Leu Arg Asp Thr Glu Glu Met Leu Ser Lys Lys
 24                  29                  34                  39

cag gag ttc ctg gag aag aaa atc gag cag gag ctg acg gcc gcc aag     256
Gln Glu Phe Leu Glu Lys Lys Ile Glu Gln Glu Leu Thr Ala Ala Lys
 40                  45                  50                  55

aag cac ggc acc aaa aac aag cgc gcg gcc ctc cag gca ctg aag cgt     304
Lys His Gly Thr Lys Asn Lys Arg Ala Ala Leu Gln Ala Leu Lys Arg
 56                  61                  66                  71

aag aag agg tat gag aag cag ctg gcg cag atc gac ggc aca tta tca     352
Lys Lys Arg Tyr Glu Lys Gln Leu Ala Gln Ile Asp Gly Thr Leu Ser
 72                  77                  82                  87

acc atc gag ttc cag cgg gag gcc ctg gag aat gcc aac acc aac acc     400
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Thr Ile Glu Phe Gln Arg Glu Ala Leu Glu Asn Ala Asn Thr Asn Thr
 88                  93                  98                  103

gag gtg ctc aag aac atg ggc tat gcc gcc aag gcc atg aag gcg gcc      448
Glu Val Leu Lys Asn Met Gly Tyr Ala Ala Lys Ala Met Lys Ala Ala
104                 109                 114                 119

cat gac aac atg gac atc gat aaa gtt gat gag tta atg cag gac att      496
His Asp Asn Met Asp Ile Asp Lys Val Asp Glu Leu Met Gln Asp Ile
120                 125                 130                 135

gct gac cag caa gaa ctt gca gag gag att tca aca gca att tcg aaa      544
Ala Asp Gln Gln Glu Leu Ala Glu Glu Ile Ser Thr Ala Ile Ser Lys
136                 141                 146                 151

cct gta ggg ttt gga gaa gag ttt gac gag gat gag ctc atg gcg gaa      592
Pro Val Gly Phe Gly Glu Glu Phe Asp Glu Asp Glu Leu Met Ala Glu
152                 157                 162                 167

tta gaa gaa cta gaa cag gag gaa cta gac aag aat ttg ctg gaa atc      640
Leu Glu Glu Leu Glu Gln Glu Glu Leu Asp Lys Asn Leu Leu Glu Ile
168                 173                 178                 183

agt gga ccc gaa aca gtc cct cta cca aat gtt ccc tct ata gcc cta      688
Ser Gly Pro Glu Thr Val Pro Leu Pro Asn Val Pro Ser Ile Ala Leu
184                 189                 194                 199

cca tca aaa ccc gcc aag aag aaa gaa gag gag gac gac gac atg aag      736
Pro Ser Lys Pro Ala Lys Lys Lys Glu Glu Glu Asp Asp Asp Met Lys
200                 205                 210                 215

gaa ttg gag aac tgg gct gga tcc atg taa t ggggtccagc gctggctggg      787
Glu Leu Glu Asn Trp Ala Gly Ser Met  *
216                 221

cccagacaga ctgtggtggc ctgcgcagcg agcaggcgtg tgcgtgtgtg gggcaggcag    847

gatgtggtgc aggcaggttc catcgctttc gactctcact ccaaagcagt agggccgcgt    907

tgctgctcac tctctgcata gcatggtctg cacctgggag atgggcgggg ggaggggggc    967

gagcgggctg gcacgtgcct gctgtttata atgttgaatt tctgtaaaat aaactgtatt   1027

tgcaaatcca aaaaaaaaaa a                                            1048
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<210> 278
<211> 2091
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (242)..(1267)

<400> 278
tttcggcggc tgacccataa aatctaccta gttctaaaat tcttaaccca cccatttaca 60

aaaaccggag gtaataggta aacagaaacg ccagggaaag atcgcactta aaggaccaaa 120

agcacccaag gaggaaaaag aggcctgaga tttccacgaa ttacaagtga acttcctgtc 180

ctgggtaaac ttccggaatc aacaacagga agacccaatc agaatcttcc tccgggagcc 240

a atg gga gag cac att aca aag agc caa tcc cag cgc cgc tgt cac 286
Met Gly Glu His Ile Thr Lys Ser Gln Ser Gln Arg Arg Cys His
1 5 10

tgt tat ggt cct gtc agg gtg ccg gcg tcg tgg tgc ttg ggt ggt cgc 334
Cys Tyr Gly Pro Val Arg Val Pro Ala Ser Trp Cys Leu Gly Gly Arg
16 21 26 31

cac caa gaa gac ttt ggt ggg gta gtc tcg ggg cag ctc agc ggc ccg 382
His Gln Glu Asp Phe Gly Gly Val Val Ser Gly Gln Leu Ser Gly Pro
32 37 42 47

ctg tgc ccg ttt ctg gcc tcg ctc gca gct tgc acg tcg aga ctc gta 430
Leu Cys Pro Phe Leu Ala Ser Leu Ala Ala Cys Thr Ser Arg Leu Val
48 53 58 63

ggc cgc acc gta ggc gag cgt gcg ggt cgc cgc cgc ggc cgc ctc ggg 478
Gly Arg Thr Val Gly Glu Arg Ala Gly Arg Arg Arg Gly Arg Leu Gly
64 69 74 79

gtc tgg gcc cag ccg cag cct ctt cta ccg cgg ccg gtt ggg agt cgc 526
Val Trp Ala Gln Pro Gln Pro Leu Leu Pro Arg Pro Val Gly Ser Arg
80 85 90 95

cgc gag atg cag cct ccg ggc ccg ccc ccg gcc tat gcc ccc act aac 574
Arg Glu Met Gln Pro Pro Gly Pro Pro Pro Ala Tyr Ala Pro Thr Asn
96 101 106 111

ggg gac ttc acc ttt gtc tcc tca gca gac gcg gaa gat ctc agt ggt 622
Gly Asp Phe Thr Phe Val Ser Ser Ala Asp Ala Glu Asp Leu Ser Gly
112 117 122 127

tca ata gca tcc cca gat gtc aaa tta aat ctt ggt gga gat ttt atc 670
Ser Ile Ala Ser Pro Asp Val Lys Leu Asn Leu Gly Gly Asp Phe Ile
128 133 138 143

aaa gaa tct aca gct act aca ttt ctg aga caa aga ggt tat ggc tgg 718
Lys Glu Ser Thr Ala Thr Thr Phe Leu Arg Gln Arg Gly Tyr Gly Trp
144 149 154 159

ctt ctg gaa gtt gaa gat gat gat cct gaa gat aac aag cca ctc ttg 766
Leu Leu Glu Val Glu Asp Asp Asp Pro Glu Asp Asn Lys Pro Leu Leu
160 165 170 175

gaa gaa ttg gac att gat cta aag gat att tac tac aaa atc cga tgt 814
Glu Glu Leu Asp Ile Asp Leu Lys Asp Ile Tyr Tyr Lys Ile Arg Cys
176 181 186 191

```
gtt ttg atg cca atg cca tca ctt ggt ttt aat aga caa gtg gtg aga      862
Val Leu Met Pro Met Pro Ser Leu Gly Phe Asn Arg Gln Val Val Arg
192                 197                 202                 207

gac aat cct gac ttt tgg ggt cct ctg gct gtt gtt ctt ttc ttt tcc      910
Asp Asn Pro Asp Phe Trp Gly Pro Leu Ala Val Val Leu Phe Phe Ser
208                 213                 218                 223

atg ata tca tta tat gga cag ttt agg gtg gtc tca tgg att ata acc      958
Met Ile Ser Leu Tyr Gly Gln Phe Arg Val Val Ser Trp Ile Ile Thr
224                 229                 234                 239

att tgg ata ttt ggt tca cta aca att ttc tta ctg gcc aga gtt ctt     1006
Ile Trp Ile Phe Gly Ser Leu Thr Ile Phe Leu Leu Ala Arg Val Leu
240                 245                 250                 255

ggt gga gaa gtt gca tat ggc caa gtc ctt gga gtt ata gga tat tca     1054
Gly Gly Glu Val Ala Tyr Gly Gln Val Leu Gly Val Ile Gly Tyr Ser
256                 261                 266                 271

tta ctt cct ctc att gta ata gcc cct gta ctt ttg gtg gtt gga tca     1102
Leu Leu Pro Leu Ile Val Ile Ala Pro Val Leu Leu Val Val Gly Ser
272                 277                 282                 287

ttt gaa gtg gtg tct aca ctt ata aaa ctg ttt ggt gtg ttt tgg gct     1150
Phe Glu Val Val Ser Thr Leu Ile Lys Leu Phe Gly Val Phe Trp Ala
288                 293                 298                 303

gcc tac agt gct gct tca ttg tta gtg ggt gaa gaa ttc aag acc aaa     1198
Ala Tyr Ser Ala Ala Ser Leu Leu Val Gly Glu Glu Phe Lys Thr Lys
304                 309                 314                 319

aag cct ctt ctg att tat cca atc ttt tta tta tac att tat ttt ttg     1246
Lys Pro Leu Leu Ile Tyr Pro Ile Phe Leu Leu Tyr Ile Tyr Phe Leu
320                 325                 330                 335

tcg tta tat act ggt gtg tga tc caagttatac atgaatagaa aaagatggtg     1299
Ser Leu Tyr Thr Gly Val  *
336                 341

ttaaatttgt gtgtaggctg ggaattcttg ctgaaggaat tggagaaaac ctgttgctgc   1359

aaaattttac atgttccaga tggaaaggga agtctaagcg ctttttaaaa caatttttt    1419

ttgtatttaa ttaagcaatt gcagttatct gggatttttg ggtcagaatt ttaaattctg   1479

tttgattctc catattccag tgaataaaat acaaaagcat tgtgttttta agattgtgtc   1539

gatattcacc taaaaacttg tgccaaaagc acctggattg gtaattatat ttcacttaaa   1599

gggtaaattt gacaatatct tgataatcaa aagtgcaatt tttttcttca aaatgttttc   1659

tccagcatca cagatcctgc agatatatat ttatatttat acatatatat ttatgaaata   1719

attcttactc acaaaatata tttctgataa acattaagat attaaatctg atgcacaaac   1779

tttttaattt ggccattaat ctttttttatt taaaaattta aatttgtttt taaaattgta   1839
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tatagttttt aaaatctcac acatgcttcg atacttcctt gttaagaatt cttaataact   1899

actaaaactg atttttaata gttgctgata tatatttggt ttgtttgggt atacttttca   1959

aaaccatttt tgaatgtcca aacatctgat ttaaagtttc tgtttatctt tctgaccaaa   2019

ggagcaagag gtataatgga tatggcattc attaaaatct ttactatgta caaaaacagt   2079

aaaaaaaaaa aa                                                      2091
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<210> 279
<211> 789
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (76)..(372)

<400> 279

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ggtgggctgc attcaaagct gtcctgggcc acatgcagct cgctgcccgt gggttagcaa     60

ggctgctcta agaca atg agt gta ggt agg ccc ttc tat agg tcc tct gag     111
                Met Ser Val Gly Arg Pro Phe Tyr Arg Ser Ser Glu
                  1               5                  10

ttc atg gag caa ctt ctc agc agc cat ctc cac cag gtt ccc ttc ttc      159
Phe Met Glu Gln Leu Leu Ser Ser His Leu His Gln Val Pro Phe Phe
 13                  18                  23                  28

tgt tgt ttc act gtg gtt tgc ctc tgt aac tgc ttg ttc gag aac tct      207
Cys Cys Phe Thr Val Val Cys Leu Cys Asn Cys Leu Phe Glu Asn Ser
 29                  34                  39                  44

gtc agc aaa ctc tac atg ctc tgc ttc aac ttc ttc atg tcc att ttt      255
Val Ser Lys Leu Tyr Met Leu Cys Phe Asn Phe Phe Met Ser Ile Phe
 45                  50                  55                  60

ttt tat agc ctt agc ata aca aag tta aat ttg att tac ctt tgg ggg      303
Phe Tyr Ser Leu Ser Ile Thr Lys Leu Asn Leu Ile Tyr Leu Trp Gly
 61                  66                  71                  76

ctc agc tat caa agc cta ctc ctt ctt cta ctc tca ggc cat cgg ccc      351
Leu Ser Tyr Gln Ser Leu Leu Leu Leu Leu Leu Ser Gly His Arg Pro
 77                  82                  87                  92

tgg ggc tcc agc atg gtt tga tg gtctggtcat ccgatcatca gcactgaagt      404
Trp Gly Ser Ser Met Val  *
 93                  98

ctctcacagg attcaaaaat ggctccatga cacatgaaca ctgtgatctt gagtatatct    464

cttaatttct ctgcaactcc atttccacat cagcaaaact gggataataa tacttacctt    524
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gcagagatac tgcaaagatt aaatgagaga atgcatattg aacccagaat ggtggctgac    584

atgtagcagg tatataatag atgagcctcc tagtatgtta gaggtgtttc ctgaagggat    644

tctaatctcc tgaggaagac tagggcccaa gaccttaagc aaacccaggc aagagcctct    704

gtgtcttaga tgtgtgtgtg tattaccccc tagtggctcc acagtaatga ttctcgtgcc    764

gaattcttgg cctcgagggc caaat                                          789
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<210> 280
<211> 1403
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (138)..(599)

<400> 280

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gcacgaggcc tcgtgccact ggaagaattc gcagccgggc agccgcttcc cgcccccgag     60

caggagccgg tgcgagcgga gcagagccga ggtcgggccg cgagcggagc cggctgagcg    120

ggcgccgagc tcccgcc   atg gcc cgg aac acg ctg tcc tcg cgc ttc cgc     170
                    Met Ala Arg Asn Thr Leu Ser Ser Arg Phe Arg
                      1               5

cgg gtg gac atc gac gaa ttt gac gag aac aaa ttt gtg gac gag cag      218
Arg Val Asp Ile Asp Glu Phe Asp Glu Asn Lys Phe Val Asp Glu Gln
 12                  17                  22                  27

gag gag gcg gcg gcg gcg gcg gcg gag cca ggc ccg gac ccg agc gag      266
Glu Glu Ala Ala Ala Ala Ala Ala Glu Pro Gly Pro Asp Pro Ser Glu
 28                  33                  38                  43

gtg gac ggg ctc ctg cgg caa ggg gac atg ctt cgg gca ttc cat gca      314
Val Asp Gly Leu Leu Arg Gln Gly Asp Met Leu Arg Ala Phe His Ala
 44                  49                  54                  59

gcc ttg cgg aac tct ccc gtc aac acc aag aat caa gct gtg aag gag      362
Ala Leu Arg Asn Ser Pro Val Asn Thr Lys Asn Gln Ala Val Lys Glu
 60                  65                  70                  75

cga gcc cag ggc gtg gtg ctg aaa gtg ctc aca aac ttc aag agc agt      410
Arg Ala Gln Gly Val Val Leu Lys Val Leu Thr Asn Phe Lys Ser Ser
 76                  81                  86                  91

gag att gag cag gct gtg cag tca ctg gac aga aac ggc gtt gac ttg      458
Glu Ile Glu Gln Ala Val Gln Ser Leu Asp Arg Asn Gly Val Asp Leu
 92                  97                 102                 107

tta atg aag tac att tat aaa ggc ttt gag aag ccc aca gaa aat agc      506
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Leu Met Lys Tyr Ile Tyr Lys Gly Phe Glu Lys Pro Thr Glu Asn Ser
108                 113                 118                 123

agc gca gtg tta ctc cag tgg cac gaa aag gcc tta gca gta gga gga      554
Ser Ala Val Leu Leu Gln Trp His Glu Lys Ala Leu Ala Val Gly Gly
124                 129                 134                 139

cta ggc tcc att ata aga gtt ctt aca gca aga aag act gtt taa aaa      602
Leu Gly Ser Ile Ile Arg Val Leu Thr Ala Arg Lys Thr Val  *
140                 145                 150

aaataaaaag actcatgtta ccttgagaag aattctggat gcccaggctg gtgaagaagg    662

gattgacaat ggaccatctt cctaggaact cccaagtaaa ctatttcagg acatgtatct    722

gctgaaatgt attttatttt caaggtggag gggaaaatcg tctgtttcct aaatcctgtt    782

taggatctga tagtctatgc ctttgtctcc gagtactgca gaactgacat tttgacggtc    842

taccagcgtg gcggctggtg ttggtcagat gcacctgtgt gcactggggg agggatggtt    902

tgggcaggtg cagatccaag ggctgtggta aacgggagag cttgtgtttt tgaagtggaa    962

aaaaacccaa gagtttgtac agacatcctg tcttcccaga gaaggtggac actcttgggc   1022

tcattgtaaa gtgcctgctg catcaataaa gctcttggct tattagtcta tacattgcgg   1082

tgtgtttcgt gtatgtaaaa aaaaatggta atgaatggga tggtaatgaa tgagagttca   1142

gttgttgttc cggaaacccg atgtggaagg agtagacctg tgtccctgtt gagccacccc   1202

tgggagcgag catggcaatc cacaggccct ctgccacagg acgccagcct cggcctcaga   1262

gctgccggct gctgcagaga ggtgtttgct gaataaacta tttattgttt cttattcctt   1322

tgatttgtat gtaattaatt ttggagctta tttaattaat ttaataaagt gccaaacatt   1382

taataattga aaaaaaaaaa a                                            1403
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<213> Homo sapiens

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<222> (244)..(972)

<400> 281

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acagggaggg caagggtttc cttttggcgc ttccctttgg accccggagt gaaaaactct    120

aacgtccaga tcagtggaga gaaacgcaga tttaggaccc tgaggagtct ttttcacccg    180
```

```
tttcccgtca ctcgctcagg cgcgccgagg gcagtccttg tggggtcctc gtggccagcc    240

aag  atg gtt gcc ccc gca gtg aag gtt gcc cga gga tgg tcg ggc ctg     288
     Met Val Ala Pro Ala Val Lys Val Ala Arg Gly Trp Ser Gly Leu
       1               5                  10

gcg ttg ggc gtg cgg cgg gct gtc ttg cag ctt cca ggg cta act cag      336
Ala Leu Gly Val Arg Arg Ala Val Leu Gln Leu Pro Gly Leu Thr Gln
 16                  21                  26                  31

gtg aga tgg agc cgc tat agt cct gaa ttc aag gat ccc ttg att gac      384
Val Arg Trp Ser Arg Tyr Ser Pro Glu Phe Lys Asp Pro Leu Ile Asp
 32                  37                  42                  47

aag gaa tat tat cgc aag cca gtg gag gag cta act gag gag gag aaa      432
Lys Glu Tyr Tyr Arg Lys Pro Val Glu Glu Leu Thr Glu Glu Glu Lys
 48                  53                  58                  63

tat gtt cgg gag ctc aag aag act cag ctc atc aaa gct gct cca gca      480
Tyr Val Arg Glu Leu Lys Lys Thr Gln Leu Ile Lys Ala Ala Pro Ala
 64                  69                  74                  79

ggg aaa aca agt tct gtg ttt gaa gac cca gtc atc agt aaa ttc acc      528
Gly Lys Thr Ser Ser Val Phe Glu Asp Pro Val Ile Ser Lys Phe Thr
 80                  85                  90                  95

aac atg atg atg ata gga gga aac aaa gta ctg gcc aga tcc ctc atg      576
Asn Met Met Met Ile Gly Gly Asn Lys Val Leu Ala Arg Ser Leu Met
 96                 101                 106                 111

att cag act ctg gaa gct gtg aaa agg aag cag ttt gag aag tac cat      624
Ile Gln Thr Leu Glu Ala Val Lys Arg Lys Gln Phe Glu Lys Tyr His
112                 117                 122                 127

gcc gct tct gca gag gaa cag gca acc atc gaa cgc aac ccc tac acc      672
Ala Ala Ser Ala Glu Glu Gln Ala Thr Ile Glu Arg Asn Pro Tyr Thr
128                 133                 138                 143

atc ttc cat caa gca ctg aaa aac tgt gag cct atg att ggg ctg gta      720
Ile Phe His Gln Ala Leu Lys Asn Cys Glu Pro Met Ile Gly Leu Val
144                 149                 154                 159

ccc atc ctc aag gga ggc cgt ttc tac cag gtc cct gta ccc cta ccc      768
Pro Ile Leu Lys Gly Gly Arg Phe Tyr Gln Val Pro Val Pro Leu Pro
160                 165                 170                 175

gac cgg cgt cgc cgc ttc cta gcc atg aag tgg atg atc act gag tgc      816
Asp Arg Arg Arg Arg Phe Leu Ala Met Lys Trp Met Ile Thr Glu Cys
176                 181                 186                 191

cgg gat aaa aag cac cag cgg aca ctg atg ccg gag aag ctg tca cac      864
Arg Asp Lys Lys His Gln Arg Thr Leu Met Pro Glu Lys Leu Ser His
192                 197                 202                 207

aag ctg ctg gag gct ttc cat aac cag ggc ccc gtg atc aag agg aag      912
Lys Leu Leu Glu Ala Phe His Asn Gln Gly Pro Val Ile Lys Arg Lys
```

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208                 213                 218                 223

cat gac ttg cac aag atg gca gag gcc aac cgt gcc ctg gcc cac tac      960
His Asp Leu His Lys Met Ala Glu Ala Asn Arg Ala Leu Ala His Tyr
224                 229                 234                 239

cgc tgg tgg tag agt ctccaggagg agcccagggc cctctgccgc aagaaacagt     1015
Arg Trp Trp  *
240

gtgagctact gccacgctga aaactacctg tgggttaagg atgtagttcc tttgtaaggg   1075

tgggcaggcc tcgtaagaaa gatgtagcag catattcact atccgttaat ccttctttct   1135

ttgaggctgg aacttgctct ctctgcccct atttccttgt aaagagggag cacattgact   1195

tgggaatttc ctccaggaaa ctcagggctg ttttctcttc ccttaggttg gggcggacct   1255

ttggacatat aaaggaagca gttttagtat cagaaaagat ttattagaaa attctcacgc   1315

tgaactggtg tagcatgtgg tgcagcattc agtgaaactg gctggaggaa ataggcttgt   1375

ttccagagtt gtccttatac aaaatgtata aaaagcagtt tctggtgtga cttgtgctct   1435

gcctccaccc cttgacatcc caaaatatcc caccagtggc tatgcttacc cattttacag   1495

atgggtaaac tgaggcacca aggtagtagt tgcactaatg gttacacagt gcagtggctc   1555

ttgggagttg cccttctctg cctggccgtg gtgggttgtg gtggggaaag gggctcaggg   1615

caggaccacg gcataagtgg gaaacatctc accaggagat gggaaagtct agaagggaag   1675

acactcaaag tctggaaggg aaaagtcttt gggtgaggca gagactccac tgccagcttt   1735

agaggtgggt agaagaaagg ccagtgctgg tgaggaagcc ctgatctg               1783
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US 9,550,834 B2

<210> 282
<211> 3181
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<213> Homo sapiens

<220>
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<222> (129)..(1124)

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<223> n = a,t,c or g

<400> 282

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atctctacca caggaagctc agagaggtag agcggaatgg gatcccccgg cagccaaagg    120
```

```
atgtcttc atg gac acg cac cag ggt ctg acg gat gta cga gca aag gtg     170
         Met Asp Thr His Gln Gly Leu Thr Asp Val Arg Ala Lys Val
           1               5                  10

act ggc ttc agt gaa ggt gtg gtg gat agt gtc aaa ggt ggg ttt tcc     218
Thr Gly Phe Ser Glu Gly Val Val Asp Ser Val Lys Gly Gly Phe Ser
 15                  20                  25                  30

agc ttc tcc cag gcc acc cat tca gca gca ggc gct gta gtc tca aag     266
Ser Phe Ser Gln Ala Thr His Ser Ala Ala Gly Ala Val Val Ser Lys
 31                  36                  41                  46

ccc aga gag att gcc tca ctc att cgg aac aaa ttt ggc agt gca gac     314
Pro Arg Glu Ile Ala Ser Leu Ile Arg Asn Lys Phe Gly Ser Ala Asp
 47                  52                  57                  62

aac atc ccc aac ctg aag gac tct tta gag gaa ggg caa gtg gat gat     362
Asn Ile Pro Asn Leu Lys Asp Ser Leu Glu Glu Gly Gln Val Asp Asp
 63                  68                  73                  78

gcg ggg aag gct ttg gga gtg att tca aac ttt cag tct agc cca aaa     410
Ala Gly Lys Ala Leu Gly Val Ile Ser Asn Phe Gln Ser Ser Pro Lys
 79                  84                  89                  94

tat ggt agt gaa gaa gat tgt tct agt gcc act tca ggc tca gtg gga     458
Tyr Gly Ser Glu Glu Asp Cys Ser Ser Ala Thr Ser Gly Ser Val Gly
 95                 100                 105                 110

gcc aac agc acc aca ggg ggc atc gct gta gga gca tcc agc tcc aaa     506
Ala Asn Ser Thr Thr Gly Gly Ile Ala Val Gly Ala Ser Ser Ser Lys
111                 116                 121                 126

aca aac acc ctg gac atg cag agc tca gga ttt gat gca cta cta cat     554
Thr Asn Thr Leu Asp Met Gln Ser Ser Gly Phe Asp Ala Leu Leu His
127                 132                 137                 142

gag atc cag gag atc cgg gaa acc cag gcc aga cta gag gaa tcc ttt     602
Glu Ile Gln Glu Ile Arg Glu Thr Gln Ala Arg Leu Glu Glu Ser Phe
143                 148                 153                 158

gag act ctc aag gaa cat tat cag agg gac tat tcc tta ata atg cag     650
Glu Thr Leu Lys Glu His Tyr Gln Arg Asp Tyr Ser Leu Ile Met Gln
159                 164                 169                 174

acc tta cag gag gag cga tat aga tgt gaa cga ttg gaa gaa cag cta     698
Thr Leu Gln Glu Glu Arg Tyr Arg Cys Glu Arg Leu Glu Glu Gln Leu
175                 180                 185                 190

aat gac cta aca gag ctc cac cag aat gaa atc ttg aac ttg aag cag     746
Asn Asp Leu Thr Glu Leu His Gln Asn Glu Ile Leu Asn Leu Lys Gln
191                 196                 201                 206

gaa ctg gca agc atg gaa gaa aaa atc gcg tat cag tcc tat gaa cgg     794
Glu Leu Ala Ser Met Glu Glu Lys Ile Ala Tyr Gln Ser Tyr Glu Arg
207                 212                 217                 222
```

```
gcc cgg gac atc cag gag gcc ctg gag gca tgc cag acg cgc atc tcc      842
Ala Arg Asp Ile Gln Glu Ala Leu Glu Ala Cys Gln Thr Arg Ile Ser
223                 228                 233                 238

aag atg gag ctg cag cag cag cag cag cag gtg gtg cag cta gaa ggg      890
Lys Met Glu Leu Gln Gln Gln Gln Gln Gln Val Val Gln Leu Glu Gly
239                 244                 249                 254

ctg gag aat gcc act gcc cgg aac ctt ctg ggc aaa ctc atc aac atc      938
Leu Glu Asn Ala Thr Ala Arg Asn Leu Leu Gly Lys Leu Ile Asn Ile
255                 260                 265                 270

ctc ctg gct gtc atg gca gtc ctt ttg gtc ttt gtc tcc act gta gcc      986
Leu Leu Ala Val Met Ala Val Leu Leu Val Phe Val Ser Thr Val Ala
271                 276                 281                 286

aac tgt gtg gtc ccc ctc atg aag act cgc aac agg acg ttc agc act     1034
Asn Cys Val Val Pro Leu Met Lys Thr Arg Asn Arg Thr Phe Ser Thr
287                 292                 297                 302

tta ttc ctt gtg gtt ttt att gcc ttt ctc tgg aag cac tgg gac gcc     1082
Leu Phe Leu Val Val Phe Ile Ala Phe Leu Trp Lys His Trp Asp Ala
303                 308                 313                 318

ctc ttc agc tat gtg gaa cgg ttc ttt tca tcc cct aga tga tgctggc     1131
Leu Phe Ser Tyr Val Glu Arg Phe Phe Ser Ser Pro Arg  *
319                 324                 329

acagaaggca ttgttcccta ccctctggcg agtgcatgca gcagagagtt agacagcaac   1191

ttacctactc tgaagttttc tacaacaaaa aaagagttga gtgaatctgt ttacatttag   1251

aataatgttt ttttcttcaa gagacgcaat tgcaatagta ttttttagat tttatccaag   1311

aagtttttg ggcgaaaatc ttggatcatt tttatgtagc atgattttcc ttgggatgca   1371

aatcttaaaa cagtccttta atatgaacca acaatctgga gcacaccgaa gggcaatcta   1431

aattgtggct tgaaggactg cactaaaacc cactaaaaag atgcgaaaac ctgatgaggg   1491

caaaccagtt aaacctaaca ccctgccttg tctgggctca tcacctctcc ctatcccaga   1551

ctaactttac tgtgaaatcc taccacattc catgtctgaa tttttggatt cggggtggat   1611

tttcgttgtc cgtggaagaa cacatggatc tctctggctt tctcacccaa gttggccact   1671

tacgctaatc ctggaagtat gatcactttt gaacctgccc cttaaccttg acgaggatac   1731

aaaagtgaaa gcatcatccc ccaaaggatc actgcacagt cctactacag tatttttaag   1791

tagccctcta aatacttaat tttaagcaaa atcccttggc cgcactttta aggttttttt   1851

atatgtgtat agttaccaac ctaaaaataa aaaatccgaa cagcatactt gaagaatgta   1911

atactcaaac tctcagtgct tccttatggt ttctaatagg atttttttatt attgttatta   1971

ttattattgg gttttttttgg acagggttgg gagggtcttt tatttttcct ttgaaataaa   2031
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gaagtgatgt ttttaaatga agaaatgtgt ggatatttaa gtgtgctgct ccctcttgtc 2091

ttgaaacagt ttgagtaaga aagtcttgct gtaaatgctg ccctctgccg cctttgtttt 2151

gagatgcagt ttaaactccc tctggctgct gctgctgctt tttggtgtcc cgacatacct 2211

acgcccccgt tttatgggtt tggcttagtt gaagaggaaa gggttgtgca aggagagcag 2271

gaggctgttt ccaaaaacca gtgtagtagg atagggattt ttttttttt ttttgcccca 2331

agaaaacgtt cacccagtga tcttgggctg gggttgtctt taggaaaagt tgagactata 2391

agagtcataa ataagtcctt gtgtttcctt aatttatttt gttaacaccc ctaattacaa 2451

ccaaagtgat gatgtggagt cttctgtctt cattttggcc ccagcattct taatttcaaa 2511

gctttattct gtctgcctaa gagaatcaac caaaggtgat tctcctaaag agcagtgaag 2571

gaaatgtcag gttagcagga cccaagtttt gggtgtgaaa tgttgccagc ttcctataat 2631

gtaaacggac ttgttaacct aacctaatta tgctcagtgg acttctatag atggttttga 2691

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gaacatttag agtttatcta gagagcttgg ttaatctttc catattattt gtagtattgg 2811

tcacaaatgc tgttccctct tagcctcatt ctgtgcaacc aagtgcatat aagatgccct 2871

gaaaagagta acaaagtatg ctttgcctgt ttccacttac caggaaattc cttcagaact 2931

agattagcat tgccctgcct gtctgaaagg acagtttacc taatggtgcc agcctccttt 2991

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ttaactcagg tactccagtc ttcaccccaa cctcagctga ttgtagtaca cctgctagct 3111

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aaaaaaaaaa 3181

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ggcaggagtc agcccgcttc cgaccgtacc ccgcccgcct cccggggctc ctgttctttg 120

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gccccgggac cctaaccttc tcccggggcg gttccctccg tctgggcgtc cgagcgctgc    180

ccacatcttt cattcctccc tgcacctcct tcccttcact tttgccccgg ctctctttct    240

cctctctgtc ctgctgtcgc ctcctctcct cactccagcc tccttccctg gcttattctg    300

cccaggaaag tttggaaccc ccgccccccc tccccaatca ggtcaacctg actaggagta    360

gggggagatg taggaaggcc tgagagttcg gggggggggga agctggaagc tggtttccca    420

gaaaatttcc ccccatcttc tccatttagg gggggggggaa ttttttttaa tcctgttttt    480

gaggaggtgg taggtgttta gaaaaggatg tgggaatgga aggggtagat gagtcaaccc    540

tctttcaaga ttccaagggt ggtgtgttac ctgatccttt tcgtgtgtgg agttcagggg    600

gtcgggaggt ttggccttta ttcccacatt caaagttgga acctccccca aattaagaat    660

ggagttttag tacccacttg tggcaggaat cctgggggga aggggtcctt ttttcctttt    720

tcttttcttt tttccctttt ttttcctttt ggcaacccac acccttccac acacgctcac    780

cccaaaatta aacaccaaga tcctctaact tgtttggatt gactgatgaa gacataaagc    840

tctatgtttt ttgaggtgga gtgagtggtt tttcttcatt tttaaatggc caaatgacag    900

cttgacccag tttgctttcc aatcaaaggg catttatttt ga   atg tct ctt tgt     954
                                                    Met Ser Leu Cys
                                                      1

ggc gca aga gcc aac gca aaa atg atg gcg gct tac aat ggc ggt aca     1002
Gly Ala Arg Ala Asn Ala Lys Met Met Ala Ala Tyr Asn Gly Gly Thr
  5                  10                  15                  20

tct gca gca gca gca ggt cac cac cac cac cat cac cac cac ctt cca     1050
Ser Ala Ala Ala Ala Gly His His His His His His His His Leu Pro
 21                  26                  31                  36

cac ctc cct cct cct cac ctg cac cac cac cac cac cct caa cac cat     1098
His Leu Pro Pro Pro His Leu His His His His His Pro Gln His His
 37                  42                  47                  52

ctt cat ccg ggg tcg gct gcc gct gta cac cct gta cag cag cac acc     1146
Leu His Pro Gly Ser Ala Ala Ala Val His Pro Val Gln Gln His Thr
 53                  58                  63                  68

tct tcg gca gct gcg gca gcc gca gca gcg gct gca gct gca gcc atg     1194
Ser Ser Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Met
 69                  74                  79                  84

tta aac cct ggg caa caa cag cca tat ttc cca tca ccg gca ccg ggg     1242
Leu Asn Pro Gly Gln Gln Gln Pro Tyr Phe Pro Ser Pro Ala Pro Gly
 85                  90                  95                 100

cag gct cct gga cca gct gca gca gcc cca gct cag gta cag gct gcc     1290
Gln Ala Pro Gly Pro Ala Ala Ala Ala Pro Ala Gln Val Gln Ala Ala
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101                 106                 111                 116

gca gct gct aca gtt aag gcg cac cat cat cag cac tcg cat cat cca     1338
Ala Ala Ala Thr Val Lys Ala His His His Gln His Ser His His Pro
117                 122                 127                 132

cag cag cag ctg gat att gag ccg gat aga cct att gga tat gga gcc     1386
Gln Gln Gln Leu Asp Ile Glu Pro Asp Arg Pro Ile Gly Tyr Gly Ala
133                 138                 143                 148

ttt ggt gtt gtc tgg tca gta aca gat cca aga gat gga aag aga gta     1434
Phe Gly Val Val Trp Ser Val Thr Asp Pro Arg Asp Gly Lys Arg Val
149                 154                 159                 164

gcg ctc aaa aag atg ccc aac gtc ttc cag aat ctg gtc tct tgc aaa     1482
Ala Leu Lys Lys Met Pro Asn Val Phe Gln Asn Leu Val Ser Cys Lys
165                 170                 175                 180

agg gtc ttc cgg gaa ttg aag atg ttg tgt ttt ttt aag cat gat aat     1530
Arg Val Phe Arg Glu Leu Lys Met Leu Cys Phe Phe Lys His Asp Asn
181                 186                 191                 196

gta ctc tct gcc ctt gac ata ctc caa cct cca cac att gac tat ttt     1578
Val Leu Ser Ala Leu Asp Ile Leu Gln Pro Pro His Ile Asp Tyr Phe
197                 202                 207                 212

gaa gaa ata tat gtt gtc aca gaa ttg atg cag agt gac cta cat aaa     1626
Glu Glu Ile Tyr Val Val Thr Glu Leu Met Gln Ser Asp Leu His Lys
213                 218                 223                 228

att atc gtc tct cct caa cca ctc agc tca gat cat gtc aaa gtt ttt     1674
Ile Ile Val Ser Pro Gln Pro Leu Ser Ser Asp His Val Lys Val Phe
229                 234                 239                 244

ctt tat cag att ttg cga ggt ttg aaa tat ctc cat tca gct ggc att     1722
Leu Tyr Gln Ile Leu Arg Gly Leu Lys Tyr Leu His Ser Ala Gly Ile
245                 250                 255                 260

tta cat cga gac att aag cca ggg aat ctc ctt gtg aac agc aac tgt     1770
Leu His Arg Asp Ile Lys Pro Gly Asn Leu Leu Val Asn Ser Asn Cys
261                 266                 271                 276

gtt cta aag att tgt gat ttt gga ttg gcc aga gtg gaa gaa tta gat     1818
Val Leu Lys Ile Cys Asp Phe Gly Leu Ala Arg Val Glu Glu Leu Asp
277                 282                 287                 292

gaa tcc cgt cat atg act cag gaa gtt gtt act cag tat tat cgg gct     1866
Glu Ser Arg His Met Thr Gln Glu Val Val Thr Gln Tyr Tyr Arg Ala
293                 298                 303                 308

cca gaa atc ctg atg ggc agc cgt cat tac agc aat gct att gac atc     1914
Pro Glu Ile Leu Met Gly Ser Arg His Tyr Ser Asn Ala Ile Asp Ile
309                 314                 319                 324

tgg tct gtg gga tgt atc ttt gca gaa cta cta gga cga aga ata ttg     1962
Trp Ser Val Gly Cys Ile Phe Ala Glu Leu Leu Gly Arg Arg Ile Leu
325                 330                 335                 340
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ttt cag gca cag agt ccc att cag cag ttg gat ttg atc acg gat ctg     2010
Phe Gln Ala Gln Ser Pro Ile Gln Gln Leu Asp Leu Ile Thr Asp Leu
341                 346                 351                 356

ttg ggc aca cca tca ctg gaa gca atg agg aca gct tgt gaa ggc gct     2058
Leu Gly Thr Pro Ser Leu Glu Ala Met Arg Thr Ala Cys Glu Gly Ala
357                 362                 367                 372

aag gca cat ata ctc agg ggt cct cat aaa cag cca tct ctt cct gta     2106
Lys Ala His Ile Leu Arg Gly Pro His Lys Gln Pro Ser Leu Pro Val
373                 378                 383                 388

ctc tat acc ctg tct agc cag gct aca cat gaa gct gtt cat ctc ctt     2154
Leu Tyr Thr Leu Ser Ser Gln Ala Thr His Glu Ala Val His Leu Leu
389                 394                 399                 404

tgc agg atg ttg gtc ttt gat cca tcc aaa aga ata tcc gct aag gat     2202
Cys Arg Met Leu Val Phe Asp Pro Ser Lys Arg Ile Ser Ala Lys Asp
405                 410                 415                 420

gcc tta gcc cac ccc tac cta gat gaa ggg cga cta cga tat cac aca     2250
Ala Leu Ala His Pro Tyr Leu Asp Glu Gly Arg Leu Arg Tyr His Thr
421                 426                 431                 436

tgt atg tgt aaa tgt tgc ttt tcc acc tcc act gga aga gtt tat acc     2298
Cys Met Cys Lys Cys Cys Phe Ser Thr Ser Thr Gly Arg Val Tyr Thr
437                 442                 447                 452

agt gac ttt gag cct gtc acc aat ccc aaa ttt gat gac act ttc gag     2346
Ser Asp Phe Glu Pro Val Thr Asn Pro Lys Phe Asp Asp Thr Phe Glu
453                 458                 463                 468

aag aac ctc agt tct gtc cga cag gtt aaa gaa att att cat cag ttc     2394
Lys Asn Leu Ser Ser Val Arg Gln Val Lys Glu Ile Ile His Gln Phe
469                 474                 479                 484

att ttg gaa cag cag aaa gga aac aga gtg cct ctc tgc atc aac cct     2442
Ile Leu Glu Gln Gln Lys Gly Asn Arg Val Pro Leu Cys Ile Asn Pro
485                 490                 495                 500

cag tct gct gct ttt aag agc ttt att agt tcc act gtt gct cag cca     2490
Gln Ser Ala Ala Phe Lys Ser Phe Ile Ser Ser Thr Val Ala Gln Pro
501                 506                 511                 516

tct gag atg ccc cca tct cct ctg gtg tgg gag tga tggt ggaagataat     2540
Ser Glu Met Pro Pro Ser Pro Leu Val Trp Glu  *
517                 522                 527

gtactactga agatgtaatg tagctttcca ctggagtctg ggatttgcaa ttctggaggt   2600

taatcatgct tgtactgtaa ttttactaat gaagttttaa attaacaacc actacttgta   2660

tgatatgaat aatatttaga aatgttacta gacttttaat cttgtaaagt ggttgtgctt   2720

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tggctcacct cagaacaaaa gagaattgaa ccaaatttgg gagtttgggg ttttatgttt 2840

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acacacaaac acaaaggaca gtcatacatt ttgatatttg agccattcct aaagatttgg 2960

ggttttctaa aactaaagaa tctaggaacc ttgcctgcga ccaatcatgg agccacgtga 3020

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gcggagcgcg cagcgcggcc cgagcgcgac gacctgccga gcggcggccg aggcggcggt 180

gtgggcgcgt caggccgcga cgagggcgct gagacaaatt tacatgtatt ggagaccaga 240

ccagaagccc ttctgaatta agatctcaca ttcttgaagg tggcattgaa gagcactaag 300

atcggaag atg agt gag ctt gac cag tta cgg cag gag gcc gag caa ctt 350
Met Ser Glu Leu Asp Gln Leu Arg Gln Glu Ala Glu Gln Leu
1 5 10

aag aac cag att cga gac gcc agg aaa gca tgt gca gat gca act ctc 398
Lys Asn Gln Ile Arg Asp Ala Arg Lys Ala Cys Ala Asp Ala Thr Leu
15 20 25 30

tct cag atc aca aac aac atc gac cca gtg gga aga atc caa atg cgc 446
Ser Gln Ile Thr Asn Asn Ile Asp Pro Val Gly Arg Ile Gln Met Arg
31 36 41 46

acg agg agg aca ctg cgg ggg cac ctg gcc aag atc tac gcc atg cac 494
Thr Arg Arg Thr Leu Arg Gly His Leu Ala Lys Ile Tyr Ala Met His
47 52 57 62

tgg ggc aca gac tcc agg ctt ctc gtc agt gcc tcg cag gat ggt aaa 542
Trp Gly Thr Asp Ser Arg Leu Leu Val Ser Ala Ser Gln Asp Gly Lys
63 68 73 78

ctt atc atc tgg gac agc tac acc acc aac aag gtc cac gcc atc cct 590
Leu Ile Ile Trp Asp Ser Tyr Thr Thr Asn Lys Val His Ala Ile Pro
79 84 89 94

ctg cgc tcc tcc tgg gtc atg acc tgt gca tat gcc cct tct ggg aac 638
Leu Arg Ser Ser Trp Val Met Thr Cys Ala Tyr Ala Pro Ser Gly Asn
95 100 105 110

tat gtg gcc tgc ggt ggc ctg gat aac att tgc tcc att tac aat ctg 686
Tyr Val Ala Cys Gly Gly Leu Asp Asn Ile Cys Ser Ile Tyr Asn Leu
111 116 121 126

aaa act cgt gag ggg aac gtg cgc gtg agt cgt gag ctg gca gga cac 734
Lys Thr Arg Glu Gly Asn Val Arg Val Ser Arg Glu Leu Ala Gly His
127 132 137 142

aca ggt tac ctg tcc tgc tgc cga ttc ctg gat gac aat cag atc gtc 782
Thr Gly Tyr Leu Ser Cys Cys Arg Phe Leu Asp Asp Asn Gln Ile Val
143 148 153 158

acc agc tct gga gac acc acg tgt gcc ctg tgg gac atc gag acc ggc 830

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Thr Ser Ser Gly Asp Thr Thr Cys Ala Leu Trp Asp Ile Glu Thr Gly
159                 164                 169                 174

cag cag acg acc acg ttt acc gga cac act gga gat gtc atg agc ctt      878
Gln Gln Thr Thr Thr Phe Thr Gly His Thr Gly Asp Val Met Ser Leu
175                 180                 185                 190

tct ctt gct cct gac acc aga ctg ttc gtc tct ggt gct tgt gat gct      926
Ser Leu Ala Pro Asp Thr Arg Leu Phe Val Ser Gly Ala Cys Asp Ala
191                 196                 201                 206

tca gcc aaa ctc tgg gat gtg cga gaa ggc atg tgc cgg cag acc ttc      974
Ser Ala Lys Leu Trp Asp Val Arg Glu Gly Met Cys Arg Gln Thr Phe
207                 212                 217                 222

act ggc cac gag tct gac atc aat gcc att tgc ttc ttt cca aat ggc     1022
Thr Gly His Glu Ser Asp Ile Asn Ala Ile Cys Phe Phe Pro Asn Gly
223                 228                 233                 238

aat gca ttt gcc act ggc tca gac gac gcc acc tgc agg ctg ttt gac     1070
Asn Ala Phe Ala Thr Gly Ser Asp Asp Ala Thr Cys Arg Leu Phe Asp
239                 244                 249                 254

ctt cgt gct gac cag gag ctc atg act tac tcc cat gac aac atc atc     1118
Leu Arg Ala Asp Gln Glu Leu Met Thr Tyr Ser His Asp Asn Ile Ile
255                 260                 265                 270

tgc ggg atc acc tct gtc tcc ttc tcc aag agc ggg cgc ctc ctc ctt     1166
Cys Gly Ile Thr Ser Val Ser Phe Ser Lys Ser Gly Arg Leu Leu Leu
271                 276                 281                 286

gct ggg tac gac gac ttc aac tgc aac gtc tgg gat gca ctc aaa gcc     1214
Ala Gly Tyr Asp Asp Phe Asn Cys Asn Val Trp Asp Ala Leu Lys Ala
287                 292                 297                 302

gac cgg gca ggt gtc ttg gct ggg cat gac aac cgc gtc agc tgc ctg     1262
Asp Arg Ala Gly Val Leu Ala Gly His Asp Asn Arg Val Ser Cys Leu
303                 308                 313                 318

ggc gtg act gac gat ggc atg gct gtg gcg aca ggg tcc tgg gat agc     1310
Gly Val Thr Asp Asp Gly Met Ala Val Ala Thr Gly Ser Trp Asp Ser
319                 324                 329                 334

ttc ctc aag atc tgg aac taa cg ccagtagcat gtggatgcca tggagactgg     1363
Phe Leu Lys Ile Trp Asn  *
335                 340

aagaccattc caacttggac gcgttaccat gagagcatat cctatccaac cgtactaacg   1423

tggacaccct acacctcccc tcagaacttc aaaagggcaa gatcttttt ccttcactta   1483

ttgctgaaac caagagcaca attcccattg agagaaagat ctctgtgctg taaactaaaa   1543

caaattgtgc attccttccg gggccatcgt ctttgttttc ttttttgtct tgaatgaatt   1603

ttaaaaggaa atatataata aaaatgttaa ccagaaggta aacttgagtg taattgtcag   1663
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acagacacac ttttccacca gtgtatttga attttagacc agtgaccctg ttttgtggca 1723

ttcatgcaaa acatgctgag ggctttgttc atctggtcat cgtgtccaaa tttcagtcat 1783

gtttgtagca agattttgga agcattcata tttccttttt aaaatgtatt cctttgtgtt 1843

caacagttaa tcaaaaccag agagtctagg gcagcctctc tgatgttgtc aatgatgtaa 1903

attcagtccc tggtttttaa ttttctgtct gatgtcacag atcattgttg cacacaaacg 1963

tggcatagaa aagaacatgt tcagaagcca tggggccaag cacatgcggg gacggtctca 2023

aatgcgtgat cagagaatcc ttcacctttg ctgaaaagtg agctcagatc cagcaccatg 2083

ttcctcctga cccatcctgt ctatcttctc agttgagttt ttaatctcac tttgggtttc 2143

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gcggagcgcg cagcgcggcc cgagcgcgac gacctgccga gcggcggccg aggcggcggt 180

gtgggcgcgt caggccgcga cgagggcgct gagacaaatt tacatgtatt ggagaccaga 240

ccagaagccc ttctgaatta agatctcaca ttcttgaagg tggcattgaa gagcactaag 300

atcggaag atg agt gag ctt gac cag tta cgg cag gag gcc gag caa ctt 350
Met Ser Glu Leu Asp Gln Leu Arg Gln Glu Ala Glu Gln Leu

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          1               5                  10

aag aac cag att cga atc aca aac aac atc gac cca gtg gga aga atc      398
Lys Asn Gln Ile Arg Ile Thr Asn Asn Ile Asp Pro Val Gly Arg Ile
 15                  20                  25                  30

caa atg cgc acg agg agg aca ctg cgg ggg cac ctg gcc aag atc tac      446
Gln Met Arg Thr Arg Arg Thr Leu Arg Gly His Leu Ala Lys Ile Tyr
 31                  36                  41                  46

gcc atg cac tgg ggc aca gac tcc agg ctt ctc gtc agt gcc tcg cag      494
Ala Met His Trp Gly Thr Asp Ser Arg Leu Leu Val Ser Ala Ser Gln
 47                  52                  57                  62

gat ggt aaa ctt atc atc tgg gac agc tac acc acc aac aag gtc cac      542
Asp Gly Lys Leu Ile Ile Trp Asp Ser Tyr Thr Thr Asn Lys Val His
 63                  68                  73                  78

gcc atc cct ctg cgc tcc tcc tgg gtc atg acc tgt gca tat gcc cct      590
Ala Ile Pro Leu Arg Ser Ser Trp Val Met Thr Cys Ala Tyr Ala Pro
 79                  84                  89                  94

tct ggg aac tat gtg gcc tgc ggt ggc ctg gat aac att tgc tcc att      638
Ser Gly Asn Tyr Val Ala Cys Gly Gly Leu Asp Asn Ile Cys Ser Ile
 95                 100                 105                 110

tac aat ctg aaa act cgt gag ggg aac gtg cgc gtg agt cgt gag ctg      686
Tyr Asn Leu Lys Thr Arg Glu Gly Asn Val Arg Val Ser Arg Glu Leu
111                 116                 121                 126

gca gga cac aca ggt tac ctg tcc tgc tgc cga ttc ctg gat gac aat      734
Ala Gly His Thr Gly Tyr Leu Ser Cys Cys Arg Phe Leu Asp Asp Asn
127                 132                 137                 142

cag atc gtc acc agc tct gga gac acc acg tgt gcc ctg tgg gac atc      782
Gln Ile Val Thr Ser Ser Gly Asp Thr Thr Cys Ala Leu Trp Asp Ile
143                 148                 153                 158

gag acc ggc cag cag acg acc acg ttt acc gga cac act gga gat gtc      830
Glu Thr Gly Gln Gln Thr Thr Thr Phe Thr Gly His Thr Gly Asp Val
159                 164                 169                 174

atg agc ctt tct ctt gct cct gac acc aga ctg ttc gtc tct ggt gct      878
Met Ser Leu Ser Leu Ala Pro Asp Thr Arg Leu Phe Val Ser Gly Ala
175                 180                 185                 190

tgt gat gct tca gcc aaa ctc tgg gat gtg cga gaa ggc atg tgc cgg      926
Cys Asp Ala Ser Ala Lys Leu Trp Asp Val Arg Glu Gly Met Cys Arg
191                 196                 201                 206

cag acc ttc act ggc cac gag tct gac atc aat gcc att tgc ttc ttt      974
Gln Thr Phe Thr Gly His Glu Ser Asp Ile Asn Ala Ile Cys Phe Phe
207                 212                 217                 222

cca aat ggc aat gca ttt gcc act ggc tca gac gac gcc acc tgc agg     1022
Pro Asn Gly Asn Ala Phe Ala Thr Gly Ser Asp Asp Ala Thr Cys Arg
223                 228                 233                 238
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ctg ttt gac ctt cgt gct gac cag gag ctc atg act tac tcc cat gac     1070
Leu Phe Asp Leu Arg Ala Asp Gln Glu Leu Met Thr Tyr Ser His Asp
239                 244                 249                 254

aac atc atc tgc ggg atc acc tct gtc tcc ttc tcc aag agc ggg cgc     1118
Asn Ile Ile Cys Gly Ile Thr Ser Val Ser Phe Ser Lys Ser Gly Arg
255                 260                 265                 270

ctc ctc ctt gct ggg tac gac gac ttc aac tgc aac gtc tgg gat gca     1166
Leu Leu Leu Ala Gly Tyr Asp Asp Phe Asn Cys Asn Val Trp Asp Ala
271                 276                 281                 286

ctc aaa gcc gac cgg gca ggt gtc ttg gct ggg cat gac aac cgc gtc     1214
Leu Lys Ala Asp Arg Ala Gly Val Leu Ala Gly His Asp Asn Arg Val
287                 292                 297                 302

agc tgc ctg ggc gtg act gac gat ggc atg gct gtg gcg aca ggg tcc     1262
Ser Cys Leu Gly Val Thr Asp Asp Gly Met Ala Val Ala Thr Gly Ser
303                 308                 313                 318

tgg gat agc ttc ctc aag atc tgg aac taa c gccagtagca tgtggatgcc     1313
Trp Asp Ser Phe Leu Lys Ile Trp Asn  *
319                 324

atggagactg gaagaccatt ccaacttgga cgcgttacca tgagagcata tcctatccaa   1373

ccgtactaac gtggacaccc tacacctccc ctcagaactt caaaagggca agatcttttt   1433

tccttcactt attgctgaaa ccaagagcac aattcccatt gagagaaaga tctctgtgct   1493

gtaaactaaa acaaattgtg cattccttcc ggggccatcg tctttgtttt ctttttgtc    1553

ttgaatgaat tttaaaagga aatatataat aaaaatgtta accagaaggt aaacttgagt   1613

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ctttgggttt ccttgtgaag ttggagggaa gtttataata gcctaacact accccacccc   2153

caactaggag gaacctctgt tttcaagaga gatgcctgtc ctgtgcttgg atagtcagtc   2213

aattatttgt gtatgaaaca atgtacaaat caatgttttg aaaataatga tctcagactt   2273
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05050-7006US

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cttttaagaa ataacctctt acagttgtaa ccattgcggc tctgtccact tctcgttgct   2453

gctctgtggc acatatcgga agcagtacag cgcgcggctc tacacgcttg ggtagcggga   2513

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tcctccacaa actgggattc atccccgctg aaaaagcaca atctaacagc aagggaacaa    120

aaaaacc  atg cta tca cat aat act atg atg aag cag aga aaa cag caa      169
         Met Leu Ser His Asn Thr Met Met Lys Gln Arg Lys Gln Gln
           1               5                  10

gca aca gcc atc atg aag gaa gtc cat gga aat gat gtt gat ggc atg      217
Ala Thr Ala Ile Met Lys Glu Val His Gly Asn Asp Val Asp Gly Met
 15                  20                  25                  30

gac ctg ggc aaa aag gtc agc atc ccc aga gac atc atg ttg gaa gaa      265
Asp Leu Gly Lys Lys Val Ser Ile Pro Arg Asp Ile Met Leu Glu Glu
 31                  36                  41                  46

tta tcc cat ctc agt aac cgt ggt gcc agg cta ttt aag atg cgt caa      313
Leu Ser His Leu Ser Asn Arg Gly Ala Arg Leu Phe Lys Met Arg Gln
 47                  52                  57                  62

aga aga tct gac aaa tac aca ttt gaa aat ttc cag tat caa tct aga      361
Arg Arg Ser Asp Lys Tyr Thr Phe Glu Asn Phe Gln Tyr Gln Ser Arg
 63                  68                  73                  78

gca caa ata aat cac agt att gct atg cag aat ggg aaa gtg gat gga      409
Ala Gln Ile Asn His Ser Ile Ala Met Gln Asn Gly Lys Val Asp Gly
 79                  84                  89                  94

agt aac ttg gaa ggt ggt tcg cag caa gcc ccc ttg act cct ccc aac      457
Ser Asn Leu Glu Gly Gly Ser Gln Gln Ala Pro Leu Thr Pro Pro Asn
 95                 100                 105                 110

acc cca gat cca cga agc cct cca aat cca gac aac att gct cca gga      505
Thr Pro Asp Pro Arg Ser Pro Pro Asn Pro Asp Asn Ile Ala Pro Gly
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111                 116                 121                 126

tat tct gga cca ctg aag gaa att cct cct gaa aaa ttc aac acc aca      553
Tyr Ser Gly Pro Leu Lys Glu Ile Pro Pro Glu Lys Phe Asn Thr Thr
127                 132                 137                 142

gct gtc cct aag tac tat caa tct ccc tgg gaa caa gcc att agc aat      601
Ala Val Pro Lys Tyr Tyr Gln Ser Pro Trp Glu Gln Ala Ile Ser Asn
143                 148                 153                 158

gat ccg gag ctt tta gag gct tta tat cct aaa ctt ttc aag cct gaa      649
Asp Pro Glu Leu Leu Glu Ala Leu Tyr Pro Lys Leu Phe Lys Pro Glu
159                 164                 169                 174

gga aag gca gaa ctg cct gat tac agg agc ttt aac agg gtt gcc aca      697
Gly Lys Ala Glu Leu Pro Asp Tyr Arg Ser Phe Asn Arg Val Ala Thr
175                 180                 185                 190

cca ttt gga ggt ttt gaa aaa gca tca aga atg gtt aaa ttt aaa gtt      745
Pro Phe Gly Gly Phe Glu Lys Ala Ser Arg Met Val Lys Phe Lys Val
191                 196                 201                 206

cca gat ttt gag cta cta ttg cta aca gat ccc agg ttt atg tcc ttt      793
Pro Asp Phe Glu Leu Leu Leu Leu Thr Asp Pro Arg Phe Met Ser Phe
207                 212                 217                 222

gtc aat ccc ctt tct ggc aga cgg tcc ttt aat agg act cct aag gga      841
Val Asn Pro Leu Ser Gly Arg Arg Ser Phe Asn Arg Thr Pro Lys Gly
223                 228                 233                 238

tgg ata tct gag aat att cct ata gtg ata aca acc gaa cct aca gat      889
Trp Ile Ser Glu Asn Ile Pro Ile Val Ile Thr Thr Glu Pro Thr Asp
239                 244                 249                 254

gat acc act gta cca gaa tca gaa gac cta tga aaagaaag ttgtatgtgc      940
Asp Thr Thr Val Pro Glu Ser Glu Asp Leu  *
255                 260                 265

cacataaaac tctgaatata aaagttgctg ttctactatt ttaactactg gcaaagccac   1000

ttgcattttt cattagtagc aacaatagca atttagtgat tttccttttc tgacattcaa   1060

tttcaatctc agatcaaata ctaataaaca attagaaatc ttactttaaa aaaaaaaaa    1119
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             Met Asp Lys Leu Phe Thr Phe His Leu Phe Thr Phe His
               1               5                  10

gga ttg tta cac ttc ctc gat ggg agc att caa aaa cta ata caa gct      158
Gly Leu Leu His Phe Leu Asp Gly Ser Ile Gln Lys Leu Ile Gln Ala
 14                  19                  24                  29

gag att ata ctg tct gac aat tca agt att tta gtt tta gaa aac aat      206
Glu Ile Ile Leu Ser Asp Asn Ser Ser Ile Leu Val Leu Glu Asn Asn
 30                  35                  40                  45

ttc cta ttt aaa gta aaa agc aaa gaa ttt atc cat ctg att gct aag      254
Phe Leu Phe Lys Val Lys Ser Lys Glu Phe Ile His Leu Ile Ala Lys
 46                  51                  56                  61

aag ttt tac atc tcc att aca att gtg tct gca tca aac gga gag tcc      302
Lys Phe Tyr Ile Ser Ile Thr Ile Val Ser Ala Ser Asn Gly Glu Ser
 62                  67                  72                  77

ttc gtc ctc agt atg att gtt act ggc tga g aacatacggt gacctgtgtt      353
Phe Val Leu Ser Met Ile Val Thr Gly  *
 78                  83

ctgagtgcct gattggaaaa gacctccctg tcatctgcca tactacggga caaatcagta    413

tctactcaaa ttcccacttc cagaatgaga ggactcatca ggggtttagg agtttggcaa    473

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tccggaattc ccgggtcgac ccacgcgtcc gaggcgccgg agcccagcgg ctggcgccag      60

atccaggctc ctggaagaac catgtccggc agctactggt catgccaggc acacactgct     120

gcccaagagg agctgctgtt tgaattatct gtgaatgttg ggaagaggaa tgccagagct     180

gccggctgaa aattacccaa ccaagagaaa tgtaggctgg gtaccctgaa tcacccccctg    240

cagg atg gac ttt ctg gtc ctc ttc ttg ttc tac ctg gct tcg gtg ctg      289
     Met Asp Phe Leu Val Leu Phe Leu Phe Tyr Leu Ala Ser Val Leu
```

```
       1               5                  10

atg ggt ctt gtt ctt atc tgc gtc tgc tcg aaa acc cat agc ttg aaa      337
Met Gly Leu Val Leu Ile Cys Val Cys Ser Lys Thr His Ser Leu Lys
 16                  21                  26                  31

ggc ctg gcc agg gga gga gca cag ata ttt tcc tgt ata att cca gaa      385
Gly Leu Ala Arg Gly Gly Ala Gln Ile Phe Ser Cys Ile Ile Pro Glu
 32                  37                  42                  47

tgt ctt cag aga gcc atg cat gga ttg ctt cat tac ctt ttc cat acg      433
Cys Leu Gln Arg Ala Met His Gly Leu Leu His Tyr Leu Phe His Thr
 48                  53                  58                  63

aga aac cac acc ttc att gtc ctg cac ctg gtc ttg caa ggg atg gtt      481
Arg Asn His Thr Phe Ile Val Leu His Leu Val Leu Gln Gly Met Val
 64                  69                  74                  79

tat act gag tac acc tgg gaa gta ttt ggc tac tgt cag gag ctg gag      529
Tyr Thr Glu Tyr Thr Trp Glu Val Phe Gly Tyr Cys Gln Glu Leu Glu
 80                  85                  90                  95

ttg tcc ttg cat tac ctt ctt ctg ccc tat ctg ctg cta ggt gta aac      577
Leu Ser Leu His Tyr Leu Leu Leu Pro Tyr Leu Leu Leu Gly Val Asn
 96                 101                 106                 111

ctg ttt ttt ttc acc ctg act tgt gga acc aat cct ggc att ata aca      625
Leu Phe Phe Phe Thr Leu Thr Cys Gly Thr Asn Pro Gly Ile Ile Thr
112                 117                 122                 127

aaa gca aat gaa tta tta ttt ctt cat gtt tat gaa ttt gat gaa gtg      673
Lys Ala Asn Glu Leu Leu Phe Leu His Val Tyr Glu Phe Asp Glu Val
128                 133                 138                 143

atg ttt cca aag aac gtg agg tgc tct act tgt gat tta agg aaa cca      721
Met Phe Pro Lys Asn Val Arg Cys Ser Thr Cys Asp Leu Arg Lys Pro
144                 149                 154                 159

gct cga tcc aag cac tgc agt gtg tgt aac tgg tgt gtg cac cgt ttc      769
Ala Arg Ser Lys His Cys Ser Val Cys Asn Trp Cys Val His Arg Phe
160                 165                 170                 175

gac cat cac tgt gtt tgg gtg aac aac tgc atc ggg gcc tgg aac atc      817
Asp His His Cys Val Trp Val Asn Asn Cys Ile Gly Ala Trp Asn Ile
176                 181                 186                 191

agg tac ttc ctc atc tac gtc ttg acc ttg acg gcc tcg gct gcc acc      865
Arg Tyr Phe Leu Ile Tyr Val Leu Thr Leu Thr Ala Ser Ala Ala Thr
192                 197                 202                 207

gtc gcc att gtg agc acc act ttt ctg gtc cac ttg gtg gtg atg tca      913
Val Ala Ile Val Ser Thr Thr Phe Leu Val His Leu Val Val Met Ser
208                 213                 218                 223

gat tta tac cag gag act tac atc gat gac ctt gga cac ctc cat gtt      961
Asp Leu Tyr Gln Glu Thr Tyr Ile Asp Asp Leu Gly His Leu His Val
224                 229                 234                 239
```

```
atg gac acg gtc ttt ctt att cag tac ctg ttc ctg act ttt cca cgg     1009
Met Asp Thr Val Phe Leu Ile Gln Tyr Leu Phe Leu Thr Phe Pro Arg
240                 245                 250                 255

att gtc ttc atg ctg ggc ttt gtc gtg gtt ctg agc ttc ctc ctg ggt     1057
Ile Val Phe Met Leu Gly Phe Val Val Val Leu Ser Phe Leu Leu Gly
256                 261                 266                 271

ggc tac ctg ttt gtc ctg tat ctg gcg gcc acc aac cag act act aac     1105
Gly Tyr Leu Phe Val Leu Tyr Leu Ala Ala Thr Asn Gln Thr Thr Asn
272                 277                 282                 287

gag tgg tac aga ggt gac tgg gcc tgg tgc cag cgt tgt ccc ctt gtg     1153
Glu Trp Tyr Arg Gly Asp Trp Ala Trp Cys Gln Arg Cys Pro Leu Val
288                 293                 298                 303

gcc tgg cct ccg tca gca gag ccc caa gtc cac cgg aac att cac tcc     1201
Ala Trp Pro Pro Ser Ala Glu Pro Gln Val His Arg Asn Ile His Ser
304                 309                 314                 319

cat ggg ctt cgg agc aac ctt caa gag atc ttt cta cct gcc ttt cca     1249
His Gly Leu Arg Ser Asn Leu Gln Glu Ile Phe Leu Pro Ala Phe Pro
320                 325                 330                 335

tgt cat gag agg aag aaa caa gaa tga caagt gtatgactgc ctttgagctg     1301
Cys His Glu Arg Lys Lys Gln Glu  *
336                 341

tagttcccgt ttatttacac atgtggatcc tcgttttcc                         1340
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US 2006/0063160 A1

<210> 289
<211> 1009
<212> DNA
<213> Homo sapiens

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<222> (117)..(893)

<400> 289

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gggacgtgga gacccggggt cccggcagcc gggcggcccg cgggcccagg gtgggg   116

atg cac cgc cgc ggg gtg gga gct ggc gcc atc gcc aag aag aaa ctt      164
Met His Arg Arg Gly Val Gly Ala Gly Ala Ile Ala Lys Lys Lys Leu
  1               5                  10                  15

gca gag gcc aag tat aag gag cga ggg acg gtc ttg gct gag gac cag      212
Ala Glu Ala Lys Tyr Lys Glu Arg Gly Thr Val Leu Ala Glu Asp Gln
 17                  22                  27                  32

cta gcc cag atg tca aag cag ttg gac atg ttc aag acc aac ctg gag      260
```

```
Leu Ala Gln Met Ser Lys Gln Leu Asp Met Phe Lys Thr Asn Leu Glu
 33                  38                  43                  48

gaa ttt gcc agc aaa cac aag cag gag atc cgg aag aat cct gag ttc      308
Glu Phe Ala Ser Lys His Lys Gln Glu Ile Arg Lys Asn Pro Glu Phe
 49                  54                  59                  64

cgt gtg cag ttc cag gac atg tgt gca acc att ggc gtg gat ccg ctg      356
Arg Val Gln Phe Gln Asp Met Cys Ala Thr Ile Gly Val Asp Pro Leu
 65                  70                  75                  80

gcc tct gga aaa gga ttt tgg tct gag atg ctg ggc gtg ggg gac ttc      404
Ala Ser Gly Lys Gly Phe Trp Ser Glu Met Leu Gly Val Gly Asp Phe
 81                  86                  91                  96

tat tac gaa cta ggt gtc caa att atc gaa gtg tgc ctg gcg ctg aag      452
Tyr Tyr Glu Leu Gly Val Gln Ile Ile Glu Val Cys Leu Ala Leu Lys
 97                 102                 107                 112

cat cgg aat gga ggt ctg ata act ttg gag gaa cta cat caa cag gtg      500
His Arg Asn Gly Gly Leu Ile Thr Leu Glu Glu Leu His Gln Gln Val
113                 118                 123                 128

ttg aag gga agg ggc aag ttc gcc cag gat gtc agt caa gat gac ctg      548
Leu Lys Gly Arg Gly Lys Phe Ala Gln Asp Val Ser Gln Asp Asp Leu
129                 134                 139                 144

atc aga gcc atc aag aaa cta aag gca ctt ggc act ggc ttc ggc atc      596
Ile Arg Ala Ile Lys Lys Leu Lys Ala Leu Gly Thr Gly Phe Gly Ile
145                 150                 155                 160

atc cct gtg ggc ggc act tac ctc att cag tct gtt cca gct gag ctc      644
Ile Pro Val Gly Gly Thr Tyr Leu Ile Gln Ser Val Pro Ala Glu Leu
161                 166                 171                 176

aat atg gat cac acc gtg gtg ctg cag ctg gca gag aag aat ggc tac      692
Asn Met Asp His Thr Val Val Leu Gln Leu Ala Glu Lys Asn Gly Tyr
177                 182                 187                 192

gtg act gtc agt gag atc aaa gcc agt ctt aaa tgg gag acc gag cga      740
Val Thr Val Ser Glu Ile Lys Ala Ser Leu Lys Trp Glu Thr Glu Arg
193                 198                 203                 208

gcg cgg caa gtg ctg gaa cac ctg ctg aag gaa ggg ttg gcg tgg ctg      788
Ala Arg Gln Val Leu Glu His Leu Leu Lys Glu Gly Leu Ala Trp Leu
209                 214                 219                 224

gac tta cag gcc cca ggg gag gcc cac tac tgg ctg cca gct ctc ttc      836
Asp Leu Gln Ala Pro Gly Glu Ala His Tyr Trp Leu Pro Ala Leu Phe
225                 230                 235                 240

act gac ctc tac tcc cag gag att aca gct gag gag gcc aga gaa gcc      884
Thr Asp Leu Tyr Ser Gln Glu Ile Thr Ala Glu Glu Ala Arg Glu Ala
241                 246                 251                 256

ctc ccc tga ctgcatg tggaagggca cacagcagca ggcagggagg aggcggaggt      940
Leu Pro  *
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257

ggcaaataaa cctgggcaat tttgtttata caaaaaatag aaaaaaagtt ccaagttaaa 1000

aaaaaaaaa 1009

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<213> Homo sapiens

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tcagcgtctg agccaggcca acaatgacca aggagg atg gga tcc tgg gtg cag 114
Met Gly Ser Trp Val Gln
1

ctc atc aca agc gtc ggg gtg cag caa aac cat cca ggc tgg aca gtg 162
Leu Ile Thr Ser Val Gly Val Gln Gln Asn His Pro Gly Trp Thr Val
7 12 17 22

gct gga cag ttc caa gaa aag aaa cgc ttc act gaa gaa gtc att gaa 210
Ala Gly Gln Phe Gln Glu Lys Lys Arg Phe Thr Glu Glu Val Ile Glu
23 28 33 38

tac ttc cag aag aaa gtt agc cca gtg cat ctg aaa atc ctg ctg act 258
Tyr Phe Gln Lys Lys Val Ser Pro Val His Leu Lys Ile Leu Leu Thr
39 44 49 54

agc gat gaa gcc tgg aag aga ttt gtg cgt gtg gct gaa ttg ccc agg 306
Ser Asp Glu Ala Trp Lys Arg Phe Val Arg Val Ala Glu Leu Pro Arg
55 60 65 70

gaa gag gca gat gct ctc tat gaa gct ctg aag aat ctt aca cca tat 354
Glu Glu Ala Asp Ala Leu Tyr Glu Ala Leu Lys Asn Leu Thr Pro Tyr
71 76 81 86

gtg act att gag gac aaa gac atg cag caa aaa gaa cag cag ttt agg 402
Val Thr Ile Glu Asp Lys Asp Met Gln Gln Lys Glu Gln Gln Phe Arg
87 92 97 102

gag tgg ttt ttg aaa gag ttt cct caa atc aga tgg aag att cag gag 450
Glu Trp Phe Leu Lys Glu Phe Pro Gln Ile Arg Trp Lys Ile Gln Glu
103 108 113 118

tcc ata gaa agg ctt cgt gtc att gca aat gag att gaa aag gtc cac 498
Ser Ile Glu Arg Leu Arg Val Ile Ala Asn Glu Ile Glu Lys Val His
119 124 129 134

```
aga ggc tgc gtc atc gcc aat gtg gtg tct ggc tcc act ggc atc ctg      546
Arg Gly Cys Val Ile Ala Asn Val Val Ser Gly Ser Thr Gly Ile Leu
135                 140                 145                 150

tct gtc att ggc gtt atg ttg gca cca ttt aca gca ggg ctg agc ctg      594
Ser Val Ile Gly Val Met Leu Ala Pro Phe Thr Ala Gly Leu Ser Leu
151                 156                 161                 166

agc att act gca gct ggg gta ggg ctg gga ata gca tct gcc acg gct      642
Ser Ile Thr Ala Ala Gly Val Gly Leu Gly Ile Ala Ser Ala Thr Ala
167                 172                 177                 182

ggg atc gcc tcc agc atc gtg gag aac aca tac aca agg tca gca gaa      690
Gly Ile Ala Ser Ser Ile Val Glu Asn Thr Tyr Thr Arg Ser Ala Glu
183                 188                 193                 198

ctc aca gcc agc agg ctg act gca acc agc act gac caa ttg gag gca      738
Leu Thr Ala Ser Arg Leu Thr Ala Thr Ser Thr Asp Gln Leu Glu Ala
199                 204                 209                 214

tta agg gac att ctg cat gac atc aca ccc aat gtg ctt tcc ttt gca      786
Leu Arg Asp Ile Leu His Asp Ile Thr Pro Asn Val Leu Ser Phe Ala
215                 220                 225                 230

ctt gat ttt gac gaa gcc aca aaa atg att gcg aat gat gtc cat aca      834
Leu Asp Phe Asp Glu Ala Thr Lys Met Ile Ala Asn Asp Val His Thr
231                 236                 241                 246

ctc agg aga tct aaa gcc act gtt gga cgc cct ttg att gct tgg cga      882
Leu Arg Arg Ser Lys Ala Thr Val Gly Arg Pro Leu Ile Ala Trp Arg
247                 252                 257                 262

tat gta cct ata aat gtt gtt gag aca ctg aga aca cgt ggg gcc ccc      930
Tyr Val Pro Ile Asn Val Val Glu Thr Leu Arg Thr Arg Gly Ala Pro
263                 268                 273                 278

acc cgg ata gtg aga aaa gta gcc cgg aac ctg ggc aag gcc act tca      978
Thr Arg Ile Val Arg Lys Val Ala Arg Asn Leu Gly Lys Ala Thr Ser
279                 284                 289                 294

ggt gtc ctt gtt gtg ctg gat gta gtc aac ctt gtg caa gac tca ctg     1026
Gly Val Leu Val Val Leu Asp Val Val Asn Leu Val Gln Asp Ser Leu
295                 300                 305                 310

gac ttg cac aag ggg gca aaa tcc gag tct gct gag tcg ctg agg cag     1074
Asp Leu His Lys Gly Ala Lys Ser Glu Ser Ala Glu Ser Leu Arg Gln
311                 316                 321                 326

tgg gct cag gag ctg gag gag aat ctc aat gag ctc acc cat atc cat     1122
Trp Ala Gln Glu Leu Glu Glu Asn Leu Asn Glu Leu Thr His Ile His
327                 332                 337                 342

cag agt cta aaa gca ggc tag gc ccaattgttg cgggaagtca gggaccccaa     1175
Gln Ser Leu Lys Ala Gly  *
343                 348

acggagggac tggctgaagc catggcagaa gaacgtggat tgtgaagatt tcatggacat   1235
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ttattagttc cccaaattaa tacttttata atttcctatg cctgtcttta ccgcaatctc 1295

taaacacaaa ttgtgaagat ttcatggaca cttatcactt ccccaatcaa tacccttgtg 1355

atttcttatg cctgtcttta ctttaatctc ctaatcctgt cagctgagga ggatgtatgt 1415

cacctcagga ccatgtgata attgcgttaa ctgcacaaat tgtagagcat gtgtgtttga 1475

acaatatgaa atctgggcac cttgaaaaaa gaacaggata acagcaattg ttcagggaat 1535

aagagagata accttaaact ctgaccaaca gtgagccggg tggaacagag tcatatttct 1595

cttctttcaa aagcaaatgg gagaaatatc gctgaattct ttttctcagc aaggaacatc 1655

cctgagaaag agaatgcacc cctgagggtg ggtctataaa tggcctcctt gggtgtggcc 1715

atcttctatg gtcgagactg tagggatgaa ataaacccca gtctcccata gtgctcccag 1775

gcttattagg aagaggaaat tcccgcctaa taaattttgg tcagaccggt tgctctcaaa 1835

accctgtctc ctgataagat gttatcaatg acaatggtgc ctgaaacctc attagcaatt 1895

ttaatttctc cccggtcctg tggtcctgtg atctcaccct gcctccactt gccttgtgat 1955

attctattac cttgtgaagt aggtgatctt tgtgacccac accctattca tacactccct 2015

ccccttttga aagtccctaa taaaaacttg ctggttttgc agcttgtgag gcatcacgga 2075

acctactgat gtgtgatgtc tcccctggac acctagcttt aaaatttcaa aaa 2128

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<211> 716
<212> DNA
<213> Homo sapiens

<220>
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<222> (41)..(586)

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ctgcagaatt cggcacgagc tctgagggtc cccaaggaac atg gct ggg agc cgt 55
Met Ala Gly Ser Arg
1

gag gtg gtg gcc atg gac tgc gag atg gtg ggg ctg ggg ccc cac cgg 103
Glu Val Val Ala Met Asp Cys Glu Met Val Gly Leu Gly Pro His Arg
6 11 16 21

gag agt ggc ctg gct cgt tgc agc ctc gtg aac gtc cac ggt gct gtg 151
Glu Ser Gly Leu Ala Arg Cys Ser Leu Val Asn Val His Gly Ala Val
22 27 32 37

ctg tac gac aag ttc atc cgg cct gag gga gag atc acc gat tac aga 199

```
Leu Tyr Asp Lys Phe Ile Arg Pro Glu Gly Glu Ile Thr Asp Tyr Arg
 38                  43                  48                  53

acc cgg gtc agc ggg gtc acc cct cag cac atg gtg ggg gcc aca cca      247
Thr Arg Val Ser Gly Val Thr Pro Gln His Met Val Gly Ala Thr Pro
 54                  59                  64                  69

ttt gcc gtg gcc agg cta gag atc ctg cag ctc ctg aaa ggc aag ctg      295
Phe Ala Val Ala Arg Leu Glu Ile Leu Gln Leu Leu Lys Gly Lys Leu
 70                  75                  80                  85

gtg gtg ggt cat gac ctg aag cac gac ttc cag gca ctg aaa gag gac      343
Val Val Gly His Asp Leu Lys His Asp Phe Gln Ala Leu Lys Glu Asp
 86                  91                  96                 101

atg agc ggc tac aca atc tac gac acg tcc act gac agg ctg ttg tgg      391
Met Ser Gly Tyr Thr Ile Tyr Asp Thr Ser Thr Asp Arg Leu Leu Trp
102                 107                 112                 117

cgt gag gcc aag ctg gac cac tgc agg cgt gtc tcc ctg cgg gtg ctg      439
Arg Glu Ala Lys Leu Asp His Cys Arg Arg Val Ser Leu Arg Val Leu
118                 123                 128                 133

agt gag cgc ctc ctg cac aag agc atc cag aac agc ctg ctt gga cac      487
Ser Glu Arg Leu Leu His Lys Ser Ile Gln Asn Ser Leu Leu Gly His
134                 139                 144                 149

agc tcg gtg gaa gat gcg agg gca acg atg gag ctc tat caa atc tcc      535
Ser Ser Val Glu Asp Ala Arg Ala Thr Met Glu Leu Tyr Gln Ile Ser
150                 155                 160                 165

cag aga atc cga gcc cgc cga ggg ctg ccc cgc ctg gct gtg tca gac      583
Gln Arg Ile Arg Ala Arg Arg Gly Leu Pro Arg Leu Ala Val Ser Asp
166                 171                 176                 181

tga agcc ccatccagcc cgttccgcag ggactagagg ctttcggctt tttgggacag      640
 *
182

caactacctt gcttttggaa aatacatttt taatagtaaa gtggctctat attttctcta    700

cgccaaaaaa aaaaaa                                                   716
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<210> 292
<211> 4322
<212> DNA
<213> Homo sapiens

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<222> (617)..(997)

<220>
<221> misc_feature

09/15/2006 17:06:30

<222> (1)...(4322)
<223> n = a,t,c or g

<400> 292

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ttttttagac aacggcgcga ctggcagcct ttctctatca agggtcagac ggtaaacgtt     120

ttcagctttg cagaccagag gccctgtggc tacagtagcg cagacacagc cacaggcatg     180

tcattgaatg gctgcggcta tgttccaata aaaacttatt tacaataaca ggtggtggcc     240

aaattggccc atgggcctta tttggtgaac cctgttctat gagatcacct aggcttcagc     300

cttaaacagt ggaagccatc ccctgaatga caagtcacaa gggtatcaaa gaaagacccc     360

tgaattttca tggaaaaagc tattcagacc cctgcttgga aagctaaggc acactgccac     420

gaagcagcaa ggacgcctta caagtttcag tgcaacagag atggacacct gggctgggct     480

ggacaatgtt taaggttcct tttagtccat gactcaagtg atactgtttt aggctatcag     540

gtagtaaaca cgatcttaga catccccatc tttgtaagca gaacagtacg gcacttcacc     600

acatctgctt cccacc    atg ctt cta agc agc tgt ctt ccc cct gct aat      649
                     Met Leu Leu Ser Ser Cys Leu Pro Pro Ala Asn
                       1               5

gtt aca acc aaa gca gcc acc cca cct cct ctc gtg ttg agc ctc acg      697
Val Thr Thr Lys Ala Ala Thr Pro Pro Pro Leu Val Leu Ser Leu Thr
 12                  17                  22                  27

acc gct gac cca gct gga aag cca gcg ccc tgc cgc gtc acc ctg act      745
Thr Ala Asp Pro Ala Gly Lys Pro Ala Pro Cys Arg Val Thr Leu Thr
 28                  33                  38                  43

ctg ctc aga gcc agc att cca gcc aca aag agg gcc tcc ttc ctt tcc      793
Leu Leu Arg Ala Ser Ile Pro Ala Thr Lys Arg Ala Ser Phe Leu Ser
 44                  49                  54                  59

tct ttc ata aaa atg ttt ttt gaa gag tta gag tat att tta ggc ttt      841
Ser Phe Ile Lys Met Phe Phe Glu Glu Leu Glu Tyr Ile Leu Gly Phe
 60                  65                  70                  75

tta tct tta tta aaa ttt cat gtg cat gtg tct gtg tat tct gca att      889
Leu Ser Leu Leu Lys Phe His Val His Val Ser Val Tyr Ser Ala Ile
 76                  81                  86                  91

tgt cat ttt cag aaa gaa gga aca ggc aat tcg aga agt ttc acc tgt      937
Cys His Phe Gln Lys Glu Gly Thr Gly Asn Ser Arg Ser Phe Thr Cys
 92                  97                 102                 107

act ccc gag ctg ttc ccc agg ctc cag acc cac ttg aga gca gaa ggt      985
Thr Pro Glu Leu Phe Pro Arg Leu Gln Thr His Leu Arg Ala Glu Gly
108                 113                 118                 123

gga gct caa tga agg gtctcgagct cagcgaaggg tcactgggtg aactgagaga     1040
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Gly Ala Gln *
124

aaccacgttc acaaacgcgt actgcggact tcctgccgcc ctgggacctg tcactgtttg 1100

tccatgtaag ctacagcatt actagcagat gctaagatcg agtgatatca ctggaaaagt 1160

aggtgaatcc tactaggaaa ctttctactc cctactagga cctcaagccc ctcagccaca 1220

cagcaaatgc taatatgctc cagtgttagc ttagaagcct tgtgtcaaca agaactggct 1280

cctgagtccc aagcttggtg ccacacagca aatgctaata tgctccagtg ttagcttaga 1340

agccttgtgt caacaagaac tggctcctga gtcccaagct tggtgccaca cagcaaatgc 1400

taatatgctc cagtgttagc ttagaagcct tgtgtcaaca agaactggct cctgagtccc 1460

aagtgctgtc acaggacttg cccattggga tgttttccac attaaatatc aagtaaaaag 1520

acttcctggt gctcaggaat tacagttcgt tcttgaaaca ttccaaagag gccaccacag 1580

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acccaaggaa attagtaata atagaatcag aaaactgtca ggagcataaa gatttctgta 1700

tcaaaatgaa agaagcaatc ctgagttgct gaattaccca tctgctaatg aaaccgggat 1760

ggactgatca tctaacaaag tgcagactga ggattctact tagtcctccg actgggtaca 1820

acaacagcct aggttctagg gagggtggca gtgaccggga tgccacaatg gaagagaaaa 1880

tgaaaacact ggcacagtga aatgtctcat ttccaaacag ttttgcctat ggccaagcaa 1940

ggcaataaag acaaactctc ccttttcccc attgcgtgtg ggctgccagg tacaagtaag 2000

ggaatctttg ctgtgcccac tgtcctccag tagagaaccc aacaggcaag ggccccactc 2060

aggtatcagc tcacctcctg cacctcccct tagcaggaac tccttccact ggcaaaggac 2120

tgccactgcc atctgactca actgtggcga tgtggacgga gtcaccgagc tgcttttctt 2180

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caaaagcacc tagatttcag tgctgaatcc ccacaattgc atgcagctca cacctaccag 2300

gggtattcca gtgcataggg gaaaggaacc cggctgaaaa accagctcct tatttttctt 2360

ttaaataaaa taatacgatc ctaagtccat ttaccatctg aagttgtcac gagtgaacag 2420

tcacattact gttgtggacc aggccttaga tgagtttctc aggctcagca ctgacattct 2480

gggccggatc atcctctctt gtgggaccat cctgtgcact gcaggatgtt tcacagcacc 2540

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gaatgctacc aaggagactt gaattttggt cccatcatca aaaatgcctt ctgcatcaat 2660

cctatgccag tttcccctaa aagagggcta actggaatgt tctaggatgt accaatcctc 2720

caggaccctc ttagagctca tgccatcaga gacaggcctc tatctcaggg atcaccccgg 2780

ctgacatcaa attcctcttc tcttttccca acatttcaaa ttgttcttcg gactcattga 2840

gttccctaag gtgacaagcc ccccccccccc cccccaaaac caccttgggg ggtcacggat 2900

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Thr Ser Glu Leu Ser Cys Glu Val Ser Glu Glu Asn Cys Glu Arg Arg
  3                   8                  13                  18

gag gcc ttc tgg gca gaa tgg aag gat ctg aca ctg tcc aca cgg ccc      152
Glu Ala Phe Trp Ala Glu Trp Lys Asp Leu Thr Leu Ser Thr Arg Pro
 19                  24                  29                  34

gag gag ggc tgc tcc ctg cat gag gag gac acc cag aga cat gag acc      200
Glu Glu Gly Cys Ser Leu His Glu Glu Asp Thr Gln Arg His Glu Thr
 35                  40                  45                  50

tac cac cag cag ggg cag tgc cag gtg ctg gtg cag cgc tcg ccc tgg      248
Tyr His Gln Gln Gly Gln Cys Gln Val Leu Val Gln Arg Ser Pro Trp
 51                  56                  61                  66

ctg atg atg cgg atg ggc atc ctc ggc cgt ggg ctg cag gag tac cag      296
Leu Met Met Arg Met Gly Ile Leu Gly Arg Gly Leu Gln Glu Tyr Gln
 67                  72                  77                  82

ctg ccc tac cag cgg gta ctg ccg ctg ccc atc ttc acc cct gcc aag      344
Leu Pro Tyr Gln Arg Val Leu Pro Leu Pro Ile Phe Thr Pro Ala Lys
 83                  88                  93                  98

atg ggc gcc acc aag gag gag cgg ggg gtc ccc agc acc ctc tgt tag      392
Met Gly Ala Thr Lys Glu Glu Arg Gly Val Pro Ser Thr Leu Cys  *
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gattggtccc tgact atg gct ccc cag agc ctg cct tca tct agg atg gct 171
Met Ala Pro Gln Ser Leu Pro Ser Ser Arg Met Ala
1 5 10

cct ctg ggc atg ctg ctt ggg ctg ctg atg gcc gcc tgc ttc acc ttc 219
Pro Leu Gly Met Leu Leu Gly Leu Leu Met Ala Ala Cys Phe Thr Phe
13 18 23 28

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Cys Leu Ser His Gln Asn Leu Lys Glu Phe Ala Leu Thr Asn Pro Glu
29 34 39 44

aag agc agc acc aaa gaa acg gag aga aaa gaa acc aaa gcc gag gag 315
Lys Ser Ser Thr Lys Glu Thr Glu Arg Lys Glu Thr Lys Ala Glu Glu
45 50 55 60

gag ctg gat gcc gaa gtc ctg gag gtg ttc cac ccg acg cat gag tgg 363
Glu Leu Asp Ala Glu Val Leu Glu Val Phe His Pro Thr His Glu Trp
61 66 71 76

cag gcc ctt cag cca ggg cag gct gtc cct gca gga tcc cac gta cgg 411
Gln Ala Leu Gln Pro Gly Gln Ala Val Pro Ala Gly Ser His Val Arg
77 82 87 92

ctg aat ctt cag act ggg gaa aga gag gca aaa ctc caa tat gag gac 459
Leu Asn Leu Gln Thr Gly Glu Arg Glu Ala Lys Leu Gln Tyr Glu Asp
93 98 103 108

aag ttc cga aat aat ttg aaa ggc aaa agg ctg gat atc aac acc aac 507
Lys Phe Arg Asn Asn Leu Lys Gly Lys Arg Leu Asp Ile Asn Thr Asn
109 114 119 124

acc tac aca tct cag gat ctc aag agt gca ctg gca aaa ttc aag gag 555
Thr Tyr Thr Ser Gln Asp Leu Lys Ser Ala Leu Ala Lys Phe Lys Glu
125 130 135 140

ggg gca gag atg gag agt tca aag gaa gac aag gca agg cag gct gag 603
Gly Ala Glu Met Glu Ser Ser Lys Glu Asp Lys Ala Arg Gln Ala Glu
141 146 151 156

gta aag cgg ctc ttc cgc ccc att gag gaa ctg aag aaa gac ttt gat 651
Val Lys Arg Leu Phe Arg Pro Ile Glu Glu Leu Lys Lys Asp Phe Asp
157 162 167 172

gag ctg aat gtt gtc att gag act gac atg cag atc atg gta cgg ctg 699
Glu Leu Asn Val Val Ile Glu Thr Asp Met Gln Ile Met Val Arg Leu
173 178 183 188

atc aac aag ttc aat agt tcc agc tcc agt ttg gaa gag aag att gct 747
Ile Asn Lys Phe Asn Ser Ser Ser Ser Ser Leu Glu Glu Lys Ile Ala
189 194 199 204

Docket No.: 0609.2110-000

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gcg ctc ttt gat ctt gaa tat tat gtc cat cag atg gac aat gcg cag      795
Ala Leu Phe Asp Leu Glu Tyr Tyr Val His Gln Met Asp Asn Ala Gln
205                 210                 215                 220

gac ctg ctt tcc ttt ggt ggt ctt caa gtg gtg atc aat ggg ctg aac      843
Asp Leu Leu Ser Phe Gly Gly Leu Gln Val Val Ile Asn Gly Leu Asn
221                 226                 231                 236

agc aca gag ccc ctc gtg aag gag tat gct gcg ttt gtg ctg ggc gct      891
Ser Thr Glu Pro Leu Val Lys Glu Tyr Ala Ala Phe Val Leu Gly Ala
237                 242                 247                 252

gcc ttt tcc agc aac ccc aag gtc cag gtg gag gcc atc gaa ggg gga      939
Ala Phe Ser Ser Asn Pro Lys Val Gln Val Glu Ala Ile Glu Gly Gly
253                 258                 263                 268

gcc ctg cag aag ctg ctg gtc atc ctg gcc acg gag cag ccg ctc act      987
Ala Leu Gln Lys Leu Leu Val Ile Leu Ala Thr Glu Gln Pro Leu Thr
269                 274                 279                 284

gca aag aag aag gtc ctg ttt gca ctg tgc tcc ctg ctg cgc cac ttc     1035
Ala Lys Lys Lys Val Leu Phe Ala Leu Cys Ser Leu Leu Arg His Phe
285                 290                 295                 300

ccc tat gcc cag cgg cag ttc ctg aag ctc ggg ggg ctg cag gtc ctg     1083
Pro Tyr Ala Gln Arg Gln Phe Leu Lys Leu Gly Gly Leu Gln Val Leu
301                 306                 311                 316

agg acc ctg gtg cag gag aag ggc acg gag gtg ctc gcc gtg cgc gtg     1131
Arg Thr Leu Val Gln Glu Lys Gly Thr Glu Val Leu Ala Val Arg Val
317                 322                 327                 332

gtc aca ctg ctc tac gac ctg gtc acg gag aag atg ttc gcc gag gag     1179
Val Thr Leu Leu Tyr Asp Leu Val Thr Glu Lys Met Phe Ala Glu Glu
333                 338                 343                 348

gag gct gag ctg acc cag gag atg tcc cca gag aag ctg cag cag tat     1227
Glu Ala Glu Leu Thr Gln Glu Met Ser Pro Glu Lys Leu Gln Gln Tyr
349                 354                 359                 364

cgc cag gta cac ctc ctg cca ggc ctg tgg gaa cag ggc tgg tgc gag     1275
Arg Gln Val His Leu Leu Pro Gly Leu Trp Glu Gln Gly Trp Cys Glu
365                 370                 375                 380

atc acg gcc cac ctc ctg gcg ctg ccc gag cat gat gcc cgt gag aag     1323
Ile Thr Ala His Leu Leu Ala Leu Pro Glu His Asp Ala Arg Glu Lys
381                 386                 391                 396

gtg ctg cag aca ctg ggc gtc ctc ctg acc acc tgc cgg gac cgc tac     1371
Val Leu Gln Thr Leu Gly Val Leu Leu Thr Thr Cys Arg Asp Arg Tyr
397                 402                 407                 412

cgt cag gac ccc cag ctc ggc agg aca ctg gcc agc ctg cag gct gag     1419
Arg Gln Asp Pro Gln Leu Gly Arg Thr Leu Ala Ser Leu Gln Ala Glu
413                 418                 423                 428
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tac cag gtg ctg gcc agc ctg gag ctg cag gat ggt gag gac gag ggc     1467
Tyr Gln Val Leu Ala Ser Leu Glu Leu Gln Asp Gly Glu Asp Glu Gly
429                 434                 439                 444

tac ttc cag gag ctg ctg ggc tct gtc aac agc ttg ctg aag gag ctg     1515
Tyr Phe Gln Glu Leu Leu Gly Ser Val Asn Ser Leu Leu Lys Glu Leu
445                 450                 455                 460

aga tga ggccccacac caggactgga ctgggatgcc gctagtgagg ctgaggggtg      1571
Arg  *
461

ccagcgtggg tgggcttctc aggcaggagg acatcttggc agtgctggct tggccattaa   1631

atggaaacct gaaggccatc ctctttctgc tgtgtgtctg tgtagactgg gcacagccct   1691

gtggccgggg ggtcaggtga gtggttgggt gatgggctct gctgacgtgc agggctcagc   1751

ccagggcatc caggaacagg ctccagggca ggaacctggg cccaggagtt gcaagtctct   1811

gcttcttacc aagcagcagc tctgtacctt gggaagtcgc                         1851
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US 2006/0063160 A1

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gtcccagaac tttgggaggc caaggtgggc gaatcacgag gtcaggagtt tgagactggc    180

ctggccaata tggtggagcc ccgtctctac caaaaatata agaattggct gggtgtggtg    240

gcgggtgcct gtggtcccag ctgctcggga ggctgaggtg ggagaattgc ttgaacctgg    300

gaggcggagg ttgcagtgag ccgagatcgc gccactgcac tccagcctgg gtgacagacc    360

gagactccgt ctcaaaaaaa aaaaaaaaaa aaaaaaaaag aatggagata ctagaggttg    420

cacagtgctg agaaatatga ggttctgacc tagccagagt ggagagaact ttttaacatc    480

ataggcattc aattgaaaaa ccacacctta ggggaaagaa ccacctccta gagtaaagac    540

tactctaggc agggtgtggt ggctcacacc tgtaatccca gaactttggg aggccaaggt    600

gggcgaatca cgaggtcagg agtttgagac tggcctggcc aatatggtga aaccccgtct    660
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tcacgccact gccctccagc ctgggtgaca gagggagact ccatctcaaa aaacaaacaa    840

accaaaaacc aaaaaccaaa aaaccaccca ggggtcttgt taaaatgcag atgttgaatc    900

agtaggtctg gtggtgcggc ctgagattct gcatttccag caagctccca ggag  atg     957
                                                             Met
                                                               1

cca gtg ctg gtg ggt aga ggt agg gag ggt cct gct ctg cag tta tct     1005
Pro Val Leu Val Gly Arg Gly Arg Glu Gly Pro Ala Leu Gln Leu Ser
  2                   7                  12                  17

ggg tgt ctt att acg act cct tta ccc tcc tcc ttt gct aag gac tgg     1053
Gly Cys Leu Ile Thr Thr Pro Leu Pro Ser Ser Phe Ala Lys Asp Trp
 18                  23                  28                  33

gag act tct cca ctg cct ggg atg ctg gcc ccg gca gct ggc cct gcc     1101
Glu Thr Ser Pro Leu Pro Gly Met Leu Ala Pro Ala Ala Gly Pro Ala
 34                  39                  44                  49

ttt gac agt gac cct gag atc tcc gac gtg gat gag gat gag cca ggg     1149
Phe Asp Ser Asp Pro Glu Ile Ser Asp Val Asp Glu Asp Glu Pro Gly
 50                  55                  60                  65

ggt ctg gtg ggc tct gcg gat gtt gtc tcc ccc agc ggc cac tca gat     1197
Gly Leu Val Gly Ser Ala Asp Val Val Ser Pro Ser Gly His Ser Asp
 66                  71                  76                  81

gcc cag acc ctg gcc atg atg ctg cag gag cag ctg gat gcc atc aat     1245
Ala Gln Thr Leu Ala Met Met Leu Gln Glu Gln Leu Asp Ala Ile Asn
 82                  87                  92                  97

gag gaa atc agg atg att cag gaa gag aag gag tcc acg gag ctc cgc     1293
Glu Glu Ile Arg Met Ile Gln Glu Glu Lys Glu Ser Thr Glu Leu Arg
 98                 103                 108                 113

gcg gag gag att gag acg cgt gta acc agt ggc agc atg gaa gcc cta     1341
Ala Glu Glu Ile Glu Thr Arg Val Thr Ser Gly Ser Met Glu Ala Leu
114                 119                 124                 129

aac ctg aag cag ctg cgc aag cgt ggt tcc atc ccc acc tct ctg acg     1389
Asn Leu Lys Gln Leu Arg Lys Arg Gly Ser Ile Pro Thr Ser Leu Thr
130                 135                 140                 145

gcc ctg tcc ctg gcc agc gcg tcc cca cca ctc agc ggc cgc tcc aca     1437
Ala Leu Ser Leu Ala Ser Ala Ser Pro Pro Leu Ser Gly Arg Ser Thr
146                 151                 156                 161

cct aag ctc acc tcc cgc agt gct gcc cag gac ctg gac cga atg ggg     1485
Pro Lys Leu Thr Ser Arg Ser Ala Ala Gln Asp Leu Asp Arg Met Gly
162                 167                 172                 177

gtc atg acc ctg ccc agt gac tta aga aag cat agg agg aag ctg ctg     1533
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Val Met Thr Leu Pro Ser Asp Leu Arg Lys His Arg Arg Lys Leu Leu
178                 183                 188                 193

tcg cca gtg tct cgg gaa gag aac cga gag gat aaa gcc acc ata aaa     1581
Ser Pro Val Ser Arg Glu Glu Asn Arg Glu Asp Lys Ala Thr Ile Lys
194                 199                 204                 209

tgt gag act tct cct cct tcc tca ccc agg acg ctg cgg cta gag aag     1629
Cys Glu Thr Ser Pro Pro Ser Ser Pro Arg Thr Leu Arg Leu Glu Lys
210                 215                 220                 225

ctt ggc cac cca gcc ctg agc cag gaa gaa ggc aag agt gcc ttg gag     1677
Leu Gly His Pro Ala Leu Ser Gln Glu Glu Gly Lys Ser Ala Leu Glu
226                 231                 236                 241

gat cag ggc agc aac ccc agc agc agc aac agc agc cag gac tcc ctg     1725
Asp Gln Gly Ser Asn Pro Ser Ser Ser Asn Ser Ser Gln Asp Ser Leu
242                 247                 252                 257

cac aag ggc gcc aag cgc aag ggc atc aag tcg tcc att ggc cgc ctg     1773
His Lys Gly Ala Lys Arg Lys Gly Ile Lys Ser Ser Ile Gly Arg Leu
258                 263                 268                 273

ttt ggg aag aag gag aag ggc agg ctg atc cag ctg agt cgg gat gga     1821
Phe Gly Lys Lys Glu Lys Gly Arg Leu Ile Gln Leu Ser Arg Asp Gly
274                 279                 284                 289

gcc aca ggc cat gtt ctg cta aca gac tcc gaa ttc agt atg cag gag     1869
Ala Thr Gly His Val Leu Leu Thr Asp Ser Glu Phe Ser Met Gln Glu
290                 295                 300                 305

cct atg gtg cct gcc aag ctg ggg acc cag gca gag aag gac cgg cgg     1917
Pro Met Val Pro Ala Lys Leu Gly Thr Gln Ala Glu Lys Asp Arg Arg
306                 311                 316                 321

cta aag aag aaa cac cag ctg ctt gaa gat gcc cgc agg aaa gga atg     1965
Leu Lys Lys Lys His Gln Leu Leu Glu Asp Ala Arg Arg Lys Gly Met
322                 327                 332                 337

ccc ttt gcc cag tgg gat ggt cct act gtg gtc tcc tgg ttg gag ctc     2013
Pro Phe Ala Gln Trp Asp Gly Pro Thr Val Val Ser Trp Leu Glu Leu
338                 343                 348                 353

tgg gtg ggg atg cct gcc tgg tat gtg gca gcc tgc cgg gcc aac gtc     2061
Trp Val Gly Met Pro Ala Trp Tyr Val Ala Ala Cys Arg Ala Asn Val
354                 359                 364                 369

aag agt ggt gcc atc atg tcc gct ctg tcg gac aca gag atc cag cgg     2109
Lys Ser Gly Ala Ile Met Ser Ala Leu Ser Asp Thr Glu Ile Gln Arg
370                 375                 380                 385

gag atc ggc atc agc aat gcc ctg cac cgg ctc aag ctc cgc ctg gcc     2157
Glu Ile Gly Ile Ser Asn Ala Leu His Arg Leu Lys Leu Arg Leu Ala
386                 391                 396                 401

att cag gag atg gtg tca ttg acc agc ccc tct gcc cca ccc acc tcc     2205
Ile Gln Glu Met Val Ser Leu Thr Ser Pro Ser Ala Pro Pro Thr Ser
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US 20150050265 A1

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agg act tct tct ggg aat gtc tgg gtc acc cat gaa gag atg gaa act     2253
Arg Thr Ser Ser Gly Asn Val Trp Val Thr His Glu Glu Met Glu Thr
418                 423                 428                 433

ctg gaa aca tct act aaa aca gac agt gag gag ggc agc tgg gct cag     2301
Leu Glu Thr Ser Thr Lys Thr Asp Ser Glu Glu Gly Ser Trp Ala Gln
434                 439                 444                 449

acc ctg gcc tat ggg gac atg aac cat gag tgg att ggg aat gaa tgg     2349
Thr Leu Ala Tyr Gly Asp Met Asn His Glu Trp Ile Gly Asn Glu Trp
450                 455                 460                 465

cta ccc agc ctg ggg ctc ccg cag tac cgc agc tac ttc atg gag tgc     2397
Leu Pro Ser Leu Gly Leu Pro Gln Tyr Arg Ser Tyr Phe Met Glu Cys
466                 471                 476                 481

ctg gtg gac gcc cgc atg ctg gac cac ctc acc aag aag gac ctg cgg     2445
Leu Val Asp Ala Arg Met Leu Asp His Leu Thr Lys Lys Asp Leu Arg
482                 487                 492                 497

gtc cac ctg aag atg gtg gac agc ttc cat cga acc agt ctt cag tat     2493
Val His Leu Lys Met Val Asp Ser Phe His Arg Thr Ser Leu Gln Tyr
498                 503                 508                 513

ggc atc atg tgt ctg aag agg ctg aat tat gac cgg aag gag ctg gag     2541
Gly Ile Met Cys Leu Lys Arg Leu Asn Tyr Asp Arg Lys Glu Leu Glu
514                 519                 524                 529

aag agg cga gag gag agc cag cat gag atc aag gat gtg tta gtc tgg     2589
Lys Arg Arg Glu Glu Ser Gln His Glu Ile Lys Asp Val Leu Val Trp
530                 535                 540                 545

acc aac gac cag gtg gtt cat tgg gtc cag tct att ggg ctc cgg gac     2637
Thr Asn Asp Gln Val Val His Trp Val Gln Ser Ile Gly Leu Arg Asp
546                 551                 556                 561

tac gca gga aac ctg cat gag agt ggt gtg cat gga gcc ttg ctg gcc     2685
Tyr Ala Gly Asn Leu His Glu Ser Gly Val His Gly Ala Leu Leu Ala
562                 567                 572                 577

ctg gac gag aac ttc gac cac aac aca ctg gcc ctg atc ctc cag atc     2733
Leu Asp Glu Asn Phe Asp His Asn Thr Leu Ala Leu Ile Leu Gln Ile
578                 583                 588                 593

ccc aca cag aac acc cag gca cgc caa gtg atg gaa aga gag ttc aat     2781
Pro Thr Gln Asn Thr Gln Ala Arg Gln Val Met Glu Arg Glu Phe Asn
594                 599                 604                 609

aac ctg ttg gcc ttg ggc aca gac cgg aag ctg gat gac ggg gat gac     2829
Asn Leu Leu Ala Leu Gly Thr Asp Arg Lys Leu Asp Asp Gly Asp Asp
610                 615                 620                 625

aag gtg ttt cgc cgc gcg ccc tcc tgg agg aag cgc ttc cgg ccg cgg     2877
Lys Val Phe Arg Arg Ala Pro Ser Trp Arg Lys Arg Phe Arg Pro Arg
626                 631                 636                 641
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Glu His His Gly Arg Gly Gly Met Leu Ser Ala Ser Ala Glu Thr Leu
642                 647                 652                 657

ccg gcg ggc ttc cgt gtg tcc acc ctg ggg acc ctg cag ccc cca ccg     2973
Pro Ala Gly Phe Arg Val Ser Thr Leu Gly Thr Leu Gln Pro Pro Pro
658                 663                 668                 673

gcc ccg cca aag aag atc atg cct gaa gct cac tcc cac tat ctc tac     3021
Ala Pro Pro Lys Lys Ile Met Pro Glu Ala His Ser His Tyr Leu Tyr
674                 679                 684                 689

gga cac atg ctc tcc gcc ttc cgg gac tag c catggccccc agggctggct     3072
Gly His Met Leu Ser Ala Phe Arg Asp  *
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Gly Cys Leu Ile Thr Thr Pro Leu Pro Ser Ser Phe Ala Lys Asp Trp
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gag act tct cca ctg cct ggg atg ctg gcc ccg gca gct ggc cct gcc    1101
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Phe Asp Ser Asp Pro Glu Ile Ser Asp Val Asp Glu Asp Glu Pro Gly
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Ala Gln Thr Leu Ala Met Met Leu Gln Glu Gln Leu Asp Ala Ile Asn
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gag gaa atc agg atg att cag gaa gag aag gag tcc acg gag ctc cgc    1293
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Asn Leu Lys Gln Leu Arg Lys Arg Gly Ser Ile Pro Thr Ser Leu Thr
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gcc ctg tcc ctg gcc agc gcg tcc cca cca ctc agc ggc cgc tcc aca     1437
Ala Leu Ser Leu Ala Ser Ala Ser Pro Pro Leu Ser Gly Arg Ser Thr
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cct aag ctc acc tcc cgc agt gct gcc cag gac ctg gac cga atg ggg     1485
Pro Lys Leu Thr Ser Arg Ser Ala Ala Gln Asp Leu Asp Arg Met Gly
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gtc atg acc ctg ccc agt gac tta aga aag cat agg agg aag ctg ctg     1533
Val Met Thr Leu Pro Ser Asp Leu Arg Lys His Arg Arg Lys Leu Leu
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tcg cca gtg tct cgg gaa gag aac cga gag gat aaa gcc acc ata aaa     1581
Ser Pro Val Ser Arg Glu Glu Asn Arg Glu Asp Lys Ala Thr Ile Lys
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Cys Glu Thr Ser Pro Pro Ser Ser Pro Arg Thr Leu Arg Leu Glu Lys
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Leu Gly His Pro Ala Leu Ser Gln Glu Glu Gly Lys Ser Ala Leu Glu
226                 231                 236                 241

gat cag ggc agc aac ccc agc agc agc aac agc agc cag gac tcc ctg     1725
Asp Gln Gly Ser Asn Pro Ser Ser Ser Asn Ser Ser Gln Asp Ser Leu
242                 247                 252                 257

cac aag ggc gcc aag cgc aag ggc atc aag tcg tcc att ggc cgc ctg     1773
His Lys Gly Ala Lys Arg Lys Gly Ile Lys Ser Ser Ile Gly Arg Leu
258                 263                 268                 273

ttt ggg aag aag gag aag ggc agg ctg atc cag ctg agt cgg gat gga     1821
Phe Gly Lys Lys Glu Lys Gly Arg Leu Ile Gln Leu Ser Arg Asp Gly
274                 279                 284                 289

gcc aca ggc cat gtt ctg cta aca gac tcc gaa ttc agt atg cag gag     1869
Ala Thr Gly His Val Leu Leu Thr Asp Ser Glu Phe Ser Met Gln Glu
290                 295                 300                 305

cct atg gtg cct gcc aag ctg ggg acc cag gca gag aag gac cgg cgg     1917
Pro Met Val Pro Ala Lys Leu Gly Thr Gln Ala Glu Lys Asp Arg Arg
306                 311                 316                 321

cta aag aag aaa cac cag ctg ctt gaa gat gcc cgc agg aaa gga atg     1965
Leu Lys Lys Lys His Gln Leu Leu Glu Asp Ala Arg Arg Lys Gly Met
322                 327                 332                 337
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09/05/2006 15:36:05 PM

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tgg gtg ggg atg cct gcc tgg tat gtg gca gcc tgc cgg gcc aac gtc     2061
Trp Val Gly Met Pro Ala Trp Tyr Val Ala Ala Cys Arg Ala Asn Val
354                 359                 364                 369

aag agt ggt gcc atc atg tcc gct ctg tcg gac aca gag atc cag cgg     2109
Lys Ser Gly Ala Ile Met Ser Ala Leu Ser Asp Thr Glu Ile Gln Arg
370                 375                 380                 385

gag atc ggc atc agc aat gcc ctg cac cgg ctc aag ctc cgc ctg gcc     2157
Glu Ile Gly Ile Ser Asn Ala Leu His Arg Leu Lys Leu Arg Leu Ala
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att cag gag atg gtg tca ttg acc agc ccc tct gcc cca ccc acc tcc     2205
Ile Gln Glu Met Val Ser Leu Thr Ser Pro Ser Ala Pro Pro Thr Ser
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agg act tct tct ggg aat gtc tgg gtc acc cat gaa gag atg gaa act     2253
Arg Thr Ser Ser Gly Asn Val Trp Val Thr His Glu Glu Met Glu Thr
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ctg gaa aca tct act aaa aca acc ctg gcc tat ggg gac atg aac cat     2301
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gag tgg att ggg aat gaa tgg cta ccc agc ctg ggg ctc ccg cag tac     2349
Glu Trp Ile Gly Asn Glu Trp Leu Pro Ser Leu Gly Leu Pro Gln Tyr
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cgc agc tac ttc atg gag tgc ctg gtg gac gcc cgc atg ctg gac cac     2397
Arg Ser Tyr Phe Met Glu Cys Leu Val Asp Ala Arg Met Leu Asp His
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ctc acc aag aag gac ctg cgg gtc cac ctg aag atg gtg gac agc ttc     2445
Leu Thr Lys Lys Asp Leu Arg Val His Leu Lys Met Val Asp Ser Phe
482                 487                 492                 497

cat cga acc agt ctt cag tat ggc atc atg tgt ctg aag agg ctg aat     2493
His Arg Thr Ser Leu Gln Tyr Gly Ile Met Cys Leu Lys Arg Leu Asn
498                 503                 508                 513

tat gac cgg aag gag ctg gag aag agg cga gag gag agc cag cat gag     2541
Tyr Asp Arg Lys Glu Leu Glu Lys Arg Arg Glu Glu Ser Gln His Glu
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atc aag gat gtg tta gtc tgg acc aac gac cag gtg gtt cat tgg gtc     2589
Ile Lys Asp Val Leu Val Trp Thr Asn Asp Gln Val Val His Trp Val
530                 535                 540                 545

cag tct att ggg ctc cgg gac tac gca gga aac ctg cat gag agt ggt     2637
Gln Ser Ile Gly Leu Arg Asp Tyr Ala Gly Asn Leu His Glu Ser Gly
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gtg cat gga gcc ttg ctg gcc ctg gac gag aac ttc gac cac aac aca     2685
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gtg atg gaa aga gag ttc aat aac ctg ttg gcc ttg ggc aca gac cgg     2781
Val Met Glu Arg Glu Phe Asn Asn Leu Leu Ala Leu Gly Thr Asp Arg
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aag ctg gat gac ggg gat gac aag gtg ttt cgc cgc gcg ccc tcc tgg     2829
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Arg Lys Arg Phe Arg Pro Arg Glu His His Gly Arg Gly Gly Met Leu
626                 631                 636                 641

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Ser Ala Ser Ala Glu Thr Leu Pro Ala Gly Phe Arg Val Ser Thr Leu
642                 647                 652                 657

ggg acc ctg cag ccc cca ccg gcc ccg cca aag aag atc atg cct gaa     2973
Gly Thr Leu Gln Pro Pro Pro Ala Pro Pro Lys Lys Ile Met Pro Glu
658                 663                 668                 673

gct cac tcc cac tat ctc tac gga cac atg ctc tcc gcc ttc cgg gac     3021
Ala His Ser His Tyr Leu Tyr Gly His Met Leu Ser Ala Phe Arg Asp
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Ala Lys Gly Pro Gly Ala Glu Pro Phe Tyr Ile Arg Ala Asn Leu Thr
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Leu Pro Glu Arg Ala Asp Pro His Ala Leu Cys Val Lys Ala Gln Glu
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Cys Thr Arg Val Asp Pro Leu Thr Leu Arg Asp Leu Asp Arg Gly Thr
65 70 75 80

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Val Pro Asn Tyr Gln Arg Ala Gln Gln Leu Leu Glu Val Gln Glu Lys
81 86 91 96

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Cys Leu Pro Ser Ser Arg His Arg Gly Pro Arg Ser Asn Leu Lys Lys
97 102 107 112

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113 118 123 128

cct gca ggg gac tcc ccg gat cag ctg ctg ctg gag ccc tgt gca gag 550
Pro Ala Gly Asp Ser Pro Asp Gln Leu Leu Leu Glu Pro Cys Ala Glu
129 134 139 144

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Document 1 of 1 - 2006/0160760

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Ser Ala Leu Arg Pro Val Val Leu Leu Pro Glu Cys Leu Ala Pro Arg
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Leu Ile Arg Asn Leu Leu Asp Leu Pro Ser Ser Arg Leu Asp Phe Gln
177                 182                 187                 192

gtg tgc cca gcg gaa agc ctc tct ggg gag gaa ctg tgc cca tcc tca      742
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273                 278                 283                 288

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Val Gln Val Pro Ala His Glu Trp Gly His Ala Glu Glu Leu Ala Lys
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Ser Glu Pro Asp Ala Pro Arg Leu Leu Pro Ser Pro Val Thr Cys Thr
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cct aaa gag ggg gag aca cca cca gcc cct gca gca ctc tcc agt cct     144
Pro Lys Glu Gly Glu Thr Pro Pro Ala Pro Ala Ala Leu Ser Ser Pro
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ctt gct gtg ccg gcc ttg tca gca tcc tca ttg agt tcc aga gct cct     192
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129                 134                 139                 144

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Lys Lys Tyr Gln His Ile His Gln Lys Ser Phe Ser Cys Pro Glu Pro
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gcc tgt ggg aag tct ttc aac ttt aag aaa cac ctg aag gag cac atg      528
Ala Cys Gly Lys Ser Phe Asn Phe Lys Lys His Leu Lys Glu His Met
161                 166                 171                 176

aag ctg cac agt gac acc cgg gac tac atc tgt gag ttc tgc gcc cgg      576
Lys Leu His Ser Asp Thr Arg Asp Tyr Ile Cys Glu Phe Cys Ala Arg
177                 182                 187                 192

tct ttc cgc act agc agc aac ctt gtc atc cac aga cgt atc cac act      624
Ser Phe Arg Thr Ser Ser Asn Leu Val Ile His Arg Arg Ile His Thr
193                 198                 203                 208

gga gaa aaa ccc ctg cag tgt gag ata tgc ggg ttt acc tgc cgc cag      672
Gly Glu Lys Pro Leu Gln Cys Glu Ile Cys Gly Phe Thr Cys Arg Gln
209                 214                 219                 224

aag gct tcc ctg aac tgg cac cag cgc aag cat gca gag acg gtg gct      720
Lys Ala Ser Leu Asn Trp His Gln Arg Lys His Ala Glu Thr Val Ala
225                 230                 235                 240

gcc ttg cgc ttc ccc tgt gaa ttc tgc ggc aag cgc ttt gag aag cca      768
Ala Leu Arg Phe Pro Cys Glu Phe Cys Gly Lys Arg Phe Glu Lys Pro
241                 246                 251                 256

gac agt gtt gca gcc cac cgt agc aaa agt cac cca gcc ctg ctt cta      816
Asp Ser Val Ala Ala His Arg Ser Lys Ser His Pro Ala Leu Leu Leu
257                 262                 267                 272

gcc cct caa gag tca ccc agt ggt ccc cta gag ccc tgt ccc agc atc      864
Ala Pro Gln Glu Ser Pro Ser Gly Pro Leu Glu Pro Cys Pro Ser Ile
273                 278                 283                 288

tct gcc cct ggg cct ctg gga tcc agc gag ggg tcc agg ccc tct gca      912
Ser Ala Pro Gly Pro Leu Gly Ser Ser Glu Gly Ser Arg Pro Ser Ala
289                 294                 299                 304

tct cct cag gct cca acc ctg ctt cct cag caa tga gctc tcctccagct      962
Ser Pro Gln Ala Pro Thr Leu Leu Pro Gln Gln  *
305                 310                 315

ttggctttgg gaagccagac tccagggact gaaaaggagc aacaaggaga gggtctgctt   1022

gagaaatgcc agatgcttgg tccccaggaa ctaaggcgac agagtgcagg gtgggggcaa   1082
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gactgggctg taggggagct ggactacttt agtcttccta aaggacaaaa taaacagtat   1142

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cctgccagcc gggaacacgg aggggaagga ggaggagctt aaaagaggct actgaacccc    180

agttggcc atg gct gag gaa ttt gtg acc ctc aag gat gtc ggc atg gac      230
         Met Ala Glu Glu Phe Val Thr Leu Lys Asp Val Gly Met Asp
           1               5                  10

ttc acc ttg gga gac tgg gag cag ctc ggg ctg gaa cag ggg gac acg      278
Phe Thr Leu Gly Asp Trp Glu Gln Leu Gly Leu Glu Gln Gly Asp Thr
 15                  20                  25                  30

ttc tgg gac aca gcg ttg gac aat tgc cag gac ctc ttc ctg ctg gac      326
Phe Trp Asp Thr Ala Leu Asp Asn Cys Gln Asp Leu Phe Leu Leu Asp
 31                  36                  41                  46

ccc cca aga ccc aac ctg acc tcc cac cca gat ggc agt gaa gat ctg      374
Pro Pro Arg Pro Asn Leu Thr Ser His Pro Asp Gly Ser Glu Asp Leu
 47                  52                  57                  62

gag cct ctg gca gga gga agc cca gaa gca aca agc cct gat gtg act      422
Glu Pro Leu Ala Gly Gly Ser Pro Glu Ala Thr Ser Pro Asp Val Thr
 63                  68                  73                  78

gag acc aag aac tct cct ctg atg gag gat ttc ttc gaa gaa gga ttc      470
Glu Thr Lys Asn Ser Pro Leu Met Glu Asp Phe Phe Glu Glu Gly Phe
 79                  84                  89                  94

tcc cag gag att ata gag atg tta tcc aag gat ggc ttc tgg aac tcc      518
Ser Gln Glu Ile Ile Glu Met Leu Ser Lys Asp Gly Phe Trp Asn Ser
 95                 100                 105                 110

aat ttc gga gaa gcc tgt ata gag gac acc tgg tta gat agt ttg cta      566
Asn Phe Gly Glu Ala Cys Ile Glu Asp Thr Trp Leu Asp Ser Leu Leu
111                 116                 121                 126

ggc gat cca gaa agt ctt ctg agg tct gat att gcc acc aac ggg gaa      614
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Gly Asp Pro Glu Ser Leu Leu Arg Ser Asp Ile Ala Thr Asn Gly Glu
127                 132                 137                 142

agt ccc acg gaa tgc aag agt cat gaa tta aag aga gga ctc agt cct      662
Ser Pro Thr Glu Cys Lys Ser His Glu Leu Lys Arg Gly Leu Ser Pro
143                 148                 153                 158

gtg tcc acc gtt tcc acg gga gaa gat tcc atg gtg cat aat gtt tct      710
Val Ser Thr Val Ser Thr Gly Glu Asp Ser Met Val His Asn Val Ser
159                 164                 169                 174

gaa aag acc ctc aca cca gct aag tct aag gaa tat agg ggt gag ttt      758
Glu Lys Thr Leu Thr Pro Ala Lys Ser Lys Glu Tyr Arg Gly Glu Phe
175                 180                 185                 190

ttc tcc tac tcc gac cac agc cag cag gat tct gtt cag gaa ggg gag      806
Phe Ser Tyr Ser Asp His Ser Gln Gln Asp Ser Val Gln Glu Gly Glu
191                 196                 201                 206

aaa cca tat caa tgt agt gaa tgt ggg aaa agc ttc agt ggg agt tac      854
Lys Pro Tyr Gln Cys Ser Glu Cys Gly Lys Ser Phe Ser Gly Ser Tyr
207                 212                 217                 222

cgt ctt acc cag cac tgg atc act cat act agg gag aaa ccc act gtc      902
Arg Leu Thr Gln His Trp Ile Thr His Thr Arg Glu Lys Pro Thr Val
223                 228                 233                 238

cat caa gag tgt gag caa ggt ttt gac cgg aat gct tcc ctt tct gtg      950
His Gln Glu Cys Glu Gln Gly Phe Asp Arg Asn Ala Ser Leu Ser Val
239                 244                 249                 254

tat ccg aaa act cac acg ggc tac aaa ttc tat gtg tgt aat gaa tat      998
Tyr Pro Lys Thr His Thr Gly Tyr Lys Phe Tyr Val Cys Asn Glu Tyr
255                 260                 265                 270

ggg aca act ttt agt cag agt aca tac ctg tgg cat cag aaa act cac     1046
Gly Thr Thr Phe Ser Gln Ser Thr Tyr Leu Trp His Gln Lys Thr His
271                 276                 281                 286

act gga gaa aaa cca tgt aag agt caa gat agt gac cac cca ccc agt     1094
Thr Gly Glu Lys Pro Cys Lys Ser Gln Asp Ser Asp His Pro Pro Ser
287                 292                 297                 302

cat gac aca cag cct ggt gag cat cag aaa act cac aca gat agt aag     1142
His Asp Thr Gln Pro Gly Glu His Gln Lys Thr His Thr Asp Ser Lys
303                 308                 313                 318

tcc tac aac tgt aac gaa tgc ggc aag gct ttt acc cgg atc ttc cac     1190
Ser Tyr Asn Cys Asn Glu Cys Gly Lys Ala Phe Thr Arg Ile Phe His
319                 324                 329                 334

ctt act cgg cac cag aag atc cac act cgg aaa cgc tat gag tgt tcc     1238
Leu Thr Arg His Gln Lys Ile His Thr Arg Lys Arg Tyr Glu Cys Ser
335                 340                 345                 350

aag tgc cag gcg acc ttc aac ttg aga aaa cac ctc atc caa cat cag     1286
Lys Cys Gln Ala Thr Phe Asn Leu Arg Lys His Leu Ile Gln His Gln
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351                 356                 361                 366

aaa act cac gct gca aaa act acc tct gag tgt cag gag tgt ggg aag     1334
Lys Thr His Ala Ala Lys Thr Thr Ser Glu Cys Gln Glu Cys Gly Lys
367                 372                 377                 382

att ttt agg cac agt tcg ctg ctc att gaa cac cag gct ctt cat gct     1382
Ile Phe Arg His Ser Ser Leu Leu Ile Glu His Gln Ala Leu His Ala
383                 388                 393                 398

gga gag gag cct tat aag tgt aac gaa cgt ggg aaa tcc ttc agg cat     1430
Gly Glu Glu Pro Tyr Lys Cys Asn Glu Arg Gly Lys Ser Phe Arg His
399                 404                 409                 414

aac tct acc cta aag atc cat cag agg gtt cac agt gga gag aag cct     1478
Asn Ser Thr Leu Lys Ile His Gln Arg Val His Ser Gly Glu Lys Pro
415                 420                 425                 430

tac aaa tgc agt gag tgt ggg aag gcc ttc cac cgg cac act cac ctt     1526
Tyr Lys Cys Ser Glu Cys Gly Lys Ala Phe His Arg His Thr His Leu
431                 436                 441                 446

aat gaa cat cgg cga att cat aca ggc tac aga ccc cac aaa tgt cag     1574
Asn Glu His Arg Arg Ile His Thr Gly Tyr Arg Pro His Lys Cys Gln
447                 452                 457                 462

gaa tgc gtc agg agt ttc agc cgg ccc tca cat ctg atg cga cat cag     1622
Glu Cys Val Arg Ser Phe Ser Arg Pro Ser His Leu Met Arg His Gln
463                 468                 473                 478

gcc att cac acc gca gaa aag ccc tat agc tgt gct gaa tgc aag gag     1670
Ala Ile His Thr Ala Glu Lys Pro Tyr Ser Cys Ala Glu Cys Lys Glu
479                 484                 489                 494

act ttc agc gat aac aat cgc ctt gtg caa cac cag aaa atg cac act     1718
Thr Phe Ser Asp Asn Asn Arg Leu Val Gln His Gln Lys Met His Thr
495                 500                 505                 510

gtc aaa acc cca tat gaa tgt cag gag tgc gga gaa cgc ttc att tgc     1766
Val Lys Thr Pro Tyr Glu Cys Gln Glu Cys Gly Glu Arg Phe Ile Cys
511                 516                 521                 526

ggc tca acc ctg aag tgc cac gag agt gtt cac gcc aga gaa aaa caa     1814
Gly Ser Thr Leu Lys Cys His Glu Ser Val His Ala Arg Glu Lys Gln
527                 532                 537                 542

gga ttt ttt gtg agt ggg aag atc ttg gat cag aac cca gaa cag aaa     1862
Gly Phe Phe Val Ser Gly Lys Ile Leu Asp Gln Asn Pro Glu Gln Lys
543                 548                 553                 558

gag aag tgc ttt aag tgt aac aaa tgt gag aaa acc ttt agc tgc agc     1910
Glu Lys Cys Phe Lys Cys Asn Lys Cys Glu Lys Thr Phe Ser Cys Ser
559                 564                 569                 574

aaa tac cta act cag cac gag agg att cac acc agg gga gtg aag ccc     1958
Lys Tyr Leu Thr Gln His Glu Arg Ile His Thr Arg Gly Val Lys Pro
575                 580                 585                 590
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ttt gaa tgt gac cag tgt ggg aaa gcc ttt ggc caa agt act cgg ctc     2006
Phe Glu Cys Asp Gln Cys Gly Lys Ala Phe Gly Gln Ser Thr Arg Leu
591                 596                 601                 606

att cac cat caa aga atc cac tct aga gtg agg ctg tat aaa tgg ggt     2054
Ile His His Gln Arg Ile His Ser Arg Val Arg Leu Tyr Lys Trp Gly
607                 612                 617                 622

gag caa ggg aaa gcc atc agc agt gcc tcc ctt atc aaa ctt cag tcc     2102
Glu Gln Gly Lys Ala Ile Ser Ser Ala Ser Leu Ile Lys Leu Gln Ser
623                 628                 633                 638

ttc cac aca aag gag cac cct ttt aaa tgt aac gaa tgc gga aag acc     2150
Phe His Thr Lys Glu His Pro Phe Lys Cys Asn Glu Cys Gly Lys Thr
639                 644                 649                 654

ttc agc cac agt gca cac ctc tca aaa cat cag tta att cac gct gga     2198
Phe Ser His Ser Ala His Leu Ser Lys His Gln Leu Ile His Ala Gly
655                 660                 665                 670

gag aat ccc ttt aaa tgt agt aag tgt gac aga gtc ttc acc cag aga     2246
Glu Asn Pro Phe Lys Cys Ser Lys Cys Asp Arg Val Phe Thr Gln Arg
671                 676                 681                 686

aac tac ctt gtt cag cat gag cga act cat gcc aga aag aag ccg ttg     2294
Asn Tyr Leu Val Gln His Glu Arg Thr His Ala Arg Lys Lys Pro Leu
687                 692                 697                 702

gtg tgt aac gaa tgc ggg aaa acg ttc cgt cag agc tca tgc ctt tct     2342
Val Cys Asn Glu Cys Gly Lys Thr Phe Arg Gln Ser Ser Cys Leu Ser
703                 708                 713                 718

aag cat cag aga att cac tca ggt gag aag ccc tat gta tgt gat tac     2390
Lys His Gln Arg Ile His Ser Gly Glu Lys Pro Tyr Val Cys Asp Tyr
719                 724                 729                 734

tgc ggg aag gcc ttc ggc ctg agt gct gag ctt gtc cgc cac cag aga     2438
Cys Gly Lys Ala Phe Gly Leu Ser Ala Glu Leu Val Arg His Gln Arg
735                 740                 745                 750

att cac act gga gaa aag cct tat gtt tgt cag gaa tgc ggg aaa gcc     2486
Ile His Thr Gly Glu Lys Pro Tyr Val Cys Gln Glu Cys Gly Lys Ala
751                 756                 761                 766

ttc acc cag agc tca tgc ctt tct att cac cgg aga gtt cac act ggg     2534
Phe Thr Gln Ser Ser Cys Leu Ser Ile His Arg Arg Val His Thr Gly
767                 772                 777                 782

gag aag ccc tac aga tgt ggt gaa tgt ggg aaa gcc ttt gcc cag aaa     2582
Glu Lys Pro Tyr Arg Cys Gly Glu Cys Gly Lys Ala Phe Ala Gln Lys
783                 788                 793                 798

gca aat cta aca cag cac cag aga att cac aca ggg gag aag cct tac     2630
Ala Asn Leu Thr Gln His Gln Arg Ile His Thr Gly Glu Lys Pro Tyr
799                 804                 809                 814
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tcc tgt aat gtg tgt ggc aaa gct ttt gtc ctc agt gcc cat ctc aac     2678
Ser Cys Asn Val Cys Gly Lys Ala Phe Val Leu Ser Ala His Leu Asn
815                 820                 825                 830

cag cac ctg aga gtt cac acc cag gag aca ctt tat cag tgt caa cgt     2726
Gln His Leu Arg Val His Thr Gln Glu Thr Leu Tyr Gln Cys Gln Arg
831                 836                 841                 846

tgc cag aaa gcc ttt cgg tgc cac tcg agc ctc agc cgc cat cag cgt     2774
Cys Gln Lys Ala Phe Arg Cys His Ser Ser Leu Ser Arg His Gln Arg
847                 852                 857                 862

gta cac aac aag cag caa tac tgc ctg tag c cattgggtgg cagcagagtc     2825
Val His Asn Lys Gln Gln Tyr Cys Leu  *
863                 868

ccagaatatg agaccgttac tcggatgttg aaagttggaa actatcccat tgcaagtttc   2885

tctccaaata aatgcatcta aagattgatt agaaagtttg tgcgcatgtt tttcattata   2945

acaatgaaaa cacaaaagtg gagaagctgt acaacgtcag gattcagagg taggctctgg   3005

agccagtcta ccttgagtta aatcccacct ctgccatcta ctacctaagt gaccttggga   3065

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tcagagggct tttctgagga ttaaataaat aaatgtgaag cacttagaac tgatggccag   3185

cacatgaggg ctcaccaagt gtaagccaca aatacacatc agctatagca caaatatact   3245

tgtgttacaa gaaaggaatt agtaatctgt gtttactgta gttaatgttc ttacaatgta   3305

tcgcttttaa tttaagtttt ccttttttac agtttttctc cagcacttta ctcttcttaa   3365

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aaaaagaaca tgtaaactct tcacctcaac tagctacaac cttccactcc taacctccca   3485

agcttctcac ttaaagagga ctccctatcc cacaaacaca tgctccctct tcctatgacc   3545

ttcctccatt taacagtgtt ggttatgcaa taagacaccc aatttttcat gggagttgac   3605

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tggaaccaca caaccagttc cctaccagtg tcttgtcagc tctgggtgtt tgttccctgc   4025

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US 6,756,480 B2

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agttgaaact gggaacctgt tggctaacca ttggggcctt acactgtttt tcaaatggtt   4265

gcaacattta acttctcgca catggttccc gtcctctgga gctctgtctt gtcggggaga   4325

tgggcatgtt gtataccaaa agagtgtaca aagtgttgca gggctgtgac acaataggga   4385

ctctatggaa aactggcagc cattgggtgt gggggcagtc tgtaaatcag tcacctgtgt   4445

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aatagattta agataaaata gacttcccag agaacagctt ccgctgcact acactgaata    240

catacacgca taccaaggaa aaacagcact ggaggcaatg tttctataaa tcaaagaaga    300

gacagtgtga ga    atg tca gcc ctc aac tgg aag ccg ttt gtg tac ggg      348
                 Met Ser Ala Leu Asn Trp Lys Pro Phe Val Tyr Gly
                   1               5                  10

ggg ctg gcc tcc atc act gct gag tgc ggt aca ttt cca att gat tta      396
Gly Leu Ala Ser Ile Thr Ala Glu Cys Gly Thr Phe Pro Ile Asp Leu
 13                  18                  23                  28

acc aag aca cgg ctc cag att caa ggc cag acg aat gat gca aaa ttt      444
Thr Lys Thr Arg Leu Gln Ile Gln Gly Gln Thr Asn Asp Ala Lys Phe
 29                  34                  39                  44

aag gaa att aga tac cga gga atg ttg cac gca tta gtg agg ata ggc      492
Lys Glu Ile Arg Tyr Arg Gly Met Leu His Ala Leu Val Arg Ile Gly
 45                  50                  55                  60

aga gaa gaa ggg ctg aaa gca ctc tac tcg ggg att gcc ccc gcg atg      540
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Arg Glu Glu Gly Leu Lys Ala Leu Tyr Ser Gly Ile Ala Pro Ala Met
 61                  66                  71                  76

tta cgc cag gca tcc tat ggc acc atc aag ata ggc act tac cag agc      588
Leu Arg Gln Ala Ser Tyr Gly Thr Ile Lys Ile Gly Thr Tyr Gln Ser
 77                  82                  87                  92

ttg aag cga cta ttc att gaa cgc cca gaa gat gaa act cta ccg ata      636
Leu Lys Arg Leu Phe Ile Glu Arg Pro Glu Asp Glu Thr Leu Pro Ile
 93                  98                 103                 108

aat gtg ata tgt gga att ctg tct gga gtc ata tct tca acc att gct      684
Asn Val Ile Cys Gly Ile Leu Ser Gly Val Ile Ser Ser Thr Ile Ala
109                 114                 119                 124

aat cca act gat gtt ttg aaa att cgg atg caa gcg caa agc aac acc      732
Asn Pro Thr Asp Val Leu Lys Ile Arg Met Gln Ala Gln Ser Asn Thr
125                 130                 135                 140

att caa gga gga atg ata ggc aac ttc atg aac att tac cag caa gag      780
Ile Gln Gly Gly Met Ile Gly Asn Phe Met Asn Ile Tyr Gln Gln Glu
141                 146                 151                 156

ggg aca aga gga ctg tgg aag ggt gtg tcc ctt act gcg cag agg gct      828
Gly Thr Arg Gly Leu Trp Lys Gly Val Ser Leu Thr Ala Gln Arg Ala
157                 162                 167                 172

gct att gtt gtt ggt gtg gag ctg ccg gtc tat gac atc acc aag aag      876
Ala Ile Val Val Gly Val Glu Leu Pro Val Tyr Asp Ile Thr Lys Lys
173                 178                 183                 188

cat ctt att ctc tca ggc ctg atg gga gac act gtg tat acc cac ttc      924
His Leu Ile Leu Ser Gly Leu Met Gly Asp Thr Val Tyr Thr His Phe
189                 194                 199                 204

ctc tca agc ttc acc tgt ggt ctg gca ggg gcc ctg gcc tca aac cct      972
Leu Ser Ser Phe Thr Cys Gly Leu Ala Gly Ala Leu Ala Ser Asn Pro
205                 210                 215                 220

gtt gat gtt gtg agg aca cgt atg atg aat cag aga gtg ctt cga gat     1020
Val Asp Val Val Arg Thr Arg Met Met Asn Gln Arg Val Leu Arg Asp
221                 226                 231                 236

ggc aga tgt tct ggc tac aca gga acc ctg gat tgc ttg tta cag gtg     1068
Gly Arg Cys Ser Gly Tyr Thr Gly Thr Leu Asp Cys Leu Leu Gln Val
237                 242                 247                 252

ttg cct taa tgaagca aagacactta tcgtattcat ccacctgaca tcttgggaaa     1124
Leu Pro  *
253

tagtggtact ctgaatgata tctctaccac tattgcttct ttatttgtga cctgttcagg   1184

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cctttcctcc cccacccttg agttacccct ctgtctttcc tgctgttgcg cgggtgctcc 180

cacagcggag cggagattac agagccgccg gg atg ccc caa ctc tcc gga gga 233
Met Pro Gln Leu Ser Gly Gly
1 5

ggt ggc ggc ggc ggg ggg gac ccg gaa ctc tgc gcc acg gac gag atg 281
Gly Gly Gly Gly Gly Gly Asp Pro Glu Leu Cys Ala Thr Asp Glu Met
8 13 18 23

atc ccc ttc aag gac gag ggc gat cct cag aag gaa aag atc ttc gcc 329
Ile Pro Phe Lys Asp Glu Gly Asp Pro Gln Lys Glu Lys Ile Phe Ala
24 29 34 39

gag atc agt cat ccc gaa gag gaa ggc gat tta gct gac atc aag tct 377
Glu Ile Ser His Pro Glu Glu Glu Gly Asp Leu Ala Asp Ile Lys Ser
40 45 50 55

tcc ttg gtg aac gag tct gaa atc atc ccg gcc agc aac gga cac gag 425
Ser Leu Val Asn Glu Ser Glu Ile Ile Pro Ala Ser Asn Gly His Glu
56 61 66 71

gtg gcc aga caa gca caa acc tct cag gag ccc tac cac gac aag gcc 473
Val Ala Arg Gln Ala Gln Thr Ser Gln Glu Pro Tyr His Asp Lys Ala
72 77 82 87

aga gaa cac ccc gat gac gga aag cat cca gat gga ggc ctc tac aac 521
Arg Glu His Pro Asp Asp Gly Lys His Pro Asp Gly Gly Leu Tyr Asn
88 93 98 103

aag gga ccc tcc tac tcg agt tat tcc ggg tac ata atg atg cca aat 569
Lys Gly Pro Ser Tyr Ser Ser Tyr Ser Gly Tyr Ile Met Met Pro Asn
104 109 114 119

atg aat aac gac cca tac atg tca aat gga tct ctt tct cca ccc atc 617
Met Asn Asn Asp Pro Tyr Met Ser Asn Gly Ser Leu Ser Pro Pro Ile
120 125 130 135

ccg aga aca tca aat aaa gtg ccc gtg gtg cag cca tcc cat gcg gtc 665
Pro Arg Thr Ser Asn Lys Val Pro Val Val Gln Pro Ser His Ala Val

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136                 141                 146                 151

cat cct ctc acc ccc ctc atc act tac agt gac gag cac ttt tct cca      713
His Pro Leu Thr Pro Leu Ile Thr Tyr Ser Asp Glu His Phe Ser Pro
152                 157                 162                 167

gga tca cac ccg tca cac atc cca tca gat gtc aac tcc aaa caa ggc      761
Gly Ser His Pro Ser His Ile Pro Ser Asp Val Asn Ser Lys Gln Gly
168                 173                 178                 183

atg tcc aga cat cct cca gct cct gat atc cct act ttt tat ccc ttg      809
Met Ser Arg His Pro Pro Ala Pro Asp Ile Pro Thr Phe Tyr Pro Leu
184                 189                 194                 199

tct ccg ggt ggt gtt gga cag atc acc cca cct ctt ggc tgg caa ggt      857
Ser Pro Gly Gly Val Gly Gln Ile Thr Pro Pro Leu Gly Trp Gln Gly
200                 205                 210                 215

cag cct gta tat ccc atc acg ggt gga ttc agg caa ccc tac cca tcc      905
Gln Pro Val Tyr Pro Ile Thr Gly Gly Phe Arg Gln Pro Tyr Pro Ser
216                 221                 226                 231

tca ctg tca gtc gac act tcc atg tcc agg ttt tcc cat cat atg att      953
Ser Leu Ser Val Asp Thr Ser Met Ser Arg Phe Ser His His Met Ile
232                 237                 242                 247

ccc ggt cct cct ggt ccc cac aca act ggc atc cct cat cca gct att     1001
Pro Gly Pro Pro Gly Pro His Thr Thr Gly Ile Pro His Pro Ala Ile
248                 253                 258                 263

gta aca cct cag gtc aaa cag gaa cat ccc cac act gac agt gac cta     1049
Val Thr Pro Gln Val Lys Gln Glu His Pro His Thr Asp Ser Asp Leu
264                 269                 274                 279

atg cac gtg aag cct cag cat gaa cag aga aag gag cag gag cca aaa     1097
Met His Val Lys Pro Gln His Glu Gln Arg Lys Glu Gln Glu Pro Lys
280                 285                 290                 295

aga cct cac att aag aag cct ctg aat gct ttt atg tta tac atg aaa     1145
Arg Pro His Ile Lys Lys Pro Leu Asn Ala Phe Met Leu Tyr Met Lys
296                 301                 306                 311

gaa atg aga gcg aat gtc gtt gct gag tgt act cta aaa gaa agt gca     1193
Glu Met Arg Ala Asn Val Val Ala Glu Cys Thr Leu Lys Glu Ser Ala
312                 317                 322                 327

gct atc aac cag att ctt ggc aga agg tgg cat gcc ctc tcc cgt gaa     1241
Ala Ile Asn Gln Ile Leu Gly Arg Arg Trp His Ala Leu Ser Arg Glu
328                 333                 338                 343

gag cag gct aaa tat tat gaa tta gca cgg aaa gaa aga cag cta cat     1289
Glu Gln Ala Lys Tyr Tyr Glu Leu Ala Arg Lys Glu Arg Gln Leu His
344                 349                 354                 359

atg cag ctt tat cca ggc tgg tct gca aga gac aat tat ggt aag aaa     1337
Met Gln Leu Tyr Pro Gly Trp Ser Ala Arg Asp Asn Tyr Gly Lys Lys
360                 365                 370                 375
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aag aag agg aag aga gag aaa cta cag gaa tct gca tca ggt aca ggt     1385
Lys Lys Arg Lys Arg Glu Lys Leu Gln Glu Ser Ala Ser Gly Thr Gly
376                 381                 386                 391

cca aga atg aca gct gcc tac atc tga aacat ggtggaaaac gaagctcatt     1437
Pro Arg Met Thr Ala Ala Tyr Ile  *
392                 397

cccaacgtgc aaagccaagg cagcgacccc aggacctctt ctggagatgg aagcttgttg   1497

aaaacccaga ctgtctccac ggcctgccca gtcgacccca aaggaacact gacatcaatt   1557

ttaccctgag gtcactgcta gagacgctga tccataaaga caatcactgc caacccctct   1617

ttcgtctact gcaagagcca agttccaaaa taaagcataa aaaggttttt taaaaggaaa   1677

tgtaaaagca catgagaatg ctagcaggct gtggggcagc tgagcagctt ttctcccccc   1737

atatctgcgt gcacttccca gagcatcttg catccaaacc tgtaaccttt cggcaaggac   1797

ggtaacttgg ctgcatttgc ctgtcatgcg caactggagc cagcaaccag cacatccatc   1857

agcaccccag tggaggagtt catggaagag ttccctcttt gtttctgctt cattttctt    1917

tcttttcttt tctcctaaag cttttattta acagtgcaaa aggatcgttt ttttttgctt   1977

ttttaaactt gaatttttt aatttacact ttttagtttt aattttcttg tatattttgc    2037

tagctatgag cttttaaata aaattgaaag ttctggaaaa gtttgaaata atgacataaa   2097

aagaagcctt ctttttctga gacagcttgt ctggtaagtg gcttctctgt gaattgcctg   2157

taacacatag tggcttctcc gcccttgtaa ggtgttcagt agagctaaat aaatgtaata   2217

gccaaaccca ctctgttggt agcaattggc agccctattt cagtttattt tttcttctgt   2277

tttcttcttt tctttttta aacagtaaac cttaacagat gcgttcagca gactggtttg    2337

cagtgaattt tcatttcttt ccttatcacc cccttgttgt aaaaagccca gcacttgaat   2397

tgttattact ttaaatgttc tgtatttgta tctgttttta ttagccaatt agtgggattt   2457

tatgccagtt gttaaaatga gcattgatgt acccatttt taaaaaagca aggcacagcc    2517

tttgcccaaa actgtcatcc taacgtttgt cattccagtt tgagttaatg tgctgagcat   2577

ttttttaaaa gaagctttgt aataaaacat ttttaaaaat tgtaaaaaaa aaa          2630
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<210> 302
<211> 1590
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (357)..(1100)

<400> 302
agccccccca actgacgccg tgttgacggc cctgaatccc ggctcgaccc acgcgtccgg 60

gcccagaaag gtggggcagg aacgatccca gccttcagct aattctgtca cctctaacgt 120

ctggggcaag aacgtttcag gaaaccaagg gggaccgagg ctcagcgccg aagagaaaga 180

cgccaactgc gggacctgtc gcgcctcccg cgccggggtg gagctgaccc cgccgagtcc 240

cgcccctgcc tgagttcgcc agtggtccag gagccgcttt tttccactcg ggaagacttc 300

agagaagtct cacaaaggac tcggctggct gcttttctca gtgccgaagc cgcgcc 356

atg ctc gtt ctc aga agc ggc ctg acc aag gcg ctt gcc tca cgg acg 404
Met Leu Val Leu Arg Ser Gly Leu Thr Lys Ala Leu Ala Ser Arg Thr
1 5 10 15

ctc gcg cct cag gtg tgt tca tct ttt gct acg ggc cct aga caa tac 452
Leu Ala Pro Gln Val Cys Ser Ser Phe Ala Thr Gly Pro Arg Gln Tyr
17 22 27 32

gat gga acg ttc tat gaa ttt cgt act tat tac ctt aaa cct tca aat 500
Asp Gly Thr Phe Tyr Glu Phe Arg Thr Tyr Tyr Leu Lys Pro Ser Asn
33 38 43 48

atg aat gcg ttc atg gaa aat ctt aag aaa aac att cat ctt cgg acc 548
Met Asn Ala Phe Met Glu Asn Leu Lys Lys Asn Ile His Leu Arg Thr
49 54 59 64

tct tac tct gaa ttg gtt gga ttc tgg agt gta gaa ttt gga ggc aga 596
Ser Tyr Ser Glu Leu Val Gly Phe Trp Ser Val Glu Phe Gly Gly Arg
65 70 75 80

acg aat aaa gtg ttt cat att tgg aag tat gat aat ttt cct cat cga 644
Thr Asn Lys Val Phe His Ile Trp Lys Tyr Asp Asn Phe Pro His Arg
81 86 91 96

gct gaa gtt cgg aaa gcc tta gcc aac tgt aag gaa tgg caa gaa caa 692
Ala Glu Val Arg Lys Ala Leu Ala Asn Cys Lys Glu Trp Gln Glu Gln
97 102 107 112

tct atc att cca aat ttg gct cgc att gat aaa caa gag acg gaa att 740
Ser Ile Ile Pro Asn Leu Ala Arg Ile Asp Lys Gln Glu Thr Glu Ile
113 118 123 128

act tac ctg ata cca tgg tcc aaa tta caa aag cct cca aaa gaa gga 788
Thr Tyr Leu Ile Pro Trp Ser Lys Leu Gln Lys Pro Pro Lys Glu Gly
129 134 139 144

gtc tat gaa cta gct gtt ttt cag atg aaa cct ggt ggg cca gct ctg 836
Val Tyr Glu Leu Ala Val Phe Gln Met Lys Pro Gly Gly Pro Ala Leu
145 150 155 160

```
tgg ggt gat gca ttt gaa aga gca att aat gcc cat gtc aat tta ggc      884
Trp Gly Asp Ala Phe Glu Arg Ala Ile Asn Ala His Val Asn Leu Gly
161                 166                 171                 176

tac aca aaa gta gtt ggt gtt ttc cac aca gaa tat gga gaa ctc aac      932
Tyr Thr Lys Val Val Gly Val Phe His Thr Glu Tyr Gly Glu Leu Asn
177                 182                 187                 192

aga gtt cat gtt ctt tgg tgg aat gaa agt gca gat agt cgt gca gct      980
Arg Val His Val Leu Trp Trp Asn Glu Ser Ala Asp Ser Arg Ala Ala
193                 198                 203                 208

ggg aga cat aag tcc cat gag gat ccc aaa gtt gtg gca gct gtt cgg     1028
Gly Arg His Lys Ser His Glu Asp Pro Lys Val Val Ala Ala Val Arg
209                 214                 219                 224

gaa agt gtc aac tac cta ata tct cag cag aat atg ctt ctg att cct     1076
Glu Ser Val Asn Tyr Leu Ile Ser Gln Gln Asn Met Leu Leu Ile Pro
225                 230                 235                 240

aca tcg ttt tca cca ctg aaa tag ttttctactg aaatacaaaa catttcatta    1130
Thr Ser Phe Ser Pro Leu Lys  *
241                 246

actgctatag gatctgtctg ctaatggggc ttaaattctc ccaagagggt ctcactttta   1190

tttgaaggag ggggggagac aatttgctat gtttcttgca ttatgaaggc tacatctgtg   1250

ctttgtaagt accacttcaa aaaatagttc tgtttacttt ctgcatggta tttcagtgtc   1310

tgtcatacat taaaaatact tgtcactgtt ttaagatctt gactcttcat ttgtttcaga   1370

atagctcttc tactgtattc tgacaactct ttgctttata gcattttgtt gtattcaaat   1430

gataatggta gcatttccat gcttgtgaca gcatttttaa gttattaata tattttatca   1490

acctttccat catgtctgtt ttcctggttt tttttggttg ttttttgacc agtaaaattt   1550

attttgtaat accaaatagg atttaagaaa attaacgttg                         1590
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<210> 303
<211> 1376
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (158)..(1030)

<400> 303

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atttggccct cgaggccaag aattcggcac gagcgaagaa aagggagccg cgcagcgcct     60

acgggagtcc ggcggcagca gccggtaccg gcaaccacgg gcagctctca gggaatctcc    120
```

```
gtcgtgaggc cagaggctcc agtccccgcg agtccag atg cct gtc cag cct cca      175
                                          Met Pro Val Gln Pro Pro
                                            1

agc aaa gac aca gaa gag atg gaa gca gag ggt gat tct gct gct gag      223
Ser Lys Asp Thr Glu Glu Met Glu Ala Glu Gly Asp Ser Ala Ala Glu
  7                  12                  17                  22

atg aat ggg gag gag gaa gag agt gag gag gag cgg agc ggc agc cag      271
Met Asn Gly Glu Glu Glu Glu Ser Glu Glu Glu Arg Ser Gly Ser Gln
 23                  28                  33                  38

aca gag tca gaa gag gag agc tcc gag atg gat gat gag gac tat gag      319
Thr Glu Ser Glu Glu Glu Ser Ser Glu Met Asp Asp Glu Asp Tyr Glu
 39                  44                  49                  54

cga cgc cgc agc gag tgt gtc agt gag atg ctg gac cta gag aag cag      367
Arg Arg Arg Ser Glu Cys Val Ser Glu Met Leu Asp Leu Glu Lys Gln
 55                  60                  65                  70

ttc tcg gag cta aag gag aag ttg ttc agg gaa cga ctg agt cag ctg      415
Phe Ser Glu Leu Lys Glu Lys Leu Phe Arg Glu Arg Leu Ser Gln Leu
 71                  76                  81                  86

cgg ttg cgg ctg gag gaa gtg ggg gct gag aga gcc cct gaa tac acg      463
Arg Leu Arg Leu Glu Glu Val Gly Ala Glu Arg Ala Pro Glu Tyr Thr
 87                  92                  97                 102

gag ccc ctt ggg ggg ctg cag cgg agc ctc aag att cgc att cag gtg      511
Glu Pro Leu Gly Gly Leu Gln Arg Ser Leu Lys Ile Arg Ile Gln Val
103                 108                 113                 118

gca ggg atc tac aag ggc ttc tgt ctg gat gtg atc agg aat aag tac      559
Ala Gly Ile Tyr Lys Gly Phe Cys Leu Asp Val Ile Arg Asn Lys Tyr
119                 124                 129                 134

gaa tgt gag ctg cag gga gcc aaa cag cac ctg gag agt gag aag ctg      607
Glu Cys Glu Leu Gln Gly Ala Lys Gln His Leu Glu Ser Glu Lys Leu
135                 140                 145                 150

ctg ctc tat gac acg ctg cag ggg gag ctg cag gag cgg atc cag agg      655
Leu Leu Tyr Asp Thr Leu Gln Gly Glu Leu Gln Glu Arg Ile Gln Arg
151                 156                 161                 166

ctg gag gag gac cgc cag agc ctg gac ctc agc tct gaa tgg tgg gac      703
Leu Glu Glu Asp Arg Gln Ser Leu Asp Leu Ser Ser Glu Trp Trp Asp
167                 172                 177                 182

gac aaa ctg cac gcc aga ggc agc tcc agg tct tgg gac tcc ctg ccg      751
Asp Lys Leu His Ala Arg Gly Ser Ser Arg Ser Trp Asp Ser Leu Pro
183                 188                 193                 198

ccc agc gag agg aag aag gca cct ctg gtt tct ggc cca tac atc gtg      799
Pro Ser Glu Arg Lys Lys Ala Pro Leu Val Ser Gly Pro Tyr Ile Val
199                 204                 209                 214

tac atg ctt caa gag atc ggc atc ctg gag gac tgg aca gcc atc aaa      847
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```
Tyr Met Leu Gln Glu Ile Gly Ile Leu Glu Asp Trp Thr Ala Ile Lys
215                 220                 225                 230

aag gct agg gca gct gtg tcc cct cag aag aga aaa tcg gat gac ggg      895
Lys Ala Arg Ala Ala Val Ser Pro Gln Lys Arg Lys Ser Asp Asp Gly
231                 236                 241                 246

cgg acc cac agg ccc ctc agg gtc tgc cca gcc agg ctc ctg tgg tgc      943
Arg Thr His Arg Pro Leu Arg Val Cys Pro Ala Arg Leu Leu Trp Cys
247                 252                 257                 262

tgc tgg gcc ctc cca ctc cat ctg gca ctg gtc tgg act cct cct ctg      991
Cys Trp Ala Leu Pro Leu His Leu Ala Leu Val Trp Thr Pro Pro Leu
263                 268                 273                 278

ccc tcc tcg agg cct gca cag ctg tgg ccg tgg agc tga cctgaccagg      1040
Pro Ser Ser Arg Pro Ala Gln Leu Trp Pro Trp Ser  *
279                 284                 289

caaggctgct gtctccatcc ctgagccgcc tgccacctcc cactcctgaa gatccatctc   1100

ttggggctcc cctgacagag aagacagccg aagtcaaagc cacatcctct tgctgatgtt   1160

ggatgcaggc tgtccggcct cagggccagg gagccagttt ccaccgtgcg ggaactctga   1220

gtcagacgtg attatctggg ggtctgtcca ccctggctgg atctggaggc aagatgccag   1280

gccccccaag tgttctcagg gcagttcttg gtgtctgctt ctcagattcc aaggactgga   1340

attaaaacct ttcctgggac tctggaaaaa aaaaaa                              1376
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<210> 304
<211> 3043
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (108)..(2978)

<400> 304

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ccggaattcc cgggtcgacg atttcgtctc caggcagggg aagcagctag ggcagaggcc     60

ctgaagtggg accgtgtctg gcgcattgga agagcagaag gaagctg  atg ggg ctg     116
                                                     Met Gly Leu
                                                       1

gag cag atc atc aaa atc ccc gac cag ccg gac aca ctg tgc ttc cag      164
Glu Gln Ile Ile Lys Ile Pro Asp Gln Pro Asp Thr Leu Cys Phe Gln
  4                   9                  14                  19

att cgt gga gct gcc cca ccg tac gtc tat gct gtg ggg aga ggc tct      212
Ile Arg Gly Ala Ala Pro Pro Tyr Val Tyr Ala Val Gly Arg Gly Ser
 20                  25                  30                  35
```

```
gag gcc atg gct gca ggg ctc tgt gct ggt cag tgc att ctg aag gtc      260
Glu Ala Met Ala Ala Gly Leu Cys Ala Gly Gln Cys Ile Leu Lys Val
 36                  41                  46                  51

aat ggc agc aac gtg atg aac gat ggt gcc cct gag gtc ctg gag cac      308
Asn Gly Ser Asn Val Met Asn Asp Gly Ala Pro Glu Val Leu Glu His
 52                  57                  62                  67

ttc cag gca ttc cgg agt cgg cgc gaa gag gcc ctg ggc ctg tac cag      356
Phe Gln Ala Phe Arg Ser Arg Arg Glu Glu Ala Leu Gly Leu Tyr Gln
 68                  73                  78                  83

tgg atc tac cac acc cat gag gat gcc cag gaa gca cga gcc agt cag      404
Trp Ile Tyr His Thr His Glu Asp Ala Gln Glu Ala Arg Ala Ser Gln
 84                  89                  94                  99

gag gcc tcc act gag gac ccc agt ggc gag cag gcc cag gag gaa gac      452
Glu Ala Ser Thr Glu Asp Pro Ser Gly Glu Gln Ala Gln Glu Glu Asp
100                 105                 110                 115

cag gct gat tca gcc ttc cca ctg ctg tcc ctg ggt ccc cgg ctg agc      500
Gln Ala Asp Ser Ala Phe Pro Leu Leu Ser Leu Gly Pro Arg Leu Ser
116                 121                 126                 131

ctg tgt gag gac agc ccc atg gtc acc ctg act gtg gac aac gtg cac      548
Leu Cys Glu Asp Ser Pro Met Val Thr Leu Thr Val Asp Asn Val His
132                 137                 142                 147

ctg gaa cac ggc gtg gtg tat gag tat gtg agc acg gca ggc gtc agg      596
Leu Glu His Gly Val Val Tyr Glu Tyr Val Ser Thr Ala Gly Val Arg
148                 153                 158                 163

tgc cat gtg ctg gag aag atc gtg gag ccc cgc ggc tgc ttc ggc ctc      644
Cys His Val Leu Glu Lys Ile Val Glu Pro Arg Gly Cys Phe Gly Leu
164                 169                 174                 179

acc gcc aag atc ctc gag gcc ttt gct gcc aat gac agc gtc ttc gtg      692
Thr Ala Lys Ile Leu Glu Ala Phe Ala Ala Asn Asp Ser Val Phe Val
180                 185                 190                 195

gag aac tgc agg cgg ctc atg gcc ctg agc agc gcc atc gtg acc atg      740
Glu Asn Cys Arg Arg Leu Met Ala Leu Ser Ser Ala Ile Val Thr Met
196                 201                 206                 211

ccc cac ttt gag ttc cgc aac atc tgt gac acc aag ctg gag agc att      788
Pro His Phe Glu Phe Arg Asn Ile Cys Asp Thr Lys Leu Glu Ser Ile
212                 217                 222                 227

ggc cag agg att gcc tgc tac cag gag ttt gca gcc caa ctg aag agc      836
Gly Gln Arg Ile Ala Cys Tyr Gln Glu Phe Ala Ala Gln Leu Lys Ser
228                 233                 238                 243

agg gtc agc cca ccc ttc aaa caa gcc ccc ctg gag ccc cac ccg ctg      884
Arg Val Ser Pro Pro Phe Lys Gln Ala Pro Leu Glu Pro His Pro Leu
244                 249                 254                 259
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tgt ggc ctg gac ttc tgc ccc acc aat tgc cac atc aac ctc atg gaa      932
Cys Gly Leu Asp Phe Cys Pro Thr Asn Cys His Ile Asn Leu Met Glu
260                 265                 270                 275

gtg tcc tac ccc aag acc acc ccc tca gtg ggc agg tcc ttc agc atc      980
Val Ser Tyr Pro Lys Thr Thr Pro Ser Val Gly Arg Ser Phe Ser Ile
276                 281                 286                 291

cgc ttt gga cgc aaa ccc tcc ctc atc ggc ctt gac ccg gag caa ggc     1028
Arg Phe Gly Arg Lys Pro Ser Leu Ile Gly Leu Asp Pro Glu Gln Gly
292                 297                 302                 307

cac ctg aac ccc atg tcg tac acc cag cac tgc atc acc acc atg gct     1076
His Leu Asn Pro Met Ser Tyr Thr Gln His Cys Ile Thr Thr Met Ala
308                 313                 318                 323

gct ccc tcc tgg aag tgc ttg cct gct gca gag ggt gat ccc caa ggc     1124
Ala Pro Ser Trp Lys Cys Leu Pro Ala Ala Glu Gly Asp Pro Gln Gly
324                 329                 334                 339

cag ggt ctc cat gat ggc agc ttc ggg cca gcc agt ggg acc ctt ggt     1172
Gln Gly Leu His Asp Gly Ser Phe Gly Pro Ala Ser Gly Thr Leu Gly
340                 345                 350                 355

cag gaa gac cgg ggc ctc agc ttc cta ctc aag cag gag gac cgt gag     1220
Gln Glu Asp Arg Gly Leu Ser Phe Leu Leu Lys Gln Glu Asp Arg Glu
356                 361                 366                 371

atc cag gat gcc tac ctg cag ctc ttc acc aag ctg gat gtg gcc ctg     1268
Ile Gln Asp Ala Tyr Leu Gln Leu Phe Thr Lys Leu Asp Val Ala Leu
372                 377                 382                 387

aag gag atg aag caa tat gtc acc cag atc aac agg ctg ctg tcc acc     1316
Lys Glu Met Lys Gln Tyr Val Thr Gln Ile Asn Arg Leu Leu Ser Thr
388                 393                 398                 403

atc aca gag ccc acc tcg ggt ggg tcc tgc gac gca tcc ttg gct gag     1364
Ile Thr Glu Pro Thr Ser Gly Gly Ser Cys Asp Ala Ser Leu Ala Glu
404                 409                 414                 419

gag gcc tcc tcc ctg ccc ctg gtc agt gaa gag agc gag atg gac agg     1412
Glu Ala Ser Ser Leu Pro Leu Val Ser Glu Glu Ser Glu Met Asp Arg
420                 425                 430                 435

agt gac cat ggg ggc atc aag aag gtg tgc ttc aag gtg gcc gag gag     1460
Ser Asp His Gly Gly Ile Lys Lys Val Cys Phe Lys Val Ala Glu Glu
436                 441                 446                 451

gac cag gag gac tca ggc cac gac acc atg agt tat cgc gac tcc tac     1508
Asp Gln Glu Asp Ser Gly His Asp Thr Met Ser Tyr Arg Asp Ser Tyr
452                 457                 462                 467

agc gag tgt aac agc aat cga gac tcg gtc ctg tcc tac acc agc gtg     1556
Ser Glu Cys Asn Ser Asn Arg Asp Ser Val Leu Ser Tyr Thr Ser Val
468                 473                 478                 483

aga agt aac agc tcc tac ttg ggc agc gac gag atg ggg tct gga gat     1604
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Arg Ser Asn Ser Ser Tyr Leu Gly Ser Asp Glu Met Gly Ser Gly Asp
484                 489                 494                 499

gag ctg ccc tgt gac atg cgg atc cca tct gac aag cag gac aag ctt     1652
Glu Leu Pro Cys Asp Met Arg Ile Pro Ser Asp Lys Gln Asp Lys Leu
500                 505                 510                 515

cat ggc tgc ctg gag cac ctc ttt aac cag gtg gac tcc atc aat gct     1700
His Gly Cys Leu Glu His Leu Phe Asn Gln Val Asp Ser Ile Asn Ala
516                 521                 526                 531

ctc ctc aag ggg cca gtc atg agc cgg gct ttc gaa gag acc aag cat     1748
Leu Leu Lys Gly Pro Val Met Ser Arg Ala Phe Glu Glu Thr Lys His
532                 537                 542                 547

ttc cct atg aac cac agc tta caa gag ttt aaa cag aaa gaa gag tgt     1796
Phe Pro Met Asn His Ser Leu Gln Glu Phe Lys Gln Lys Glu Glu Cys
548                 553                 558                 563

aca atc cgt ggc cgg agc ctg atc cag att agc atc cag gag gac ccc     1844
Thr Ile Arg Gly Arg Ser Leu Ile Gln Ile Ser Ile Gln Glu Asp Pro
564                 569                 574                 579

tgg aac ctc ccc aac tcc atc aag acc ctg gtg gac aac att cag aga     1892
Trp Asn Leu Pro Asn Ser Ile Lys Thr Leu Val Asp Asn Ile Gln Arg
580                 585                 590                 595

tat gtg gaa gat ggg aag aac cag ctg ctc ctg gcc ttg ctg aag tgc     1940
Tyr Val Glu Asp Gly Lys Asn Gln Leu Leu Leu Ala Leu Leu Lys Cys
596                 601                 606                 611

aca gac acg gag ctg cag ctg cgc aga gac gcg atc ttc tgc cag gcc     1988
Thr Asp Thr Glu Leu Gln Leu Arg Arg Asp Ala Ile Phe Cys Gln Ala
612                 617                 622                 627

ctg gtg gcc gcc gtg tgc acc ttc tcc gag cag ctg ctg gcg gcc ctg     2036
Leu Val Ala Ala Val Cys Thr Phe Ser Glu Gln Leu Leu Ala Ala Leu
628                 633                 638                 643

ggc tac cgc tac aac aac aat ggc gag tac gag gag agc agc cgc gac     2084
Gly Tyr Arg Tyr Asn Asn Asn Gly Glu Tyr Glu Glu Ser Ser Arg Asp
644                 649                 654                 659

gcc agc cgc aag tgg ctg gag cag gtg gcg gcc acg ggc gtc ctg ctg     2132
Ala Ser Arg Lys Trp Leu Glu Gln Val Ala Ala Thr Gly Val Leu Leu
660                 665                 670                 675

cac tgc cag tcc ctg ctc tcg cca gcc aca gtg aag gag gaa cgg acc     2180
His Cys Gln Ser Leu Leu Ser Pro Ala Thr Val Lys Glu Glu Arg Thr
676                 681                 686                 691

atg ctg gag gac atc tgg gtg acg ctg tca gag ctg gac aat gtc acc     2228
Met Leu Glu Asp Ile Trp Val Thr Leu Ser Glu Leu Asp Asn Val Thr
692                 697                 702                 707

ttc tcc ttt aag cag ctg gac gag aac tat gtg gcc aac acc aac gtc     2276
Phe Ser Phe Lys Gln Leu Asp Glu Asn Tyr Val Ala Asn Thr Asn Val
```

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708                 713                 718                 723

ttc tac cac att gag ggc agc cgg cag gcg ctg aag gtc atc ttc tac     2324
Phe Tyr His Ile Glu Gly Ser Arg Gln Ala Leu Lys Val Ile Phe Tyr
724                 729                 734                 739

ctc gac agc tac cac ttc tcc aag ctg ccc tcc cgc ctg gag ggt ggg     2372
Leu Asp Ser Tyr His Phe Ser Lys Leu Pro Ser Arg Leu Glu Gly Gly
740                 745                 750                 755

gcc agc ctg agg ctg cac aca gcg ctg ttc acg aaa gtg ctg gag aac     2420
Ala Ser Leu Arg Leu His Thr Ala Leu Phe Thr Lys Val Leu Glu Asn
756                 761                 766                 771

gtg gag ggg ctg cct tct cca ggc agc cag gcc gcg gag gat ttg cag     2468
Val Glu Gly Leu Pro Ser Pro Gly Ser Gln Ala Ala Glu Asp Leu Gln
772                 777                 782                 787

cag gac atc aac gcg cag tcc ctg gag aaa gtt cag cag tat tac cgc     2516
Gln Asp Ile Asn Ala Gln Ser Leu Glu Lys Val Gln Gln Tyr Tyr Arg
788                 793                 798                 803

aaa ctc agg gca ttt tac ctg gag cgg tct aac ctg ccc acg gat gcc     2564
Lys Leu Arg Ala Phe Tyr Leu Glu Arg Ser Asn Leu Pro Thr Asp Ala
804                 809                 814                 819

agc acc acg gcg gta aag ata gac cag ctg atc cgc ccc atc aat gcc     2612
Ser Thr Thr Ala Val Lys Ile Asp Gln Leu Ile Arg Pro Ile Asn Ala
820                 825                 830                 835

ctg gat gag ctc tgc cgc ctc atg aag tcc ttt gtc cac cca aag cct     2660
Leu Asp Glu Leu Cys Arg Leu Met Lys Ser Phe Val His Pro Lys Pro
836                 841                 846                 851

ggt gct gct ggg agt gtg ggc gcc ggc ctc atc ccc atc tcc tcg gag     2708
Gly Ala Ala Gly Ser Val Gly Ala Gly Leu Ile Pro Ile Ser Ser Glu
852                 857                 862                 867

ctc tgc tac cgc ctg ggg gcc tgc cag atg gtc atg tgt ggc aca ggc     2756
Leu Cys Tyr Arg Leu Gly Ala Cys Gln Met Val Met Cys Gly Thr Gly
868                 873                 878                 883

atg cag agg agc acc ctg agc gtg tcc ctg gag cag gcg gcc atc ttg     2804
Met Gln Arg Ser Thr Leu Ser Val Ser Leu Glu Gln Ala Ala Ile Leu
884                 889                 894                 899

gca cgg agc cac ggg ttg ctg ccc aag tgc atc atg cag gcc acg gac     2852
Ala Arg Ser His Gly Leu Leu Pro Lys Cys Ile Met Gln Ala Thr Asp
900                 905                 910                 915

atc atg cgg aag cag ggc cca agg gtg gag att ctg gcc aaa aac ctg     2900
Ile Met Arg Lys Gln Gly Pro Arg Val Glu Ile Leu Ala Lys Asn Leu
916                 921                 926                 931

cga gtc aag gac cag atg ccc cag ggt gct ccg cgc ctc tac cgc ctc     2948
Arg Val Lys Asp Gln Met Pro Gln Gly Ala Pro Arg Leu Tyr Arg Leu
932                 937                 942                 947
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Cys Gln Pro Pro Val Asp Gly Asp Leu  *
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gagccgtgcc gagatgaacc ccagtgcccc cagctacccc atggcctcgc tctacgtggg     360

ggacctccac cccgacgtga ccgaggcgat gctctacggg aaacagcgga agacctaaga     420

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gtccctgcgg agagggaggg ggaagggcag agggggaggg gaaggagccg gaggggcgca     660

cacttggagc tgaagccctc tccagggctc cgggccggtg ccccaacgga cagaggtcga     720

ggaggacccg cagaggtggc agcggccggg ggcaggagg  atg gtg cag aag gag      774
                                            Met Val Gln Lys Glu
                                              1

agt caa gcg acg ttg gag gag cgg gag agc gag ctc agc tcc aac cct      822
Ser Gln Ala Thr Leu Glu Glu Arg Glu Ser Glu Leu Ser Ser Asn Pro
  6                 11                  16                  21

gcc gcc tct gcg ggg gca tcg ctg gag ccg ccg gca gct ccg gca cct      870
Ala Ala Ser Ala Gly Ala Ser Leu Glu Pro Pro Ala Ala Pro Ala Pro
 22                 27                  32                  37

gga gaa gac aac ccc gcc ggg gct ggg gga gcg gcg gtg gcc ggg gct      918
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Gly Glu Asp Asn Pro Ala Gly Ala Gly Gly Ala Ala Val Ala Gly Ala
 38                  43                  48                  53

gca gga ggg gct cgg cgg ttc ctc tgc ggt gtg gtg gaa gga ttt tat      966
Ala Gly Gly Ala Arg Arg Phe Leu Cys Gly Val Val Glu Gly Phe Tyr
 54                  59                  64                  69

gga aga cct tgg gtt atg gaa cag aga aaa gaa ctc ttt aga agg ctc     1014
Gly Arg Pro Trp Val Met Glu Gln Arg Lys Glu Leu Phe Arg Arg Leu
 70                  75                  80                  85

cag aaa tgg gaa tta aat aca tac ttg tat gcc cca aaa gat gac tac     1062
Gln Lys Trp Glu Leu Asn Thr Tyr Leu Tyr Ala Pro Lys Asp Asp Tyr
 86                  91                  96                 101

aaa cat agg atg ttt tgg cga gag atg tat tca gtg gag gaa gct gag     1110
Lys His Arg Met Phe Trp Arg Glu Met Tyr Ser Val Glu Glu Ala Glu
102                 107                 112                 117

caa ctt atg act ctc atc tct gct gca cga gaa tat gag ata gag ttc     1158
Gln Leu Met Thr Leu Ile Ser Ala Ala Arg Glu Tyr Glu Ile Glu Phe
118                 123                 128                 133

atc tat gcg atc tca cct gga ttg gat atc act ttt tct aac ccc aag     1206
Ile Tyr Ala Ile Ser Pro Gly Leu Asp Ile Thr Phe Ser Asn Pro Lys
134                 139                 144                 149

gaa gta tcc aca ttg aaa cgt aaa ttg gac cag gtt tct cag ttt ggg     1254
Glu Val Ser Thr Leu Lys Arg Lys Leu Asp Gln Val Ser Gln Phe Gly
150                 155                 160                 165

tgc aga tca ttt gct ttg ctt ttt gat gat ata gac cat aat atg tgt     1302
Cys Arg Ser Phe Ala Leu Leu Phe Asp Asp Ile Asp His Asn Met Cys
166                 171                 176                 181

gca gca gac aaa gag gta ttc agt tct ttt gct cat gcc caa gtc tcc     1350
Ala Ala Asp Lys Glu Val Phe Ser Ser Phe Ala His Ala Gln Val Ser
182                 187                 192                 197

atc aca aat gaa atc tat cag tac cta gga gag cca gaa act ttc ctc     1398
Ile Thr Asn Glu Ile Tyr Gln Tyr Leu Gly Glu Pro Glu Thr Phe Leu
198                 203                 208                 213

ttc tgt ccc aca gaa tac tgt ggc act ttc tgt tat cca aat gtg tct     1446
Phe Cys Pro Thr Glu Tyr Cys Gly Thr Phe Cys Tyr Pro Asn Val Ser
214                 219                 224                 229

cag tct cca tat tta agg act gtg ggt gaa aag ctt cta cct gga att     1494
Gln Ser Pro Tyr Leu Arg Thr Val Gly Glu Lys Leu Leu Pro Gly Ile
230                 235                 240                 245

gaa gtg ctt tgg aca ggt ccc aaa gtt gtt tct aaa gaa att cca gta     1542
Glu Val Leu Trp Thr Gly Pro Lys Val Val Ser Lys Glu Ile Pro Val
246                 251                 256                 261

gag tcc atc gaa gag gtt tct aag att att aag aga gct cca gta atc     1590
Glu Ser Ile Glu Glu Val Ser Lys Ile Ile Lys Arg Ala Pro Val Ile
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262                 267                 272                 277

tgg gat aac att cat gct aat gat tat gat cag aag aga ctg ttt ctg     1638
Trp Asp Asn Ile His Ala Asn Asp Tyr Asp Gln Lys Arg Leu Phe Leu
278                 283                 288                 293

ggc ccg tac aaa gga aga tcc aca gaa ctc atc cca cgg tta aaa gga     1686
Gly Pro Tyr Lys Gly Arg Ser Thr Glu Leu Ile Pro Arg Leu Lys Gly
294                 299                 304                 309

gtc ctc act aat cca aat tgt gaa ttt gaa gcc aac tac gtt gct atc     1734
Val Leu Thr Asn Pro Asn Cys Glu Phe Glu Ala Asn Tyr Val Ala Ile
310                 315                 320                 325

cac acc ctt gcc acc tgg tac aaa tca aac atg aat gga gtg aga aaa     1782
His Thr Leu Ala Thr Trp Tyr Lys Ser Asn Met Asn Gly Val Arg Lys
326                 331                 336                 341

gat gta gtg atg act gac agt gaa gat agt act gtg tcc atc cag ata     1830
Asp Val Val Met Thr Asp Ser Glu Asp Ser Thr Val Ser Ile Gln Ile
342                 347                 352                 357

aaa tta gaa aat gaa ggc agt gat gaa gat att gaa act gat gta ctc     1878
Lys Leu Glu Asn Glu Gly Ser Asp Glu Asp Ile Glu Thr Asp Val Leu
358                 363                 368                 373

tat agt cca cag atg gct cta aag cta gca tta aca gaa tgg ttg caa     1926
Tyr Ser Pro Gln Met Ala Leu Lys Leu Ala Leu Thr Glu Trp Leu Gln
374                 379                 384                 389

gag ttt ggt gtg cct cat caa tac agc agt agg caa gtt gca cac agt     1974
Glu Phe Gly Val Pro His Gln Tyr Ser Ser Arg Gln Val Ala His Ser
390                 395                 400                 405

gga gct aaa gca agt gta gtt gat ggg act cct tta gtt gca gca ccc     2022
Gly Ala Lys Ala Ser Val Val Asp Gly Thr Pro Leu Val Ala Ala Pro
406                 411                 416                 421

tct tta aat gcc aca acc gta gta aca aca gtt tat cag gag ccc att     2070
Ser Leu Asn Ala Thr Thr Val Val Thr Thr Val Tyr Gln Glu Pro Ile
422                 427                 432                 437

atg agc cag gga gca gcc ttg agt ggt gag cct act act ctg acc aag     2118
Met Ser Gln Gly Ala Ala Leu Ser Gly Glu Pro Thr Thr Leu Thr Lys
438                 443                 448                 453

gaa gaa gaa aag aaa cag cct gat gaa gaa ccc atg gac atg gtg gtg     2166
Glu Glu Glu Lys Lys Gln Pro Asp Glu Glu Pro Met Asp Met Val Val
454                 459                 464                 469

gaa aaa caa gaa gaa acg gac cac aag aat gac aat caa ata ctg agt     2214
Glu Lys Gln Glu Glu Thr Asp His Lys Asn Asp Asn Gln Ile Leu Ser
470                 475                 480                 485

gaa att gtt gaa gcg aaa atg gca gag gaa ttg aaa cca atg gac act     2262
Glu Ile Val Glu Ala Lys Met Ala Glu Glu Leu Lys Pro Met Asp Thr
486                 491                 496                 501
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gat aaa gag agc ata gct gaa tca aaa tcc cca gag atg tcc atg caa      2310
Asp Lys Glu Ser Ile Ala Glu Ser Lys Ser Pro Glu Met Ser Met Gln
502                 507                 512                 517

gaa gat tgt att agt gac att gcc ccc atg caa act gat gaa cag aca      2358
Glu Asp Cys Ile Ser Asp Ile Ala Pro Met Gln Thr Asp Glu Gln Thr
518                 523                 528                 533

aac aag gag cag ttt gtg cca ggt cca aat gaa aag cct ttg tac act      2406
Asn Lys Glu Gln Phe Val Pro Gly Pro Asn Glu Lys Pro Leu Tyr Thr
534                 539                 544                 549

gcg gaa cca gtg acc ctg gag gat ttg cag tta ctt gct gat cta ttc      2454
Ala Glu Pro Val Thr Leu Glu Asp Leu Gln Leu Leu Ala Asp Leu Phe
550                 555                 560                 565

tac ctt cct tac gag cat gga ccc aaa gga gca cag atg tta cgg gaa      2502
Tyr Leu Pro Tyr Glu His Gly Pro Lys Gly Ala Gln Met Leu Arg Glu
566                 571                 576                 581

ttt caa tgg ctt cga gca aat agt agt gtt gtc agt gtc aat tgc aaa      2550
Phe Gln Trp Leu Arg Ala Asn Ser Ser Val Val Ser Val Asn Cys Lys
582                 587                 592                 597

gga aaa gac tct gaa aaa att gaa gaa tgg cgg tca cga gca gcc aag      2598
Gly Lys Asp Ser Glu Lys Ile Glu Glu Trp Arg Ser Arg Ala Ala Lys
598                 603                 608                 613

ttt gaa gag atg tgt gga cta gtg atg gga atg ttc act cgg ctc tcc      2646
Phe Glu Glu Met Cys Gly Leu Val Met Gly Met Phe Thr Arg Leu Ser
614                 619                 624                 629

aat tgt gcc aac agg aca att ctt tat gac atg tac tcc tat gtt tgg      2694
Asn Cys Ala Asn Arg Thr Ile Leu Tyr Asp Met Tyr Ser Tyr Val Trp
630                 635                 640                 645

gat atc aag agt ata atg tct atg gtg aag tct ttt gta cag tgg tta      2742
Asp Ile Lys Ser Ile Met Ser Met Val Lys Ser Phe Val Gln Trp Leu
646                 651                 656                 661

ggg tgt cgt agt cat tct tca gca caa ttc tta att gga gac caa gaa      2790
Gly Cys Arg Ser His Ser Ser Ala Gln Phe Leu Ile Gly Asp Gln Glu
662                 667                 672                 677

ccc tgg gcc ttt aga ggt ggt cta gca gga gag ttc cag cgt ttg ctg      2838
Pro Trp Ala Phe Arg Gly Gly Leu Ala Gly Glu Phe Gln Arg Leu Leu
678                 683                 688                 693

cca att gat ggg gca aat gat ctc ttt ttt cag cca cct cca ctg act      2886
Pro Ile Asp Gly Ala Asn Asp Leu Phe Phe Gln Pro Pro Pro Leu Thr
694                 699                 704                 709

cct acc tcc aaa gtt tat act atc aga cct tat ttt cct aag gat gag      2934
Pro Thr Ser Lys Val Tyr Thr Ile Arg Pro Tyr Phe Pro Lys Asp Glu
710                 715                 720                 725
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gca tcc gtg tac aag att tgc aga gaa atg tat gac gat gga gtg ggt     2982
Ala Ser Val Tyr Lys Ile Cys Arg Glu Met Tyr Asp Asp Gly Val Gly
726                 731                 736                 741

tta ccc ttt caa agt cag cct gat ctt att gga gac aag tta gta gga     3030
Leu Pro Phe Gln Ser Gln Pro Asp Leu Ile Gly Asp Lys Leu Val Gly
742                 747                 752                 757

ggg ctg ctt tcc ctc agc ctg gat cac tgc ttt gtc cta gaa gat gaa     3078
Gly Leu Leu Ser Leu Ser Leu Asp His Cys Phe Val Leu Glu Asp Glu
758                 763                 768                 773

gat ggc ata tgt ggt tat gcc ttg ggc act gta gat gtg acc ccc ttt     3126
Asp Gly Ile Cys Gly Tyr Ala Leu Gly Thr Val Asp Val Thr Pro Phe
774                 779                 784                 789

att aaa aaa tgt aaa att tcc tgg atc ccc ttc atg cag gag aag tat     3174
Ile Lys Lys Cys Lys Ile Ser Trp Ile Pro Phe Met Gln Glu Lys Tyr
790                 795                 800                 805

acc aag cca aat ggt gac aag gaa ctc tct gag gct gag aaa ata atg     3222
Thr Lys Pro Asn Gly Asp Lys Glu Leu Ser Glu Ala Glu Lys Ile Met
806                 811                 816                 821

ttg agt ttc cat gaa gaa cag gaa gta ctg cca gaa act ttc ctt gct     3270
Leu Ser Phe His Glu Glu Gln Glu Val Leu Pro Glu Thr Phe Leu Ala
822                 827                 832                 837

aat ttc cct tct ctg ata aag atg gac att cac aaa aaa gta act gac     3318
Asn Phe Pro Ser Leu Ile Lys Met Asp Ile His Lys Lys Val Thr Asp
838                 843                 848                 853

cca agt gtg gcc aaa agc atg atg gct tgc ctc ctg tct tca ctg aag     3366
Pro Ser Val Ala Lys Ser Met Met Ala Cys Leu Leu Ser Ser Leu Lys
854                 859                 864                 869

gct aat ggc tcc cgg gga gct ttc tgt gaa gtg aga cca gat gat aaa     3414
Ala Asn Gly Ser Arg Gly Ala Phe Cys Glu Val Arg Pro Asp Asp Lys
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aga att ctg gaa ttt tac agc aag tta gga tgt ttt gaa att gca aaa     3462
Arg Ile Leu Glu Phe Tyr Ser Lys Leu Gly Cys Phe Glu Ile Ala Lys
886                 891                 896                 901

atg gaa gga ttt cca aag gat gtg gtt ata ctt ggt cgg agc ctg tga     3510
Met Glu Gly Phe Pro Lys Asp Val Val Ile Leu Gly Arg Ser Leu  *
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131                 136                 141                 146

acg acc att gtg gtg ccc aag ccc ttc cgc ccg ata ctt ggc ctg cat      776
Thr Thr Ile Val Val Pro Lys Pro Phe Arg Pro Ile Leu Gly Leu His
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ctg gac ttg gga atc ctg tac tat gtc tac atg ggg ctg ctg gca gtg      824
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Phe Cys Thr Asn Ala Ile Asn Ile Leu Ala Gly Ile Asn Gly Leu Glu
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gct ggc cag tca cta gtc att tct gct tcc atc att gtc ttc aac ctg      920
Ala Gly Gln Ser Leu Val Ile Ser Ala Ser Ile Ile Val Phe Asn Leu
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gta gag ttg gaa ggt gat tgt cgg gat gat cat gtc ttt tcc ctc tac      968
Val Glu Leu Glu Gly Asp Cys Arg Asp Asp His Val Phe Ser Leu Tyr
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ttc atg ata ccc ttt ttt ttc acc act ttg gga ttg ctc tac cac aac     1016
Phe Met Ile Pro Phe Phe Phe Thr Thr Leu Gly Leu Leu Tyr His Asn
227                 232                 237                 242

tgg tac cca tca cgg gtg ttt gtg gga gat acc ttc tgt tac ttt gct     1064
Trp Tyr Pro Ser Arg Val Phe Val Gly Asp Thr Phe Cys Tyr Phe Ala
243                 248                 253                 258

ggc atg acc ttt gcc gtg gtg ggc atc ttg gga cac ttc agc aag acc     1112
Gly Met Thr Phe Ala Val Val Gly Ile Leu Gly His Phe Ser Lys Thr
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atg cta cta ttc ttc atg ccc cag gtg ttc aac ttc ctc tac tca ctg     1160
Met Leu Leu Phe Phe Met Pro Gln Val Phe Asn Phe Leu Tyr Ser Leu
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cct cag ctc ctg cat atc atc ccc tgc cct cgc cac cgc ata ccc aga     1208
Pro Gln Leu Leu His Ile Ile Pro Cys Pro Arg His Arg Ile Pro Arg
291                 296                 301                 306

ctc aat atc aag aca ggc aaa ctg gag atg agc tat tcc aag ttc aag     1256
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acc aag agc ctc tct ttc ttg ggc acc ttt att tta aag gtg gca gag     1304
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323                 328                 333                 338

agc ctc cag ctg gtg aca gta cac cag agt gag act gaa gat ggt gaa     1352
Ser Leu Gln Leu Val Thr Val His Gln Ser Glu Thr Glu Asp Gly Glu
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atcattggca tcctgggcgt ttcttgccct ctgctgacta ctgattggat tttacctatg 1729

gctttctgca acttgctact ctctccctct ccatcccatc tttgcagcct catagggtgg 1789

gatacagcag ctttttttgc agttatccac actcacattt cagagtcctg actctcaagg 1849

aaccactggt ttttgggata gaacttgggc cagggctagg aacacaggct ccacggtgac 1909

atgtcatttg attgtaaatt aagtgttctg attagtaaga actaagcagg gggccacatg 1969

ctctcaatgg agacaataaa gtgttgtctt tttcttattg ttttaaaaaa aaaaaa 2025

<210> 307
<211> 1004
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (300)..(623)

<400> 307
atccctagtt ccagtgtggt ggaattccaa agttgccagg acttcccagg gaagctgcag 60

cagctctcgg tgccagcttc ctggcggtgg ctcctctccc agtgacagtg cgtggctccg 120

gcctggcagg aatggcagtg acatgcgatc caaaggcctt cctgtccatc tgctttgtca 180

ccttggtctt cctgcagctc ccactggcca gcatctgtca aaactgaggg acagactcct 240

gtgcaagtcg agggaaagct gactttgatg tcactgggcc tcatgcccct attctggct 299

atg gct ggg gga cac gtg gag tta cag tgc cag ctg ttc ccc aat atc 347

```
Met Ala Gly Gly His Val Glu Leu Gln Cys Gln Leu Phe Pro Asn Ile
  1               5                  10                  15

agt gcc gag gac atg gag ctg agg tgg tac agg tgc cag ccc tcc cta      395
Ser Ala Glu Asp Met Glu Leu Arg Trp Tyr Arg Cys Gln Pro Ser Leu
 17                  22                  27                  32

gct gtg cac atg cat gag aga ggg atg gac atg gat gga gag caa aag      443
Ala Val His Met His Glu Arg Gly Met Asp Met Asp Gly Glu Gln Lys
 33                  38                  43                  48

tgg cag tac aga gga agg acc acc ttc atg agt gac cac gtg gcc agg      491
Trp Gln Tyr Arg Gly Arg Thr Thr Phe Met Ser Asp His Val Ala Arg
 49                  54                  59                  64

ggc aag gcc atg gtg agg agt cac agg gtc acc acc ttt gac aac agg      539
Gly Lys Ala Met Val Arg Ser His Arg Val Thr Thr Phe Asp Asn Arg
 65                  70                  75                  80

aca tac tgc tgc cgc ttc aag gat ggt gta aag ttc ggc gag gcc act      587
Thr Tyr Cys Cys Arg Phe Lys Asp Gly Val Lys Phe Gly Glu Ala Thr
 81                  86                  91                  96

gtg cag gtg cag gtg gca ggt aag gct ggt ggc tag ctgg ctgtcagtct      637
Val Gln Val Gln Val Ala Gly Lys Ala Gly Gly  *
 97                 102                 107

acttccaggc atggccttgg ggcccagcgt gttcaggtgg agggcttttc agtagggtga    697

gagtgcactc tcccagctgc cgtgctggcc tgcactgctc ccgggaaggc acagcggtga    757

aggcagagcc accttcctca tcttcctttc cctccttaca ccagtggcct ggaaagtgaa    817

gggaagggaa agagagagat ggggggaatg agagagcccc agagaagaag agatagaatg    877

agaaagaagc agggagagcc agacagaggt ggaaagagag atggagaggg gaagagagaa    937

aaagaaaaag aaagaaagaa agaaagaaag actcgtgccg aattcttggc ctcgagggcc    997

aaattcc                                                             1004
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<210> 308
<211> 2226
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (110)..(1516)

<400> 308

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taagcttgcg gccgcggaag gggagcagct gagaaaggag ggccgctgca ggcggggttc     60

gaaccgtggg gtctgggctg ctcccgcgga gggcctgggc ggacgcggg    atg ctg     115
```

```
                                                          Met Leu
                                                            1

ggg gtc cgc tgc ctg ctg cgg tcc gtg cgc ttc tgt tcc tcc gcc ccc      163
Gly Val Arg Cys Leu Leu Arg Ser Val Arg Phe Cys Ser Ser Ala Pro
  3                   8                  13                  18

ttc ccc aag cac aaa cct tca gcc aaa ctg agc gtg cgg gac gct ctc      211
Phe Pro Lys His Lys Pro Ser Ala Lys Leu Ser Val Arg Asp Ala Leu
 19                  24                  29                  34

ggg gct cag aac gcg agt ggg gag cgc att aag atc cag gga tgg att      259
Gly Ala Gln Asn Ala Ser Gly Glu Arg Ile Lys Ile Gln Gly Trp Ile
 35                  40                  45                  50

cgt tct gtc cga tcc cag aag gaa gtc ttg ttc ctg cat gta aat gat      307
Arg Ser Val Arg Ser Gln Lys Glu Val Leu Phe Leu His Val Asn Asp
 51                  56                  61                  66

ggg tca tct ttg gaa agc ctt cag gtt gtt gca gat tca ggc ctt gac      355
Gly Ser Ser Leu Glu Ser Leu Gln Val Val Ala Asp Ser Gly Leu Asp
 67                  72                  77                  82

agt aga gaa tta act ttt ggg agt tct gtg gaa gta caa ggg cag ctg      403
Ser Arg Glu Leu Thr Phe Gly Ser Ser Val Glu Val Gln Gly Gln Leu
 83                  88                  93                  98

ata aaa agt cca tcc aaa agg caa aat gtg gaa ctg aag gca gaa aaa      451
Ile Lys Ser Pro Ser Lys Arg Gln Asn Val Glu Leu Lys Ala Glu Lys
 99                 104                 109                 114

att aaa gtt att gga aat tgt gat gcc aag gat ttc ccc atc aaa tat      499
Ile Lys Val Ile Gly Asn Cys Asp Ala Lys Asp Phe Pro Ile Lys Tyr
115                 120                 125                 130

aaa gag agg cat cct ctg gag tac ctg cga caa tat cct cac ttt agg      547
Lys Glu Arg His Pro Leu Glu Tyr Leu Arg Gln Tyr Pro His Phe Arg
131                 136                 141                 146

tgt agg act aac gtt ctg ggt tct ata ttg agg att cgc agt gaa gcg      595
Cys Arg Thr Asn Val Leu Gly Ser Ile Leu Arg Ile Arg Ser Glu Ala
147                 152                 157                 162

aca gct gct att cat tct ttc ttt aag gac agt ggc ttt gta cat att      643
Thr Ala Ala Ile His Ser Phe Phe Lys Asp Ser Gly Phe Val His Ile
163                 168                 173                 178

cat act cca ata atc aca tcc aat gac tct gag gga gct gga gaa ctt      691
His Thr Pro Ile Ile Thr Ser Asn Asp Ser Glu Gly Ala Gly Glu Leu
179                 184                 189                 194

ttt caa ctt gaa cct tca ggc aaa ctt aag gta cct gag gag aat ttc      739
Phe Gln Leu Glu Pro Ser Gly Lys Leu Lys Val Pro Glu Glu Asn Phe
195                 200                 205                 210

ttc aat gtt cct gct ttc tta act gtc tca gga caa ctt cat cta gaa      787
Phe Asn Val Pro Ala Phe Leu Thr Val Ser Gly Gln Leu His Leu Glu
```

```
211                 216                 221                 226

gtg atg tca gga gct ttt act caa gtg ttt acc ttt ggt ccg acc ttc      835
Val Met Ser Gly Ala Phe Thr Gln Val Phe Thr Phe Gly Pro Thr Phe
227                 232                 237                 242

cga gct gaa aat tct cag agc cgg agg cac ctg gca gag ttt tat atg      883
Arg Ala Glu Asn Ser Gln Ser Arg Arg His Leu Ala Glu Phe Tyr Met
243                 248                 253                 258

ata gaa gca gag att tct ttt gtt gac agc ctt caa gat ctt atg cag      931
Ile Glu Ala Glu Ile Ser Phe Val Asp Ser Leu Gln Asp Leu Met Gln
259                 264                 269                 274

gtt ata gag gaa ctg ttc aag gct aca aca atg atg gtt ctc tca aaa      979
Val Ile Glu Glu Leu Phe Lys Ala Thr Thr Met Met Val Leu Ser Lys
275                 280                 285                 290

tgt cct gaa gat gtt gaa ctc tgt cac aaa ttc ata gca cct ggc caa     1027
Cys Pro Glu Asp Val Glu Leu Cys His Lys Phe Ile Ala Pro Gly Gln
291                 296                 301                 306

aag gac aga tta gaa cat atg cta aaa aac aac ttt tta atc att tct     1075
Lys Asp Arg Leu Glu His Met Leu Lys Asn Asn Phe Leu Ile Ile Ser
307                 312                 317                 322

tat act gaa gca gtg gag atc tta aag caa gca tcc cag aac ttc acc     1123
Tyr Thr Glu Ala Val Glu Ile Leu Lys Gln Ala Ser Gln Asn Phe Thr
323                 328                 333                 338

ttt acc cca gag tgg ggt gct gac cta cgg act gaa cat gaa aag tac     1171
Phe Thr Pro Glu Trp Gly Ala Asp Leu Arg Thr Glu His Glu Lys Tyr
339                 344                 349                 354

ctg gtg aag cac tgt ggc aac ata cct gtc ttc gtt att aat tat cca     1219
Leu Val Lys His Cys Gly Asn Ile Pro Val Phe Val Ile Asn Tyr Pro
355                 360                 365                 370

tta aca ctc aag cct ttc tac atg agg gat aat gaa gat ggc cct cag     1267
Leu Thr Leu Lys Pro Phe Tyr Met Arg Asp Asn Glu Asp Gly Pro Gln
371                 376                 381                 386

cac acg gtt gct gct gtt gat ctt ctg gtt cct gga gtt ggg gaa ctc     1315
His Thr Val Ala Ala Val Asp Leu Leu Val Pro Gly Val Gly Glu Leu
387                 392                 397                 402

ttt gga gga ggc ctc aga gaa gaa cga tac cat ttc tta gag gag cgc     1363
Phe Gly Gly Gly Leu Arg Glu Glu Arg Tyr His Phe Leu Glu Glu Arg
403                 408                 413                 418

tta gcc agg tat ctg gac ctt cgt cga ttt gga tct gtg cca cat gga     1411
Leu Ala Arg Tyr Leu Asp Leu Arg Arg Phe Gly Ser Val Pro His Gly
419                 424                 429                 434

ggt ttt ggg atg gga ttt gaa cgc tac ctg cag tgc atc ttg ggt gtt     1459
Gly Phe Gly Met Gly Phe Glu Arg Tyr Leu Gln Cys Ile Leu Gly Val
435                 440                 445                 450
```

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gac aat atc aaa gat gtt atc cct ttc cca agg ttt cct cat tca tgc     1507
Asp Asn Ile Lys Asp Val Ile Pro Phe Pro Arg Phe Pro His Ser Cys
451                 456                 461                 466

ctt tta tag ctggaag attggttaag gaaaagcacc ccccatggca gagacactgc     1563
Leu Leu  *
467

acatgattgt gcatacagca gaatgcatgt ttggatttta gaaatgcaga tttcaatatg   1623

taattgttgt gccataagat atcatagaaa aaatataagt ggttgtgatt ttcttagaaa   1683

gttgagggta tttcacgtaa ggatgagctc ccgcaagaag aggtacttat agcaagggga   1743

ctctcaaatc cattacctca attaagaaat gaagaaattg aattagtctc aaagtttctt   1803

ttaaactcta aaacagaatg agataatgta ttttacgttg tctataatca ttaaatcact   1863

ccctgtgtaa tttgtgagaa ccatctagta gctcgaaata aaataatgtt gcatcttttc   1923

tcccttgcca tatactttgt gataaatcct tatctcattt tcagtacttc attaaacatt   1983

gcagaaaaaa atattcctta aggtcttaat tgatttaaag aagtagctat tctgaattga   2043

aatctccttt cattgaactg gatgaaaaaa tcatgtttaa taactgttgc ttttcaattt   2103

tcaaagctgt tgagatatta cattaagtat ttcaactctt taatcactgt tgttataatt   2163

tgtttatatt tgatgtttat aatttgtcta ataaaataga ttttttttaat agaaaaaaaa   2223

aaa                                                                 2226
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<210> 309
<211> 521
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (112)..(441)

<400> 309

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cttcagcgct ctgtgtcctc tgctcctaga ggtccaggct ctgtggccct gtgacctgca     60

ggtattggga gatctacagc taagacgcca ggaacctctg gaagcctaga a atg gag     117
                                                          Met Glu
                                                            1

aac ctg aag tct gga gtg tat cct ctc aag gaa gca agt gga tgc cct     165
Asn Leu Lys Ser Gly Val Tyr Pro Leu Lys Glu Ala Ser Gly Cys Pro
  3                   8                  13                  18

ggg gct gac agg aat ctt ctg gtg tac tct ttt tat gaa aag ggg cca     213
```

```
Gly Ala Asp Arg Asn Leu Leu Val Tyr Ser Phe Tyr Glu Lys Gly Pro
 19                  24                  29                  34

ttg aca ttt agg gat gtg gcc ata gaa ttt tct ctg gag gag tgg caa      261
Leu Thr Phe Arg Asp Val Ala Ile Glu Phe Ser Leu Glu Glu Trp Gln
 35                  40                  45                  50

tgc ctg gac act gct cag cag gat ttg tat aga aaa gtg atg tta gag      309
Cys Leu Asp Thr Ala Gln Gln Asp Leu Tyr Arg Lys Val Met Leu Glu
 51                  56                  61                  66

aac tac aga aac ctg gtc ttc ttg gca ggt att gct gtt tct aag cca      357
Asn Tyr Arg Asn Leu Val Phe Leu Ala Gly Ile Ala Val Ser Lys Pro
 67                  72                  77                  82

gac ctg atc acc tgt cta gag caa gga aaa gag ccc tgg aat atg aag      405
Asp Leu Ile Thr Cys Leu Glu Gln Gly Lys Glu Pro Trp Asn Met Lys
 83                  88                  93                  98

aga cat gcg atg gta gat caa ccc cca ggt agg tga gagt gaacacaaca      455
Arg His Ala Met Val Asp Gln Pro Pro Gly Arg  *
 99                  104                 109

gacgacatga atgagaggtc caaaaaaaaa aaaaaaaaag atctttaatt aagcggccca    515

agctta                                                              521
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<210> 310
<211> 1992
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (176)..(1936)

<400> 310

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atttaatacg acgtgctata gggaatttgg ccctcgaggc caagaattcg gcacgagaac     60

ccgagtgaca cgttgaattt gccataatca aggaaacctt ttccgggtgg ggatctctga    120

aattactcag tgagcaaccc taattaacct gatttttttgc tgataatcac tctca atg    178
                                                              Met
                                                                1

gaa tca aat cac aaa tcc ggg gat gga ttg agc ggc act cag aag gaa      226
Glu Ser Asn His Lys Ser Gly Asp Gly Leu Ser Gly Thr Gln Lys Glu
  2                   7                  12                  17

gca gcc ctc cgc gca ctg gtc cag cgc aca gga tat agc ttg gtc cag      274
Ala Ala Leu Arg Ala Leu Val Gln Arg Thr Gly Tyr Ser Leu Val Gln
 18                  23                  28                  33

gaa aat gga caa aga aaa tat ggt ggc cct cca cct ggt tgg gat gct      322
```

```
Glu Asn Gly Gln Arg Lys Tyr Gly Gly Pro Pro Pro Gly Trp Asp Ala
 34                  39                  44                  49

gca ccc cct gaa agg ggc tgt gaa att ttt att gga aaa ctt ccc cga      370
Ala Pro Pro Glu Arg Gly Cys Glu Ile Phe Ile Gly Lys Leu Pro Arg
 50                  55                  60                  65

gac ctt ttt gag gat gag ctt ata cca tta tgt gaa aaa atc ggt aaa      418
Asp Leu Phe Glu Asp Glu Leu Ile Pro Leu Cys Glu Lys Ile Gly Lys
 66                  71                  76                  81

att tat gaa atg aga atg atg atg gat ttt aat ggc aac aat aga gga      466
Ile Tyr Glu Met Arg Met Met Met Asp Phe Asn Gly Asn Asn Arg Gly
 82                  87                  92                  97

tat gca ttt gta aca ttt tca aat aaa gtg gaa gcc aag aat gca atc      514
Tyr Ala Phe Val Thr Phe Ser Asn Lys Val Glu Ala Lys Asn Ala Ile
 98                 103                 108                 113

aag caa ctt aat aat tat gaa att aga aat ggg cgc ctc tta ggg gtt      562
Lys Gln Leu Asn Asn Tyr Glu Ile Arg Asn Gly Arg Leu Leu Gly Val
114                 119                 124                 129

tgt gcc agt gtg gac aac tgc cga tta ttt gtt ggg ggc atc cca aaa      610
Cys Ala Ser Val Asp Asn Cys Arg Leu Phe Val Gly Gly Ile Pro Lys
130                 135                 140                 145

acc aaa aag aga gaa gaa atc tta tcg gag atg aaa aag gtt act gaa      658
Thr Lys Lys Arg Glu Glu Ile Leu Ser Glu Met Lys Lys Val Thr Glu
146                 151                 156                 161

ggt gtt gtc gat gtc atc gtc tac cca agc gct gca gat aaa acc aaa      706
Gly Val Val Asp Val Ile Val Tyr Pro Ser Ala Ala Asp Lys Thr Lys
162                 167                 172                 177

aac cga ggc ttt gcc ttc gtg gag tat gag agt cat cga gca gct gcc      754
Asn Arg Gly Phe Ala Phe Val Glu Tyr Glu Ser His Arg Ala Ala Ala
178                 183                 188                 193

atg gcg agg agg aaa ctg cta cca gga aga att cag tta tgg gga cat      802
Met Ala Arg Arg Lys Leu Leu Pro Gly Arg Ile Gln Leu Trp Gly His
194                 199                 204                 209

ggt att gca gta gac tgg gca gag cca gaa gta gaa gtt gat gaa gat      850
Gly Ile Ala Val Asp Trp Ala Glu Pro Glu Val Glu Val Asp Glu Asp
210                 215                 220                 225

aca atg tct tca gtg aaa atc cta tat gta aga aat ctt atg ctg tct      898
Thr Met Ser Ser Val Lys Ile Leu Tyr Val Arg Asn Leu Met Leu Ser
226                 231                 236                 241

acc tct gaa gag atg att gaa aag gaa ttc aac aat atc aaa cca ggt      946
Thr Ser Glu Glu Met Ile Glu Lys Glu Phe Asn Asn Ile Lys Pro Gly
242                 247                 252                 257

gct gtg gag agg gtg aag aaa att cga gac tat gct ttt gtg cac ttc      994
Ala Val Glu Arg Val Lys Lys Ile Arg Asp Tyr Ala Phe Val His Phe
```

```
258                 263                 268                 273

agt aac cga gaa gat gca gtt gag gct atg aaa gct tta aat ggc aag     1042
Ser Asn Arg Glu Asp Ala Val Glu Ala Met Lys Ala Leu Asn Gly Lys
274                 279                 284                 289

gtg ctg gat ggt tcc ccc att gaa gtc acc cta gca aaa cca gtg gac     1090
Val Leu Asp Gly Ser Pro Ile Glu Val Thr Leu Ala Lys Pro Val Asp
290                 295                 300                 305

aag gac agt tat gtt agg tat acc cga ggc aca ggt gga agg ggc acc     1138
Lys Asp Ser Tyr Val Arg Tyr Thr Arg Gly Thr Gly Gly Arg Gly Thr
306                 311                 316                 321

atg ctg caa gga gag tat acc tac tct ttg ggc caa gtt tat gat ccc     1186
Met Leu Gln Gly Glu Tyr Thr Tyr Ser Leu Gly Gln Val Tyr Asp Pro
322                 327                 332                 337

acc aca acc tac ctt gga gct cct gtc ttc tat gcc ccc cag acc tat     1234
Thr Thr Thr Tyr Leu Gly Ala Pro Val Phe Tyr Ala Pro Gln Thr Tyr
338                 343                 348                 353

gca gca att ccc agt ctt cat ttc cca gcc acc aaa gga cat ctc agc     1282
Ala Ala Ile Pro Ser Leu His Phe Pro Ala Thr Lys Gly His Leu Ser
354                 359                 364                 369

aac aga gcc att atc cga gcc cct tct gtt aga ggg gct gcg gga gtg     1330
Asn Arg Ala Ile Ile Arg Ala Pro Ser Val Arg Gly Ala Ala Gly Val
370                 375                 380                 385

aga gga ctg ggc ggc cgt ggc tat ttg gca tac aca ggc ctg ggt cga     1378
Arg Gly Leu Gly Gly Arg Gly Tyr Leu Ala Tyr Thr Gly Leu Gly Arg
386                 391                 396                 401

gga tac cag gtc aaa gga gac aaa aga gaa gac aaa ctc tat gac att     1426
Gly Tyr Gln Val Lys Gly Asp Lys Arg Glu Asp Lys Leu Tyr Asp Ile
402                 407                 412                 417

tta cct ggg atg gag ctc acc cca atg aat cct gtc aca tta aaa ccc     1474
Leu Pro Gly Met Glu Leu Thr Pro Met Asn Pro Val Thr Leu Lys Pro
418                 423                 428                 433

caa gga att aaa ctc gct ccc cag ata tta gaa gag att tgt cag aaa     1522
Gln Gly Ile Lys Leu Ala Pro Gln Ile Leu Glu Glu Ile Cys Gln Lys
434                 439                 444                 449

aat aac tgg gga cag cca gtg tac cag ctg cac tct gct att gga caa     1570
Asn Asn Trp Gly Gln Pro Val Tyr Gln Leu His Ser Ala Ile Gly Gln
450                 455                 460                 465

gac caa aga cag cta ttc ttg tac aaa ata act att cct gct cta gcc     1618
Asp Gln Arg Gln Leu Phe Leu Tyr Lys Ile Thr Ile Pro Ala Leu Ala
466                 471                 476                 481

agc cag aat cct gca atc cac cct ttc aca cct cca aag ctg agt gcc     1666
Ser Gln Asn Pro Ala Ile His Pro Phe Thr Pro Pro Lys Leu Ser Ala
482                 487                 492                 497
```

```
ttt gtg gat gaa gca aag acg tat gca gcc gaa tac acc ctg cag acc      1714
Phe Val Asp Glu Ala Lys Thr Tyr Ala Ala Glu Tyr Thr Leu Gln Thr
498                 503                 508                 513

ctg ggc atc ccc act gat gga ggc gat ggc acc atg gct act gct gct      1762
Leu Gly Ile Pro Thr Asp Gly Gly Asp Gly Thr Met Ala Thr Ala Ala
514                 519                 524                 529

gct gct gct act gct ttc cca gga tat gct gtc cct aat gca act gca      1810
Ala Ala Ala Thr Ala Phe Pro Gly Tyr Ala Val Pro Asn Ala Thr Ala
530                 535                 540                 545

ccc gtg tct gca gcc cag ctc aag caa gcg gta acc ctt gga caa gac      1858
Pro Val Ser Ala Ala Gln Leu Lys Gln Ala Val Thr Leu Gly Gln Asp
546                 551                 556                 561

tta gca gca tat aca acc tat gag gtc tac cca act ttt gca gtg act      1906
Leu Ala Ala Tyr Thr Thr Tyr Glu Val Tyr Pro Thr Phe Ala Val Thr
562                 567                 572                 577

gcc cga ggg gat gga tat ggc acc ttc tga a gatgcttttt taaatttaag      1957
Ala Arg Gly Asp Gly Tyr Gly Thr Phe  *
578                 583

aataagacac acaaaactct attaaaaaaa aaaaa                               1992
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<210> 311
<211> 5459
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (746)..(4522)

<220>
<221> misc_feature
<222> (1)...(5459)
<223> n = a,t,c or g

<400> 311

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agctgcggat gggggcagca ggagccgggc gggaacagag gaaagcgccg gccctgagac      60

ctagggagga gcctcggtga aggaacccgg ggcggttctg cctagatctc caagaagctc     120

caaaaatggc gggcggcaac tcggcgagcg gacgcgcagg gccaccgtgg ccgtccttcc     180

gccagccgcg ggcccaagaa ccgtccacag cgcccttatc cagaagccta cgcctctcgc     240

gattggctga actgcgcgag catccgtgtg ggggcggggc gcacgcagcc angtntgatc     300

ccgccccgct ggtgcgcgtg cgaaataccc cactggaaag cgtttgcgcg cgcccctgcc     360
```

```
gcggccccta gctcgggcct cagctccctc ccctttccgg gcaggcccgt cccgtcagca    420

aggcagtgag caccgcggcc agcagagggc ggtccggacc caagtctgca gcggcgccat    480

tggcgtgtgg aaaatgccac cagatggcgg gttaggattg cagctccgtt gaaggcgcgg    540

cccccgctcc cgaacccccg gcgaccaccc cgtaacaacc cccccacatc gggaataaca    600

caccggagac ttttgggggg aaactaggtc gatggtcggc ggcgcccgga tgggcagctg    660

aggattgcct ttgaggttat tttaaaagtt ttgagttgta cagcacttga ttattttgct    720

gcattgtgaa aggacctctc cagca  atg att act tca gaa tta cca gtg tta      772
                              Met Ile Thr Ser Glu Leu Pro Val Leu
                                1               5

cag gat tca act aat gaa act act gcc cat tcc gat gct ggc agc gag      820
Gln Asp Ser Thr Asn Glu Thr Thr Ala His Ser Asp Ala Gly Ser Glu
 10                  15                  20                  25

ctt gaa gaa aca gag gtc aaa gga aaa aga aaa agg ggt cgt cct ggc      868
Leu Glu Glu Thr Glu Val Lys Gly Lys Arg Lys Arg Gly Arg Pro Gly
 26                  31                  36                  41

cgg cct cca tct aca aat aag aaa cct cga aaa tct cca ggt gag aag      916
Arg Pro Pro Ser Thr Asn Lys Lys Pro Arg Lys Ser Pro Gly Glu Lys
 42                  47                  52                  57

agc aga att gaa gct gga att aga gga gca ggc cgt gga aga gct aat      964
Ser Arg Ile Glu Ala Gly Ile Arg Gly Ala Gly Arg Gly Arg Ala Asn
 58                  63                  68                  73

gga cac cct caa cag aat ggg gaa ggg gag cct gtc aca tta ttt gag     1012
Gly His Pro Gln Gln Asn Gly Glu Gly Glu Pro Val Thr Leu Phe Glu
 74                  79                  84                  89

gtg gtg aaa ctg ggg aaa agt gca atg cag tcc gtg gtg gat gac tgg     1060
Val Val Lys Leu Gly Lys Ser Ala Met Gln Ser Val Val Asp Asp Trp
 90                  95                 100                 105

att gaa tca tat aaa caa gac agg gac atc gca ctt ctg gat tta atc     1108
Ile Glu Ser Tyr Lys Gln Asp Arg Asp Ile Ala Leu Leu Asp Leu Ile
106                 111                 116                 121

aac ttt ttt atc cag tgt tca gga tgt cga ggt act gtg aga ata gag     1156
Asn Phe Phe Ile Gln Cys Ser Gly Cys Arg Gly Thr Val Arg Ile Glu
122                 127                 132                 137

atg ttt cga aat atg cag aat gca gaa atc atc aga aaa atg act gaa     1204
Met Phe Arg Asn Met Gln Asn Ala Glu Ile Ile Arg Lys Met Thr Glu
138                 143                 148                 153

gaa ttt gat gag gac agt ggt gat tat cct ctt acc atg cct gga cct     1252
Glu Phe Asp Glu Asp Ser Gly Asp Tyr Pro Leu Thr Met Pro Gly Pro
154                 159                 164                 169

cag tgg aaa aaa ttt cgt tca aac ttt tgt gaa ttt att gga gtc ctg     1300
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Gln Trp Lys Lys Phe Arg Ser Asn Phe Cys Glu Phe Ile Gly Val Leu
170                 175                 180                 185

att cga cag tgt cag tat agc ata att tat gat gag tat atg atg gac     1348
Ile Arg Gln Cys Gln Tyr Ser Ile Ile Tyr Asp Glu Tyr Met Met Asp
186                 191                 196                 201

aca gta atc tcc ctt ttg acg ggt ttg tca gac tcc cag gtc aga gct     1396
Thr Val Ile Ser Leu Leu Thr Gly Leu Ser Asp Ser Gln Val Arg Ala
202                 207                 212                 217

ttt agg cat aca agt acc ctg gct gcc atg aag ctc atg act gct ctg     1444
Phe Arg His Thr Ser Thr Leu Ala Ala Met Lys Leu Met Thr Ala Leu
218                 223                 228                 233

gtg aat gtt gcc tta aac ctc agt att cat cag gat aat acc cag aga     1492
Val Asn Val Ala Leu Asn Leu Ser Ile His Gln Asp Asn Thr Gln Arg
234                 239                 244                 249

caa tat gaa gcc gag aga aat aaa atg att ggg aag aga gcc aat gaa     1540
Gln Tyr Glu Ala Glu Arg Asn Lys Met Ile Gly Lys Arg Ala Asn Glu
250                 255                 260                 265

agg ttg gag tta cta ctt cag aaa cgc aaa gag ctg caa gaa aat cag     1588
Arg Leu Glu Leu Leu Leu Gln Lys Arg Lys Glu Leu Gln Glu Asn Gln
266                 271                 276                 281

gat gaa atc gaa aat atg atg aac tct att ttt aag ggt ata ttt gtt     1636
Asp Glu Ile Glu Asn Met Met Asn Ser Ile Phe Lys Gly Ile Phe Val
282                 287                 292                 297

cat aga tac cgt gat gct att gct gag att aga gcc att tgt att gaa     1684
His Arg Tyr Arg Asp Ala Ile Ala Glu Ile Arg Ala Ile Cys Ile Glu
298                 303                 308                 313

gaa att gga gta tgg atg aaa atg tat agt gat gcc ttc cta aat gac     1732
Glu Ile Gly Val Trp Met Lys Met Tyr Ser Asp Ala Phe Leu Asn Asp
314                 319                 324                 329

agt tac cta aaa tat gtt ggc tgg act ctt cat gac agg caa ggg gaa     1780
Ser Tyr Leu Lys Tyr Val Gly Trp Thr Leu His Asp Arg Gln Gly Glu
330                 335                 340                 345

gtc agg ctg aag tgt ttg aaa gct ctg cag agt cta tat acc aat aga     1828
Val Arg Leu Lys Cys Leu Lys Ala Leu Gln Ser Leu Tyr Thr Asn Arg
346                 351                 356                 361

gaa tta ttc ccc aaa ttg gaa cta ttc act aac cga ttc aag gat cgc     1876
Glu Leu Phe Pro Lys Leu Glu Leu Phe Thr Asn Arg Phe Lys Asp Arg
362                 367                 372                 377

att gta tca atg aca ctt gat aaa gaa tat gat gtt gct gtg gaa gct     1924
Ile Val Ser Met Thr Leu Asp Lys Glu Tyr Asp Val Ala Val Glu Ala
378                 383                 388                 393

att cga ttg gtt act ctg ata ctt cat gga agt gaa gaa gct ctt tcc     1972
Ile Arg Leu Val Thr Leu Ile Leu His Gly Ser Glu Glu Ala Leu Ser
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394                 399                 404                 409

aat gaa gac tgt gaa aat gtt tac cac ttg gtg tac tcg gca cat cgc     2020
Asn Glu Asp Cys Glu Asn Val Tyr His Leu Val Tyr Ser Ala His Arg
410                 415                 420                 425

cct gtt gct gtg gca gct gga gag ttc ctt cac aaa aag cta ttt agc     2068
Pro Val Ala Val Ala Ala Gly Glu Phe Leu His Lys Lys Leu Phe Ser
426                 431                 436                 441

aga cat gac cca caa gca gaa gaa gca tta gca aag agg agg gga aga     2116
Arg His Asp Pro Gln Ala Glu Glu Ala Leu Ala Lys Arg Arg Gly Arg
442                 447                 452                 457

aac agc ccg aat gga aac ctc att agg atg ctg gtt ctt ttc ttt ctt     2164
Asn Ser Pro Asn Gly Asn Leu Ile Arg Met Leu Val Leu Phe Phe Leu
458                 463                 468                 473

gaa agt gag tta cat gaa cat gca gcc tac ttg gtg gac agt tta tgg     2212
Glu Ser Glu Leu His Glu His Ala Ala Tyr Leu Val Asp Ser Leu Trp
474                 479                 484                 489

gag agc tct caa gaa ctg ttg aaa gac tgg gaa tgt atg aca gag ttg     2260
Glu Ser Ser Gln Glu Leu Leu Lys Asp Trp Glu Cys Met Thr Glu Leu
490                 495                 500                 505

cta tta gaa gaa cct gtt caa gga gag gaa gca atg tct gat cgt caa     2308
Leu Leu Glu Glu Pro Val Gln Gly Glu Glu Ala Met Ser Asp Arg Gln
506                 511                 516                 521

gag agt gct ctt ata gag cta atg gtt tgt aca att cgt caa gct gct     2356
Glu Ser Ala Leu Ile Glu Leu Met Val Cys Thr Ile Arg Gln Ala Ala
522                 527                 532                 537

gag gca cat cct cca gtg gga agg ggt acc ggc aag aga gtg cta act     2404
Glu Ala His Pro Pro Val Gly Arg Gly Thr Gly Lys Arg Val Leu Thr
538                 543                 548                 553

gcc aaa gaa agg aaa act caa att gat gat aga aac aaa ttg act gaa     2452
Ala Lys Glu Arg Lys Thr Gln Ile Asp Asp Arg Asn Lys Leu Thr Glu
554                 559                 564                 569

cat ttt att att aca ctt cct atg tta ctg tca aag tat tct gca gat     2500
His Phe Ile Ile Thr Leu Pro Met Leu Leu Ser Lys Tyr Ser Ala Asp
570                 575                 580                 585

gca gag aag gta gca aac ttg cta caa atc cca cag tat ttt gat tta     2548
Ala Glu Lys Val Ala Asn Leu Leu Gln Ile Pro Gln Tyr Phe Asp Leu
586                 591                 596                 601

gaa atc tac agc aca ggt aga atg gaa aag cat ctg gat gct tta tta     2596
Glu Ile Tyr Ser Thr Gly Arg Met Glu Lys His Leu Asp Ala Leu Leu
602                 607                 612                 617

aaa cag att aag ttt gtt gtg gag aaa cac gta gaa tca gat gtt cta     2644
Lys Gln Ile Lys Phe Val Val Glu Lys His Val Glu Ser Asp Val Leu
618                 623                 628                 633
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gaa gcc tgc agt aaa acc tat agt atc tta tgc agt gaa gaa tat acc      2692
Glu Ala Cys Ser Lys Thr Tyr Ser Ile Leu Cys Ser Glu Glu Tyr Thr
634                 639                 644                 649

atc cag aac aga gtt gac ata gct cga agc cag ctg att gat gag ttt      2740
Ile Gln Asn Arg Val Asp Ile Ala Arg Ser Gln Leu Ile Asp Glu Phe
650                 655                 660                 665

gta gat cga ttc aat cat tct gtg gaa gac cta ttg caa gag gga gaa      2788
Val Asp Arg Phe Asn His Ser Val Glu Asp Leu Leu Gln Glu Gly Glu
666                 671                 676                 681

gaa gct gat gat gat gac att tac aat gtt ctt tct aca tta aag cgg      2836
Glu Ala Asp Asp Asp Asp Ile Tyr Asn Val Leu Ser Thr Leu Lys Arg
682                 687                 692                 697

tta act tct ttt cag aat gca cat gat ctc aca aaa tgg gat ctc ttt      2884
Leu Thr Ser Phe Gln Asn Ala His Asp Leu Thr Lys Trp Asp Leu Phe
698                 703                 708                 713

ggt aat tgc tac aga tta ttg aag act gga att gaa cat gga gcc atg      2932
Gly Asn Cys Tyr Arg Leu Leu Lys Thr Gly Ile Glu His Gly Ala Met
714                 719                 724                 729

cca gaa cag ata gtc gtg caa gca ctg cag tgt tcc cat tat tcg att      2980
Pro Glu Gln Ile Val Val Gln Ala Leu Gln Cys Ser His Tyr Ser Ile
730                 735                 740                 745

ctt tgg cag ttg gtg aaa att act gat ggc tct cct tcc aaa gag gat      3028
Leu Trp Gln Leu Val Lys Ile Thr Asp Gly Ser Pro Ser Lys Glu Asp
746                 751                 756                 761

ttg ttg gta ttg agg aaa acg gtg aaa tcc ttt ttg gct gtt tgc cag      3076
Leu Leu Val Leu Arg Lys Thr Val Lys Ser Phe Leu Ala Val Cys Gln
762                 767                 772                 777

cag tgc ctg tct aat gtt aat act cca gtg aaa gaa cag gct ttc atg      3124
Gln Cys Leu Ser Asn Val Asn Thr Pro Val Lys Glu Gln Ala Phe Met
778                 783                 788                 793

tta ctc tgt gat ctt ctg atg att ttc agc cac caa tta atg aca ggt      3172
Leu Leu Cys Asp Leu Leu Met Ile Phe Ser His Gln Leu Met Thr Gly
794                 799                 804                 809

ggc aga gag ggc ctt cag cct ttg gtg ttc aat cca gat act gga ctc      3220
Gly Arg Glu Gly Leu Gln Pro Leu Val Phe Asn Pro Asp Thr Gly Leu
810                 815                 820                 825

caa tct gaa ctc ctc agt ttt gtg atg gat cac gtt ttt att gac caa      3268
Gln Ser Glu Leu Leu Ser Phe Val Met Asp His Val Phe Ile Asp Gln
826                 831                 836                 841

gac gag gag aac cag agc atg gag ggt gat gaa gaa gat gaa gct aat      3316
Asp Glu Glu Asn Gln Ser Met Glu Gly Asp Glu Glu Asp Glu Ala Asn
842                 847                 852                 857
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aaa att gag gcc tta cat aaa aga agg aat cta ctt gct gct ttc agc     3364
Lys Ile Glu Ala Leu His Lys Arg Arg Asn Leu Leu Ala Ala Phe Ser
858                 863                 868                 873

aaa ctt atc att tat gac att gtt gac atg cat gca gct gca gac atc     3412
Lys Leu Ile Ile Tyr Asp Ile Val Asp Met His Ala Ala Ala Asp Ile
874                 879                 884                 889

ttc aaa cac tac atg aag tat tac aat gac tat ggt gat att att aag     3460
Phe Lys His Tyr Met Lys Tyr Tyr Asn Asp Tyr Gly Asp Ile Ile Lys
890                 895                 900                 905

gaa aca ctg agt aaa acc agg cag att gat aaa att cag tgt gcc aag     3508
Glu Thr Leu Ser Lys Thr Arg Gln Ile Asp Lys Ile Gln Cys Ala Lys
906                 911                 916                 921

act ctc att ctc agt ttg caa cag tta ttt aat gaa ctt gtt caa gag     3556
Thr Leu Ile Leu Ser Leu Gln Gln Leu Phe Asn Glu Leu Val Gln Glu
922                 927                 932                 937

caa ggt ccc aac cta gat agg aca tct gcc cat gtc agt ggc att aaa     3604
Gln Gly Pro Asn Leu Asp Arg Thr Ser Ala His Val Ser Gly Ile Lys
938                 943                 948                 953

gaa ctg gca cgt cgc ttt gcc ctt aca ttt gga ttg gac cag att aag     3652
Glu Leu Ala Arg Arg Phe Ala Leu Thr Phe Gly Leu Asp Gln Ile Lys
954                 959                 964                 969

aca cga gaa gca gtt gcc aca ctt cac aag gat ggc ata gag ttt gca     3700
Thr Arg Glu Ala Val Ala Thr Leu His Lys Asp Gly Ile Glu Phe Ala
970                 975                 980                 985

ttt aaa tac caa aat cag aaa gga caa gag tat cca cct cct aat ctg     3748
Phe Lys Tyr Gln Asn Gln Lys Gly Gln Glu Tyr Pro Pro Pro Asn Leu
986                 991                 996                1001

gct ttt ctt gaa gta cta agt gaa ttt tct tct aaa ctt ctt cga cag     3796
Ala Phe Leu Glu Val Leu Ser Glu Phe Ser Ser Lys Leu Leu Arg Gln
1002                1007                1012                1017

gac aaa aag aca gtt cat tca tac cta gag aaa ttc ctt acc gag cag     3844
Asp Lys Lys Thr Val His Ser Tyr Leu Glu Lys Phe Leu Thr Glu Gln
1018                1023                1028                1033

atg atg gaa agg agg gag gat gta tgg ctt cca ctc atc tcc tat aga     3892
Met Met Glu Arg Arg Glu Asp Val Trp Leu Pro Leu Ile Ser Tyr Arg
1034                1039                1044                1049

aat tca tta gtc act ggg ggt gaa gat gat aga atg tct gtg aac agt     3940
Asn Ser Leu Val Thr Gly Gly Glu Asp Asp Arg Met Ser Val Asn Ser
1050                1055                1060                1065

gga agt agc agc agc aaa acc tca tca gta agg aat aag aaa gga cga     3988
Gly Ser Ser Ser Ser Lys Thr Ser Ser Val Arg Asn Lys Lys Gly Arg
1066                1071                1076                1081

cct cca ctt cat aaa aaa cga gta gaa gat gag agt ctg gat aac aca     4036
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 Pro Pro Leu His Lys Lys Arg Val Glu Asp Glu Ser Leu Asp Asn Thr
1082                1087                1092                1097

 tgg cta aac agg act gac acc atg att cag act cct ggc ccc ctg cca     4084
 Trp Leu Asn Arg Thr Asp Thr Met Ile Gln Thr Pro Gly Pro Leu Pro
1098                1103                1108                1113

 gca cca caa ctc aca tcc act gta ctg cgg gag aac agt cgg ccc atg     4132
 Ala Pro Gln Leu Thr Ser Thr Val Leu Arg Glu Asn Ser Arg Pro Met
1114                1119                1124                1129

 gga gac cag att caa gaa cct gag tct gaa cat ggt tct gaa cca gac     4180
 Gly Asp Gln Ile Gln Glu Pro Glu Ser Glu His Gly Ser Glu Pro Asp
1130                1135                1140                1145

 ttt tta cac aat cct cag atg cag atc tct tgg tta ggc cag ccg aag     4228
 Phe Leu His Asn Pro Gln Met Gln Ile Ser Trp Leu Gly Gln Pro Lys
1146                1151                1156                1161

 tta gaa gac tta aat cgg aag gac aga aca gga atg aac tac atg aaa     4276
 Leu Glu Asp Leu Asn Arg Lys Asp Arg Thr Gly Met Asn Tyr Met Lys
1162                1167                1172                1177

 gtg aga act gga gtg agg cat gct gtt cgg ggt cta atg gag gaa gat     4324
 Val Arg Thr Gly Val Arg His Ala Val Arg Gly Leu Met Glu Glu Asp
1178                1183                1188                1193

 gct gag ccc atc ttt gaa gat gtg atg atg tca tcc cga agc cag tta     4372
 Ala Glu Pro Ile Phe Glu Asp Val Met Met Ser Ser Arg Ser Gln Leu
1194                1199                1204                1209

 gaa gat atg aat gaa gaa ttt gag gac acc atg gtt att gat ctg cct     4420
 Glu Asp Met Asn Glu Glu Phe Glu Asp Thr Met Val Ile Asp Leu Pro
1210                1215                1220                1225

 cca tca aga aat cgg cga gag aga gct gag cta agg cca gac ttc ttt     4468
 Pro Ser Arg Asn Arg Arg Glu Arg Ala Glu Leu Arg Pro Asp Phe Phe
1226                1231                1236                1241

 gac tct gca gct atc ata gaa gat gat tca gga ttt gga atg cct atg     4516
 Asp Ser Ala Ala Ile Ile Glu Asp Asp Ser Gly Phe Gly Met Pro Met
1242                1247                1252                1257

 ttc tga agtctgaaga aaatttacaa atctggaact ctattattta gagctagagg     4572
 Phe  *
1258

 cctatatact gtgatagctt gtatggggaa aaacactttt gatgtgatct gatttgtttt   4632

 ttaatcaaat gattaaggtc aatccctttt tgcagtgaca gaagaggagc atgtaaatta   4692

 cccaagggaa tgttggtgaa tgtcaactca gaaagactga cctgaaaatc atttgtgtcc   4752

 tactattgga cttatcccaa tacagatgtg tgtgtttttc tggagggagg aagaaatttt   4812

 aaatttttaa aacagctgtc aagataaaca ctgttataca cctgttttat gaaaactcaa   4872
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cattgagtaa aaaaaaacat atttttaact ttattttcct gttgtacaat ttaaaaaccg   4932

ttttaacatt ttgccttttt atgttttaaa agctaaccat ttttattaaa cctatgagta   4992

agcagctcat cctaattgcg aagagtgttt tggagttcac tggatttggt tgacctttgt   5052

ggaacacaaa taatgaagga gcagaacatt gacaagctaa gatgaaattc tgacatagta   5112

catctctgcc aaaaaccaca caccctctgt ggatatggat atgaattccc agattttata   5172

tactcttgaa taaaaggttt atttttattt ataagtgggc ataaaataag aaatgtccat   5232

gcagccattt ttccaacaga tgctgtacac cgttcatttt atatagacta gggagattca   5292

aatacagtgc attttctatt ggtatttgtt ctgtgcattt ttagcaactt ctaccagcaa   5352

ataaagtatt ctcagtaaaa cgaaaaaaaa aaaaaaaggg cggccgctct agagtatccc   5412

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aaagagtcta aaacaaaata caacatttct taaatacact gtttccagaa agagctattt    120

taacagaagc aactcaaaga tatcccttcg acagaagtgg aagtgctgaa aaatgctcat    180

ctctcacaca gacttttgat ggacaggagt ttctaagtat catgcctacc aacaagctgt    240

aaa  atg atc acc ctg aac aat caa gat caa cct gtc cct ttt aac agc      288
     Met Ile Thr Leu Asn Asn Gln Asp Gln Pro Val Pro Phe Asn Ser
       1               5                  10

tca cat cca gat gaa tac aaa att gca gcc ctt gtc ttc tat agc tgt      336
Ser His Pro Asp Glu Tyr Lys Ile Ala Ala Leu Val Phe Tyr Ser Cys
 16                  21                  26                  31

atc ttc ata att gga tta ttt gtt aac atc act gca tta tgg gtt ttc      384
Ile Phe Ile Ile Gly Leu Phe Val Asn Ile Thr Ala Leu Trp Val Phe
 32                  37                  42                  47

agt tgt acc acc aag aag aga acc acg gta acc atc tat atg atg aat      432
Ser Cys Thr Thr Lys Lys Arg Thr Thr Val Thr Ile Tyr Met Met Asn
 48                  53                  58                  63
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gtg gca tta gtg gac ttg ata ttt ata atg act tta ccc ttt cga atg      480
Val Ala Leu Val Asp Leu Ile Phe Ile Met Thr Leu Pro Phe Arg Met
 64                  69                  74                  79

ttt tat tat gca aaa gat gaa tgg cca ttt gga gag tac ttc tgc cag      528
Phe Tyr Tyr Ala Lys Asp Glu Trp Pro Phe Gly Glu Tyr Phe Cys Gln
 80                  85                  90                  95

att ctt gga gct ctc aca gtg ttt tac cca agc att gct tta tgg ctt      576
Ile Leu Gly Ala Leu Thr Val Phe Tyr Pro Ser Ile Ala Leu Trp Leu
 96                 101                 106                 111

ctt gcc ttt att agt gct gac aga tac atg gcc att gta cag ccg aag      624
Leu Ala Phe Ile Ser Ala Asp Arg Tyr Met Ala Ile Val Gln Pro Lys
112                 117                 122                 127

tac gcc aaa gaa ctt aaa aac acg tgc aaa gcc gtg ctg gcg tgt gtg      672
Tyr Ala Lys Glu Leu Lys Asn Thr Cys Lys Ala Val Leu Ala Cys Val
128                 133                 138                 143

gga gtc tgg ata atg acc ctg acc acg acc acc cct ctg cta ctg ctc      720
Gly Val Trp Ile Met Thr Leu Thr Thr Thr Thr Pro Leu Leu Leu Leu
144                 149                 154                 159

tat aaa gac cca gat aaa gac tcc act ccc gcc acc tgc ctc aag att      768
Tyr Lys Asp Pro Asp Lys Asp Ser Thr Pro Ala Thr Cys Leu Lys Ile
160                 165                 170                 175

tct gac atc atc tat cta aaa gct gtg aac gtg ctg aac ctc act cga      816
Ser Asp Ile Ile Tyr Leu Lys Ala Val Asn Val Leu Asn Leu Thr Arg
176                 181                 186                 191

ctg aca ttt ttt ttc ttg att cct ttg ttc atc atg att ggg tgc tac      864
Leu Thr Phe Phe Phe Leu Ile Pro Leu Phe Ile Met Ile Gly Cys Tyr
192                 197                 202                 207

ttg gtc att att cat aat ctc ctt cac ggc agg acg tct aag ctg aaa      912
Leu Val Ile Ile His Asn Leu Leu His Gly Arg Thr Ser Lys Leu Lys
208                 213                 218                 223

ccc aaa gtc aag gag aag tcc ata agg atc atc atc acg ctg ctg gtg      960
Pro Lys Val Lys Glu Lys Ser Ile Arg Ile Ile Ile Thr Leu Leu Val
224                 229                 234                 239

cag gtg ctc gtc tgc ttt atg ccc ttc cac atc tgt ttc gct ttc ctg     1008
Gln Val Leu Val Cys Phe Met Pro Phe His Ile Cys Phe Ala Phe Leu
240                 245                 250                 255

atg ctg gga acg ggg gag aac agt tac aat ccc tgg gga gcc ttt acc     1056
Met Leu Gly Thr Gly Glu Asn Ser Tyr Asn Pro Trp Gly Ala Phe Thr
256                 261                 266                 271

acc ttc ctc atg aac ctc agc acg tgt ctg gat gtg att ctc tac tac     1104
Thr Phe Leu Met Asn Leu Ser Thr Cys Leu Asp Val Ile Leu Tyr Tyr
272                 277                 282                 287

atc gtt tca aaa caa ttt cag gct cga gtc att agt gtc atg cta tac     1152
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Ile Val Ser Lys Gln Phe Gln Ala Arg Val Ile Ser Val Met Leu Tyr
288                 293                 298                 303

cgt aat tac ctt cga agc atg cgc aga aaa agt ttc cga tct ggt agt     1200
Arg Asn Tyr Leu Arg Ser Met Arg Arg Lys Ser Phe Arg Ser Gly Ser
304                 309                 314                 319

cta cgg tca cta agc aat ata aac agt gaa atg tta tga ataataaggt      1249
Leu Arg Ser Leu Ser Asn Ile Asn Ser Glu Met Leu  *
320                 325                 330

tctttcattt caatcccatc aaaattcact tcactaacta ctctggcgtc aatggatatt   1309

ctgtataata ctatcaagtc ccttttctct tgaaaaaata aattcattat cttcatttta   1369

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Met Leu Pro Lys Arg Arg Arg Ala Arg Val Gly Ser Pro Ser Gly Asp
  1               5                  10

gcc gct tcc tcc acg ccg ccc tcg acg cgc ttc ccg gga gtc gcc atc      96
Ala Ala Ser Ser Thr Pro Pro Ser Thr Arg Phe Pro Gly Val Ala Ile
 17                  22                  27                  32

tac ctg gtc gag cct cgc atg ggt cgc agc cgc cgg gcc ttc ctc aca     144
Tyr Leu Val Glu Pro Arg Met Gly Arg Ser Arg Arg Ala Phe Leu Thr
 33                  38                  43                  48

ggc ctg gcg cgc tcc aaa ggc ttc cgc gtc ctt gac gcc tgc agc tcc     192
Gly Leu Ala Arg Ser Lys Gly Phe Arg Val Leu Asp Ala Cys Ser Ser
 49                  54                  59                  64

gaa gcg aca cat gtt gtg atg gaa gag acc tca gca gag gag gcc gtc     240
Glu Ala Thr His Val Val Met Glu Glu Thr Ser Ala Glu Glu Ala Val
 65                  70                  75                  80

agc tgg cag gag cgc agg atg gca gct gct ccc ccg ggt tgc acc ccc     288
Ser Trp Gln Glu Arg Arg Met Ala Ala Ala Pro Pro Gly Cys Thr Pro
 81                  86                  91                  96

cca gct ctg ctg gac ata agc tgg tta aca gag agc ctg gga gct ggg     336
Pro Ala Leu Leu Asp Ile Ser Trp Leu Thr Glu Ser Leu Gly Ala Gly
 97                 102                 107                 112
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cag cct gta cct gtg gag tgc cgg cac cgc ctg gag gtg gct ggg cca      384
Gln Pro Val Pro Val Glu Cys Arg His Arg Leu Glu Val Ala Gly Pro
113                 118                 123                 128

agg aag ggg cct ctg agc cca gca tgg atg cct gcc tat gcc tgc cag      432
Arg Lys Gly Pro Leu Ser Pro Ala Trp Met Pro Ala Tyr Ala Cys Gln
129                 134                 139                 144

cgc cct acg ccc ctc aca cac cac aac act ggc ctc tcc gag gct ctg      480
Arg Pro Thr Pro Leu Thr His His Asn Thr Gly Leu Ser Glu Ala Leu
145                 150                 155                 160

gag ata ctg gcc gag gca gca ggc ttt gaa ggc agt gag ggc cgc ctc      528
Glu Ile Leu Ala Glu Ala Ala Gly Phe Glu Gly Ser Glu Gly Arg Leu
161                 166                 171                 176

ctc acc ttc tgc aga gca gcc tcg gtg ctc aag gcc ctt ccc agc cct      576
Leu Thr Phe Cys Arg Ala Ala Ser Val Leu Lys Ala Leu Pro Ser Pro
177                 182                 187                 192

gtc aca acc ctg agc cag ctg cag ggg ctt ccc cac ttt gga gaa cac      624
Val Thr Thr Leu Ser Gln Leu Gln Gly Leu Pro His Phe Gly Glu His
193                 198                 203                 208

tcc tct agg gtt gtc cag gag ctg ctg gag cat gga gtg tgt gag gag      672
Ser Ser Arg Val Val Gln Glu Leu Leu Glu His Gly Val Cys Glu Glu
209                 214                 219                 224

gtg gag aga gtt cgg cgc tca gag agg tac cag acc atg aag ctc ttc      720
Val Glu Arg Val Arg Arg Ser Glu Arg Tyr Gln Thr Met Lys Leu Phe
225                 230                 235                 240

acc cag atc ttc ggg gtc ggt gtg aag act gct gac cgg tgg tac cgg      768
Thr Gln Ile Phe Gly Val Gly Val Lys Thr Ala Asp Arg Trp Tyr Arg
241                 246                 251                 256

gaa gga ctg cga acc tta gat gac ctc cga gag cag ccc cag aaa cta      816
Glu Gly Leu Arg Thr Leu Asp Asp Leu Arg Glu Gln Pro Gln Lys Leu
257                 262                 267                 272

acc caa cag cag aaa gcg ggg ctc cag cac cac cag gac ctg agc acc      864
Thr Gln Gln Gln Lys Ala Gly Leu Gln His His Gln Asp Leu Ser Thr
273                 278                 283                 288

cca gtc ctg cgg tcc gat gta gat gcc ctg cag cag gtg gtg gag gaa      912
Pro Val Leu Arg Ser Asp Val Asp Ala Leu Gln Gln Val Val Glu Glu
289                 294                 299                 304

gct gtg ggg cag gcc ctg cct ggg gcc acc gtc acg ctg acc ggc ggc      960
Ala Val Gly Gln Ala Leu Pro Gly Ala Thr Val Thr Leu Thr Gly Gly
305                 310                 315                 320

ttc cgc agg ggg aag ttg cag ggc cat gac gtg gac ttc ctc atc acc     1008
Phe Arg Arg Gly Lys Leu Gln Gly His Asp Val Asp Phe Leu Ile Thr
321                 326                 331                 336
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cac ccc aag gag ggt cag gag gcg ggg ctg ctg cct aga gtg atg tgc     1056
His Pro Lys Glu Gly Gln Glu Ala Gly Leu Leu Pro Arg Val Met Cys
337                 342                 347                 352

cgc ctg cag gac cag ggc ctc atc ctg tac cac cag cac cag cac agc     1104
Arg Leu Gln Asp Gln Gly Leu Ile Leu Tyr His Gln His Gln His Ser
353                 358                 363                 368

tgc tgt gag tcc cct acc cgc ctg gcc caa cag agc cac atg gac gct     1152
Cys Cys Glu Ser Pro Thr Arg Leu Ala Gln Gln Ser His Met Asp Ala
369                 374                 379                 384

ttt gag aga agt ttc tgc att ttc cgc cta cca caa cct cca ggg gct     1200
Phe Glu Arg Ser Phe Cys Ile Phe Arg Leu Pro Gln Pro Pro Gly Ala
385                 390                 395                 400

gct gtg ggg gga tcc acg agg ccc tgc cca tcc tgg aag gcc gtg aga     1248
Ala Val Gly Gly Ser Thr Arg Pro Cys Pro Ser Trp Lys Ala Val Arg
401                 406                 411                 416

gtg gac ttg gta gtt gca ccc gtc agc cag ttc cct ttc gcc ctg ctc     1296
Val Asp Leu Val Val Ala Pro Val Ser Gln Phe Pro Phe Ala Leu Leu
417                 422                 427                 432

ggt tgg act ggc tcc aag ctt ttc cag cgg gag ctg cgc cgc ttc agc     1344
Gly Trp Thr Gly Ser Lys Leu Phe Gln Arg Glu Leu Arg Arg Phe Ser
433                 438                 443                 448

cgg aag gag aag ggc ctg tgg ctg aac agc cat ggg ctg ttt gac ccg     1392
Arg Lys Glu Lys Gly Leu Trp Leu Asn Ser His Gly Leu Phe Asp Pro
449                 454                 459                 464

gag cag aag aca ttt ttc caa gcg gct tca gag gaa gac atc ttc aga     1440
Glu Gln Lys Thr Phe Phe Gln Ala Ala Ser Glu Glu Asp Ile Phe Arg
465                 470                 475                 480

cac ctg ggc ctt gag tac ctt cct cca gag cag aga aac gcc tga gcc     1488
His Leu Gly Leu Glu Tyr Leu Pro Pro Glu Gln Arg Asn Ala  *
481                 486                 491

tgcctgtgtc ccccacttcc actcaggaaa ttgggctgcc cccaacctgg ccactgaatg   1548

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ctcttccgga ggtcaattgt gcctgcagga tcagttgagc ccctgctggt gtgctgcagg   1668

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ggagctgtgg tggggcctgc agtcatgaat ggcaagtggt ccctgatgtg cagtgtctca   1848

ttagttgcac tgcagttaac tgtggctcct gcagggcacc ctgcccagaa tgcccagaag   1908

agaaccatgc atacctgcac tgcatttgag agccatgagc tggaggctgt ggttcgtgcc   1968

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cacgactctg aaagaggaca gcgttccca atg tcc cag ttt aag cgc cag cgg 173
Met Ser Gln Phe Lys Arg Gln Arg
1 5

atc aac ccg ctt cca ggg gga cgc aac ttc tca ggc aca gct tca aca 221
Ile Asn Pro Leu Pro Gly Gly Arg Asn Phe Ser Gly Thr Ala Ser Thr
9 14 19 24

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Ser Leu Leu Gly Pro Pro Pro Gly Leu Leu Thr Pro Pro Val Ala Thr
25 30 35 40

gaa ctg tcc cag aat gcc agg cac ctt cag ggt ggg gag aaa cag cgg 317
Glu Leu Ser Gln Asn Ala Arg His Leu Gln Gly Gly Glu Lys Gln Arg
41 46 51 56

gtc ttc act ggt att gtt acc agc ttg cat gac tac ttt ggg gtt gtg 365
Val Phe Thr Gly Ile Val Thr Ser Leu His Asp Tyr Phe Gly Val Val
57 62 67 72

gat gaa gag gtc ttt ttt cag cta agt gtg gtg aag ggc cgt ctg ccc 413

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cag ctg ggt gag aag gtg ctg gtg aag gct gca tac aac cca ggc cag      461
Gln Leu Gly Glu Lys Val Leu Val Lys Ala Ala Tyr Asn Pro Gly Gln
 89                  94                  99                 104

gca gtg ccc tgg aat gct gtc aag gtg caa acg ctc tcc aac cag ccc      509
Ala Val Pro Trp Asn Ala Val Lys Val Gln Thr Leu Ser Asn Gln Pro
105                 110                 115                 120

cta ctg aag tcc cca gca cct cct ctt ctg cat gta gca gcc ctg ggc      557
Leu Leu Lys Ser Pro Ala Pro Pro Leu Leu His Val Ala Ala Leu Gly
121                 126                 131                 136

cag aag caa ggg atc ctg gga gct cag cct cag ttg atc ttc cag cct      605
Gln Lys Gln Gly Ile Leu Gly Ala Gln Pro Gln Leu Ile Phe Gln Pro
137                 142                 147                 152

cac cgg att ccc cca ctc ttt cct cag aag cct ctg agt ctc ttc caa      653
His Arg Ile Pro Pro Leu Phe Pro Gln Lys Pro Leu Ser Leu Phe Gln
153                 158                 163                 168

aca tcc cac aca ctt cac ctg agc cac ctg aac aga ttt cct gcc cgg      701
Thr Ser His Thr Leu His Leu Ser His Leu Asn Arg Phe Pro Ala Arg
169                 174                 179                 184

ggc cct cat gga cgg ttg gat cag ggc cga agt gat gac tat gac tcc      749
Gly Pro His Gly Arg Leu Asp Gln Gly Arg Ser Asp Asp Tyr Asp Ser
185                 190                 195                 200

aag aaa cgc aaa cag cgg gct ggt gga gag ccc tgg ggt gct aag aag      797
Lys Lys Arg Lys Gln Arg Ala Gly Gly Glu Pro Trp Gly Ala Lys Lys
201                 206                 211                 216

cca agg cat gac ctg cct cct tac cgg gtc cac ctc act cct tac act      845
Pro Arg His Asp Leu Pro Pro Tyr Arg Val His Leu Thr Pro Tyr Thr
217                 222                 227                 232

gtg gac agc ccc atc tgt gac ttc cta gaa ctc cag cgc cgt tac cgc      893
Val Asp Ser Pro Ile Cys Asp Phe Leu Glu Leu Gln Arg Arg Tyr Arg
233                 238                 243                 248

agc ctc ctg gtc ccc tca gat ttt ctg tcc gtg cat ctg agt tgg cta      941
Ser Leu Leu Val Pro Ser Asp Phe Leu Ser Val His Leu Ser Trp Leu
249                 254                 259                 264

tca gcc ttc ccc ctg agc cag ccc ttt tcc ctc cat cat cca agc cgg      989
Ser Ala Phe Pro Leu Ser Gln Pro Phe Ser Leu His His Pro Ser Arg
265                 270                 275                 280

atc cag gtc tct tct gaa aag gag gca gct cca gac gct ggt gct gag     1037
Ile Gln Val Ser Ser Glu Lys Glu Ala Ala Pro Asp Ala Gly Ala Glu
281                 286                 291                 296

ccc atc act gca gac agt gac ccc gct tat agt tca aag gta ctg ctg     1085
Pro Ile Thr Ala Asp Ser Asp Pro Ala Tyr Ser Ser Lys Val Leu Leu
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09/15/2005 15:36 [ref:0000]

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313                 318                 323                 328

gtg gat gac atg gct gag cca agg gag acg cca gag cat cct ctg aag     1181
Val Asp Asp Met Ala Glu Pro Arg Glu Thr Pro Glu His Pro Leu Lys
329                 334                 339                 344

cag att aag ttt ttg ctg ggc agg aaa gaa gag gag gca gtg ctg gtt     1229
Gln Ile Lys Phe Leu Leu Gly Arg Lys Glu Glu Glu Ala Val Leu Val
345                 350                 355                 360

ggg ggt gaa tgg tct cct tcc ctg gat ggc ctc gac ccc cag gct gac     1277
Gly Gly Glu Trp Ser Pro Ser Leu Asp Gly Leu Asp Pro Gln Ala Asp
361                 366                 371                 376

ccg cag gtg ctg gtg cgt acc gcc atc cgc tgt gcg cag gcc cag act     1325
Pro Gln Val Leu Val Arg Thr Ala Ile Arg Cys Ala Gln Ala Gln Thr
377                 382                 387                 392

ggc att gat ttg agc ggc tgt acc aag tgg tgg cgc ttt gcc gag ttt     1373
Gly Ile Asp Leu Ser Gly Cys Thr Lys Trp Trp Arg Phe Ala Glu Phe
393                 398                 403                 408

cag tac ctg cag ccg gga ccc ccc cgg cgg ctt cag aca gtg gtg gtg     1421
Gln Tyr Leu Gln Pro Gly Pro Pro Arg Arg Leu Gln Thr Val Val Val
409                 414                 419                 424

tac ctg ccg gat gtc tgg acc atc atg cct act ttg gag gag tgg gag     1469
Tyr Leu Pro Asp Val Trp Thr Ile Met Pro Thr Leu Glu Glu Trp Glu
425                 430                 435                 440

gcc ctg tgc cag cag aaa gct gca gag gca gct ccc cca acc cag gag     1517
Ala Leu Cys Gln Gln Lys Ala Ala Glu Ala Ala Pro Pro Thr Gln Glu
441                 446                 451                 456

gca caa ggg gaa acg gag cct act gaa cag gca cct gat gcc ttg gag     1565
Ala Gln Gly Glu Thr Glu Pro Thr Glu Gln Ala Pro Asp Ala Leu Glu
457                 462                 467                 472

caa gca gca gac act tct aga cgg aac gca gaa act cca gag gcc acc     1613
Gln Ala Ala Asp Thr Ser Arg Arg Asn Ala Glu Thr Pro Glu Ala Thr
473                 478                 483                 488

aca cag cag gaa acg gac act gat ctc cca gag gcc cct cca ccc ccc     1661
Thr Gln Gln Glu Thr Asp Thr Asp Leu Pro Glu Ala Pro Pro Pro Pro
489                 494                 499                 504

cta gaa cct gct gtc atc gca cgc cct ggc tgt gta aac ctg tcc ctc     1709
Leu Glu Pro Ala Val Ile Ala Arg Pro Gly Cys Val Asn Leu Ser Leu
505                 510                 515                 520

cat ggg att gtg gag gat cgg agg cca aag gaa agg atc tct ttt gag     1757
His Gly Ile Val Glu Asp Arg Arg Pro Lys Glu Arg Ile Ser Phe Glu
521                 526                 531                 536
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gtg atg gtg ctg gcc gag ctg ttt ctg gag atg ctc cag agg gat ttt     1805
Val Met Val Leu Ala Glu Leu Phe Leu Glu Met Leu Gln Arg Asp Phe
537                 542                 547                 552

ggc tat aga gtt tat aag atg cta ctg agc ctt cct gaa aag gtc gtg     1853
Gly Tyr Arg Val Tyr Lys Met Leu Leu Ser Leu Pro Glu Lys Val Val
553                 558                 563                 568

tcc cca cct gaa cct gag aag gag gag gcg gcc aag gaa gaa gcc acc     1901
Ser Pro Pro Glu Pro Glu Lys Glu Glu Ala Ala Lys Glu Glu Ala Thr
569                 574                 579                 584

aag gag gaa gaa gcc atc aaa gag gag gtg gtc aag gag ccc aag gat     1949
Lys Glu Glu Glu Ala Ile Lys Glu Glu Val Val Lys Glu Pro Lys Asp
585                 590                 595                 600

gag gca cag aat gag ggc ccg gct aca gag tca gag gcc ccg ctg aag     1997
Glu Ala Gln Asn Glu Gly Pro Ala Thr Glu Ser Glu Ala Pro Leu Lys
601                 606                 611                 616

gag gat ggg ctt ttg ccc aaa cca ctc tct tct ggg gga gag gaa gaa     2045
Glu Asp Gly Leu Leu Pro Lys Pro Leu Ser Ser Gly Gly Glu Glu Glu
617                 622                 627                 632

gaa aaa ccc cgg ggc gag gct tct gag gac ctg tgt gag atg gcc ctg     2093
Glu Lys Pro Arg Gly Glu Ala Ser Glu Asp Leu Cys Glu Met Ala Leu
633                 638                 643                 648

gac cca gaa ctg ttg ctt ctg agg gat gat gga gag gag gag ttt gca     2141
Asp Pro Glu Leu Leu Leu Leu Arg Asp Asp Gly Glu Glu Glu Phe Ala
649                 654                 659                 664

gga gca aag ctg gag gat tcg gag gtc cgg tcc gtt gcc tca aac cag     2189
Gly Ala Lys Leu Glu Asp Ser Glu Val Arg Ser Val Ala Ser Asn Gln
665                 670                 675                 680

tca gag atg gag ttc tct tca ctt cag gac atg ccc aag gag ctg gat     2237
Ser Glu Met Glu Phe Ser Ser Leu Gln Asp Met Pro Lys Glu Leu Asp
681                 686                 691                 696

ccc tct gct gtg ctc ccc tta gac tgt ctg ctt gct ttt gtg ttc ttt     2285
Pro Ser Ala Val Leu Pro Leu Asp Cys Leu Leu Ala Phe Val Phe Phe
697                 702                 707                 712

gat gcc aac tgg tgt ggc tac ttg cac cgg cga gac tta gag agg atc     2333
Asp Ala Asn Trp Cys Gly Tyr Leu His Arg Arg Asp Leu Glu Arg Ile
713                 718                 723                 728

ctc ctt acc ctt ggg atc cgg ctc agt gca gag cag gcc aag cag ctg     2381
Leu Leu Thr Leu Gly Ile Arg Leu Ser Ala Glu Gln Ala Lys Gln Leu
729                 734                 739                 744

gtc agc agg gtg gtg acc cag aac atc tgc cag tac cgg agc ctt cag     2429
Val Ser Arg Val Val Thr Gln Asn Ile Cys Gln Tyr Arg Ser Leu Gln
745                 750                 755                 760
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Tyr Ser Arg Gln Glu Gly Leu Asp Gly Gly Leu Pro Glu Glu Val Leu
761                 766                 771                 776

ttc gga aac ctg gac ctg ctg ccc cct cct ggg aaa agc acg aag cca     2525
Phe Gly Asn Leu Asp Leu Leu Pro Pro Pro Gly Lys Ser Thr Lys Pro
777                 782                 787                 792

ggt gct gcc ccc aca gaa cac aaa gcc ttg gtg tcc cac aat ggc agc     2573
Gly Ala Ala Pro Thr Glu His Lys Ala Leu Val Ser His Asn Gly Ser
793                 798                 803                 808

ctg att aac gtg ggg agc ctg ctg cag cgc gcg gag cag cag gac agc     2621
Leu Ile Asn Val Gly Ser Leu Leu Gln Arg Ala Glu Gln Gln Asp Ser
809                 814                 819                 824

ggc cgg ctc tac cta gag aac aag atc cac aca ctg gag ctg aag ctg     2669
Gly Arg Leu Tyr Leu Glu Asn Lys Ile His Thr Leu Glu Leu Lys Leu
825                 830                 835                 840

gag gag agc cat aac cgt ttc tca gcc act gaa gta acc aat aag acg     2717
Glu Glu Ser His Asn Arg Phe Ser Ala Thr Glu Val Thr Asn Lys Thr
841                 846                 851                 856

ctg gcg gca gag atg cag gag ctg cga gtc cgg ctg gcg gag gcc gag     2765
Leu Ala Ala Glu Met Gln Glu Leu Arg Val Arg Leu Ala Glu Ala Glu
857                 862                 867                 872

gag acc gcc cgg acg gcg gag cga cag aag agc cag ctc cag cgg ctg     2813
Glu Thr Ala Arg Thr Ala Glu Arg Gln Lys Ser Gln Leu Gln Arg Leu
873                 878                 883                 888

ctg cag gag ctc cgc agg cgt ctg acc ccc ctg cag ctg gag atc cag     2861
Leu Gln Glu Leu Arg Arg Arg Leu Thr Pro Leu Gln Leu Glu Ile Gln
889                 894                 899                 904

cgg gtg gtg gaa aag gct gac agc tgg gtg gag aag gag gag ccg gca     2909
Arg Val Val Glu Lys Ala Asp Ser Trp Val Glu Lys Glu Glu Pro Ala
905                 910                 915                 920

cct atc aac tga cgg cctcgcacgg aactgccatc ctgtgagggc agcggtggcg     2964
Pro Ile Asn  *
921

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Leu Pro Asp Ser Val Leu Leu Glu Ile Phe Ser Tyr Leu Pro Val Arg
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gac cgg atc cgc atc tcc agg gtc tgt cac cgc tgg aag agg ctg gtg      269
Asp Arg Ile Arg Ile Ser Arg Val Cys His Arg Trp Lys Arg Leu Val
 23                  28                  33                  38

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Asp Asp Arg Trp Leu Trp Arg His Val Asp Leu Thr Leu Tyr Thr Met
 39                  44                  49                  54

cga cct aaa gtc atg tgg cac ctc ctt cga agg tac atg gca tcc cgg      365
Arg Pro Lys Val Met Trp His Leu Leu Arg Arg Tyr Met Ala Ser Arg
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ccc cag ttg tcc cct gct ctg ttg aga gcc ctg ggc cag aag tgc ccc      461
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aac ctg aag cgc ctc tgc ctg cac gtg gcc gac ctg agc atg gtg ccc      509
Asn Leu Lys Arg Leu Cys Leu His Val Ala Asp Leu Ser Met Val Pro
103                 108                 113                 118

atc acc agc ctg ccc agc acc ttg agg acc ctg gag ctg cac agc tgc      557
Ile Thr Ser Leu Pro Ser Thr Leu Arg Thr Leu Glu Leu His Ser Cys
119                 124                 129                 134

gag atc tcc atg gcc tgg ctc cac aag cag cag gac ccc acc gtg ctg      605
Glu Ile Ser Met Ala Trp Leu His Lys Gln Gln Asp Pro Thr Val Leu
135                 140                 145                 150

ccc ctg ctt gaa tgc atc gtg ctg gac cgc gtc ccc gcc ttc cgt gac      653
Pro Leu Leu Glu Cys Ile Val Leu Asp Arg Val Pro Ala Phe Arg Asp
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gag cac ctg cag ggc ctg acg cgc ttc cgg gcc ttg cgc tcg ctg gtg      701
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Gln Glu Leu Ser Tyr Leu Gln Arg Leu Glu Val Leu Gly Cys Thr Leu
199                 204                 209                 214

tct gcc gac agc acc ctg ctg gcc atc agc cgc cac ctc cga gat gtg      845
Ser Ala Asp Ser Thr Leu Leu Ala Ile Ser Arg His Leu Arg Asp Val
215                 220                 225                 230

cgc aag atc cgg ctg acc gtg agg ggc ctc tct gcc cct ggc ctg gct      893
Arg Lys Ile Arg Leu Thr Val Arg Gly Leu Ser Ala Pro Gly Leu Ala
231                 236                 241                 246

gtg ctg gag gga atg ccg gcc ctg gag agt ctg tgc ctg cag ggt ccc      941
Val Leu Glu Gly Met Pro Ala Leu Glu Ser Leu Cys Leu Gln Gly Pro
247                 252                 257                 262

ctc gtc acc cca gaa atg ccc tcc ccc act gaa atc ctc tcc tcc tgc      989
Leu Val Thr Pro Glu Met Pro Ser Pro Thr Glu Ile Leu Ser Ser Cys
263                 268                 273                 278

ctc act atg ccc aag ctc aga gtc ctt gag ctg cag ggg ctg ggg tgg     1037
Leu Thr Met Pro Lys Leu Arg Val Leu Glu Leu Gln Gly Leu Gly Trp
279                 284                 289                 294

gag ggt cag gag gcg gag aag atc ctg tgt aag ggg ctg ccc cac tgt     1085
Glu Gly Gln Glu Ala Glu Lys Ile Leu Cys Lys Gly Leu Pro His Cys
295                 300                 305                 310

atg gtc atc gtc agg gct tgc ccc aaa gag tct atg gac tgg tgg atg     1133
Met Val Ile Val Arg Ala Cys Pro Lys Glu Ser Met Asp Trp Trp Met
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327

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Leu Leu Pro Leu Leu Ile Leu Cys Thr Val Ser Val Ala Ser Phe Glu
  7                  12                  17                  22

ctg aca cag cct ttt tca gtg tcc gtg tct ccg gga cag aca gcc acc     210
Leu Thr Gln Pro Phe Ser Val Ser Val Ser Pro Gly Gln Thr Ala Thr
 23                  28                  33                  38

atc acc tgc tca gga gat gtg ttg gca aaa aaa tat gtt cgg tgg ttc     258
Ile Thr Cys Ser Gly Asp Val Leu Ala Lys Lys Tyr Val Arg Trp Phe
 39                  44                  49                  54

cag cag aag ccg ggc cag gcc cct gtg ttg ttg att tat aaa gac act     306
Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Leu Ile Tyr Lys Asp Thr
 55                  60                  65                  70

gag cgg ccc tca ggg atc cct gac cga ttc tcc ggc ttc agc tca ggg     354
Glu Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Phe Ser Ser Gly
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71 76 81 86

acc aca gtc acc ttg acc atc agc ggg gcc cag gtt gaa gat gac gct 402
Thr Thr Val Thr Leu Thr Ile Ser Gly Ala Gln Val Glu Asp Asp Ala
87 92 97 102

gac tat tat tgt tac tct gcg gct gac aat act ctg gga gtg ttc ggc 450
Asp Tyr Tyr Cys Tyr Ser Ala Ala Asp Asn Thr Leu Gly Val Phe Gly
103 108 113 118

gga ggg acc aag ctg acc gtc cta agt cag ccc aag gct gcc ccc tcg 498
Gly Gly Thr Lys Leu Thr Val Leu Ser Gln Pro Lys Ala Ala Pro Ser
119 124 129 134

gtc act ctg ttc ccg ccc tcc tct gag gag ctt caa gcc aac aag gcc 546
Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala
135 140 145 150

aca ctg gtg tgt ctc ata agt gac ttc tac ccg cga gcc gtg aca gtg 594
Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Arg Ala Val Thr Val
151 156 161 166

gcc tgg aag gca gat agc agg ccc gtc aag gcg gga gtg gag acc acc 642
Ala Trp Lys Ala Asp Ser Arg Pro Val Lys Ala Gly Val Glu Thr Thr
167 172 177 182

aca ccc tcc aaa caa agc aac aac aag tac gcg gcc agc agc tac ctg 690
Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu
183 188 193 198

agc ctg acg cct gag cag tgg aag tcc cac aaa agc tac agc tgc cag 738
Ser Leu Thr Pro Glu Gln Trp Lys Ser His Lys Ser Tyr Ser Cys Gln
199 204 209 214

gtc acg cat gaa ggg agc acc gtg gag aag aca gtg gcc tca gaa caa 786
Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val Ala Ser Glu Gln
215 220 225 230

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Arg Gln Arg Pro Leu *
231 236

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gcctggggaa taatgcagta aaggaagtga gccggctcgg cctgactgct ccaacttcct    180

gctctcacac acaccagagg ggaaaaaaaa agaggagcga gagaaagaaa aaaaggggga    240

aaaatcagga tctcattaca agagccacag accgtctgca gacgcctgtc agcatggaaa    300

gtcgggggct ttcgcccggg tcctcctaga aattcccccc gaagaagact cccccacatc    360

tgggt    atg gag agt gca atc acg ctg tgg cag ttc ctg ttg cag ttg      407
         Met Glu Ser Ala Ile Thr Leu Trp Gln Phe Leu Leu Gln Leu
           1               5                  10

ctg ctg gat caa aaa cat gag cat ttg atc tgc tgg acc tcg aac gat      455
Leu Leu Asp Gln Lys His Glu His Leu Ile Cys Trp Thr Ser Asn Asp
 15                  20                  25                  30

ggt gaa ttc aag ctc ctc aaa gca gaa gaa gtg gcc aag ctg tgg gga      503
Gly Glu Phe Lys Leu Leu Lys Ala Glu Glu Val Ala Lys Leu Trp Gly
 31                  36                  41                  46

ctc cga aaa aac aaa aca aat atg aac tat gat aag ctg agc aga gcc      551
Leu Arg Lys Asn Lys Thr Asn Met Asn Tyr Asp Lys Leu Ser Arg Ala
 47                  52                  57                  62

ctg cga tac tat tat gac aag aac atc atc aag aag gtg atc ggg cag      599
Leu Arg Tyr Tyr Tyr Asp Lys Asn Ile Ile Lys Lys Val Ile Gly Gln
 63                  68                  73                  78

aag ttt gtg tac aag ttt gtc tct ttc ccg gag atc ctg aag atg gat      647
Lys Phe Val Tyr Lys Phe Val Ser Phe Pro Glu Ile Leu Lys Met Asp
 79                  84                  89                  94

cct cac gcg gtg gag atc agc cgg gag agc ctt ctg ctg cag gac agc      695
Pro His Ala Val Glu Ile Ser Arg Glu Ser Leu Leu Leu Gln Asp Ser
 95                 100                 105                 110

gac tgc aag gcg tct ccg gag ggc cgc gag gcc cac aaa cac ggc ctg      743
Asp Cys Lys Ala Ser Pro Glu Gly Arg Glu Ala His Lys His Gly Leu
111                 116                 121                 126

gcc gcc ctc aga agc acg agc cgc aac gaa tac atc cac tca ggc ctg      791
Ala Ala Leu Arg Ser Thr Ser Arg Asn Glu Tyr Ile His Ser Gly Leu
127                 132                 137                 142

tac tcg tcc ttc acc att aat tcc ctg cag aac cca cca gac gcc ttc      839
Tyr Ser Ser Phe Thr Ile Asn Ser Leu Gln Asn Pro Pro Asp Ala Phe
143                 148                 153                 158

aag gcc atc aag acg gag aag ctg gag gag ccg ccc gaa gac agc ccc      887
Lys Ala Ile Lys Thr Glu Lys Leu Glu Glu Pro Pro Glu Asp Ser Pro
159                 164                 169                 174

ccc gtg gaa gaa gtc agg act gtg atc agg ttt gtg acc aat aaa acc      935
Pro Val Glu Glu Val Arg Thr Val Ile Arg Phe Val Thr Asn Lys Thr
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175                 180                 185                 190

gac aag cac gtc acc agg ccg gtg gtg tcc ctg cct tcc acg tca gag      983
Asp Lys His Val Thr Arg Pro Val Val Ser Leu Pro Ser Thr Ser Glu
191                 196                 201                 206

gct gcg gcg gcg tcc gcc ttc ctg gcc tcg tcc gtc tcg gcc aag atc     1031
Ala Ala Ala Ala Ser Ala Phe Leu Ala Ser Ser Val Ser Ala Lys Ile
207                 212                 217                 222

tcc tct tta atg ttg cca aac gct gcc agt att tca tcc gcc tca ccc     1079
Ser Ser Leu Met Leu Pro Asn Ala Ala Ser Ile Ser Ser Ala Ser Pro
223                 228                 233                 238

ttc tca tct cgg tcc ccg tcc ctg tcc ccc aac tca ccc ctc cct tct     1127
Phe Ser Ser Arg Ser Pro Ser Leu Ser Pro Asn Ser Pro Leu Pro Ser
239                 244                 249                 254

gaa cac aga agc ctc ttc ctg gag gcc gcc tgc cat gac tcc gat tcc     1175
Glu His Arg Ser Leu Phe Leu Glu Ala Ala Cys His Asp Ser Asp Ser
255                 260                 265                 270

ctg gag ccc ttg aac ctg tca tcg ggc tcc aag acc aag tct cca tct     1223
Leu Glu Pro Leu Asn Leu Ser Ser Gly Ser Lys Thr Lys Ser Pro Ser
271                 276                 281                 286

ctt ccc cca aag gcc aaa aaa ccc aaa ggc ttg gaa atc tca gcg ccc     1271
Leu Pro Pro Lys Ala Lys Lys Pro Lys Gly Leu Glu Ile Ser Ala Pro
287                 292                 297                 302

ccg ctg gtg ctc tcc ggc acc gac atc ggc tcc atc gcc ctc aac agc     1319
Pro Leu Val Leu Ser Gly Thr Asp Ile Gly Ser Ile Ala Leu Asn Ser
303                 308                 313                 318

cca gcc ctc ccc tcg gga tcc ctc acc cca gcc ttc ttc acc gca cag     1367
Pro Ala Leu Pro Ser Gly Ser Leu Thr Pro Ala Phe Phe Thr Ala Gln
319                 324                 329                 334

aca cca aat gga ttg ctt ctg act ccg agt cca ctg ctc tcc agc ata     1415
Thr Pro Asn Gly Leu Leu Leu Thr Pro Ser Pro Leu Leu Ser Ser Ile
335                 340                 345                 350

cat ttc tgg agc agc ctt agt cca gtt gct ccg ctg agt cct gcc agg     1463
His Phe Trp Ser Ser Leu Ser Pro Val Ala Pro Leu Ser Pro Ala Arg
351                 356                 361                 366

ctg caa ggg cca agc acg ctg ttc cag ttc ccc aca ctg ctt aat ggc     1511
Leu Gln Gly Pro Ser Thr Leu Phe Gln Phe Pro Thr Leu Leu Asn Gly
367                 372                 377                 382

cac atg cca gtg cca atc ccc agt ctg gac aga gct gct tct cca gta     1559
His Met Pro Val Pro Ile Pro Ser Leu Asp Arg Ala Ala Ser Pro Val
383                 388                 393                 398

ctg ctt tct tca aac tct cag aaa tcc tga t gacgtctggc cacaattaag     1610
Leu Leu Ser Ser Asn Ser Gln Lys Ser  *
399                 404
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gactcattaa ctgatgaaac aaatttgtcc ccacgggcta gtttacctgt gtcgtgagaa 1670

ggacattgtg aaactcttgt taatttggtt tgcacttttc ataacatgga tagtctagat 1730

ttatgttagc attttaaaaa ctgtttttga tatattcaag tatatatgaa aatctgtttg 1790

gcattaagtg aattttaatg tttttgtttt tatatccttt tagctcttaa gtgttgaaca 1850

ctgttgacag tgaagaactt ttcttaatgg ttttcagtat aactaataag gatgtgaagc 1910

ttttttctct ttagttctga gtatgctaaa ctgtgtgctt atatagacta taaccagttg 1970

tgccttcctt cgcatttaat gtaaatgaat gatttatata ttttttagta ttaagaggaa 2030

atgtttgaaa gatgaaaatt agtatcaaac agctctctag tagaatttca ttatttttca 2090

ccagtgggca atatgaaagc atatatcacg ttttgtttta ctttcaattg tataagaatt 2150

gccttagaac ctcttttgaa ctgaaattca gtaaatgtcc aagtaatgtt tttataataa 2210

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gtgataagat actgccactg tgcccagcca agtgcagtat cttatcacac ctacttggca 180

ggctgaggtg ggagaatcgc ttgagctcag gagttcgaga ccagcctggg caatgtggcg 240

aaatccccgt ctttacaaaa acaaacaaac aaacaaaaaa gatattgcag ttgtgttgta 300

agcgtcctta tctttcagag ctacatagtg gaatgtttat ggaatattta ggataa 356

atg ata tac gca ttt ggg att tgc tgc aaa atg acc cag agt cag ggg 404
Met Ile Tyr Ala Phe Gly Ile Cys Cys Lys Met Thr Gln Ser Gln Gly
1 5 10 15

tca ggg gga gag gta gag atg aga caa gag gta gag ggg aga ggt aga 452
Ser Gly Gly Glu Val Glu Met Arg Gln Glu Val Glu Gly Arg Gly Arg
17 22 27 32

ggt agc cac gag ctg ata att aca gac aag aga tgc gga gta tgt ggg 500

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Gly Ser His Glu Leu Ile Ile Thr Asp Lys Arg Cys Gly Val Cys Gly
 33                  38                  43                  48

ggc tca tta tcc tgc ata gtc tat ctt tgt ata tct ttg aac ttt tca      548
Gly Ser Leu Ser Cys Ile Val Tyr Leu Cys Ile Ser Leu Asn Phe Ser
 49                  54                  59                  64

aga ata aaa aag ctt aaa aag tat aca tgg cct ggt cct acc aga gac      596
Arg Ile Lys Lys Leu Lys Lys Tyr Thr Trp Pro Gly Pro Thr Arg Asp
 65                  70                  75                  80

tca ccc aat gcc agc ctc cag cca ggg aga gcc aag ttt gca ttt tca      644
Ser Pro Asn Ala Ser Leu Gln Pro Gly Arg Ala Lys Phe Ala Phe Ser
 81                  86                  91                  96

cac gca tct cac act cct ctg cac tct caa ctt gga gag ctc caa aca      692
His Ala Ser His Thr Pro Leu His Ser Gln Leu Gly Glu Leu Gln Thr
 97                 102                 107                 112

ggg aaa ccc caa gcc ttg ctg gct tct gcc aac ccc ctg agc aga agc      740
Gly Lys Pro Gln Ala Leu Leu Ala Ser Ala Asn Pro Leu Ser Arg Ser
113                 118                 123                 128

atg ggt ccc cct gat cac cac ctc acc acc ctc atc ctg atc tca ctg      788
Met Gly Pro Pro Asp His His Leu Thr Thr Leu Ile Leu Ile Ser Leu
129                 134                 139                 144

tac act ccc ttt cct ggt ctg cta agt agc ggg tgt ttt cct tga cac      836
Tyr Thr Pro Phe Pro Gly Leu Leu Ser Ser Gly Cys Phe Pro  *
145                 150                 155

taacgctaca gctagaccac ggtgggcttg gcaacaggtg tcttcccaga tgctggcgtt    896

accgctagac caaggagccc tctggtggcc ctgtccgggc ataacagaaa gctcgcactc    956

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Document 2 - Page 948 of 1000

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tgccgccgtt cctaggagac caaggagcag caagcctgcg ggggaggggg agcaagtggg    180

ttgctgcttt tagcagctga aagggctgca gggagctctg ggtaagacat tttctgttgc    240
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tgctgctttt gcggtagaag ctgctgcgag taagtcagag gaaggaggat tgagaaggga    300

ggaggcttca cttgcagcca tgctgaatca ctgttgctga tcagatttcc cactggtctg    360

ctgggagaat caagaacaga actaggatcc ccgagtgcat acacagttca gcagctacca    420

ccctggctgg gcctcacaca    atg gag ggt gaa agt gtc aag ctg agc tcc      470
                         Met Glu Gly Glu Ser Val Lys Leu Ser Ser
                           1               5

cag act ctg ata cag gct ggg gat gat gag aag aac cag agg acg atc      518
Gln Thr Leu Ile Gln Ala Gly Asp Asp Glu Lys Asn Gln Arg Thr Ile
 11                  16                  21                  26

act gtc aac cct gcc cac atg ggg aaa gca ttc aag gtt atg aat gaa      566
Thr Val Asn Pro Ala His Met Gly Lys Ala Phe Lys Val Met Asn Glu
 27                  32                  37                  42

ctg cgg agt aaa cag ctg ttg tgt gac gtg atg att gtg gca gaa gat      614
Leu Arg Ser Lys Gln Leu Leu Cys Asp Val Met Ile Val Ala Glu Asp
 43                  48                  53                  58

gtc gag ata gaa gcc cac cgt gtg gtc ctg gca gcc tgc agc ccc tac      662
Val Glu Ile Glu Ala His Arg Val Val Leu Ala Ala Cys Ser Pro Tyr
 59                  64                  69                  74

ttc tgt gcg atg ttc aca ggt gac atg tct gag agt aaa gcc aaa aag      710
Phe Cys Ala Met Phe Thr Gly Asp Met Ser Glu Ser Lys Ala Lys Lys
 75                  80                  85                  90

ata gaa atc aag gac gtg gat ggg cag acg ctg agt aag ctg att gac      758
Ile Glu Ile Lys Asp Val Asp Gly Gln Thr Leu Ser Lys Leu Ile Asp
 91                  96                 101                 106

tac atc tat act gct gaa atc gag gtg act gaa gag aat gtc cag gtg      806
Tyr Ile Tyr Thr Ala Glu Ile Glu Val Thr Glu Glu Asn Val Gln Val
107                 112                 117                 122

ctg ctc ccg gca gcc agc ttg ctg cag ctc atg gat gtt cgg cag aac      854
Leu Leu Pro Ala Ala Ser Leu Leu Gln Leu Met Asp Val Arg Gln Asn
123                 128                 133                 138

tgc tgt gac ttc ctg cag tct cag ttg cat ccc acc aat tgc ctg ggc      902
Cys Cys Asp Phe Leu Gln Ser Gln Leu His Pro Thr Asn Cys Leu Gly
139                 144                 149                 154

atc cgt gcg ttt gca gat gta cac acc tgc act gac ctt ctg cag cag      950
Ile Arg Ala Phe Ala Asp Val His Thr Cys Thr Asp Leu Leu Gln Gln
155                 160                 165                 170

gcc aat gcc tac gca gag cag cac ttt cca gag gtg atg cta gga gaa      998
Ala Asn Ala Tyr Ala Glu Gln His Phe Pro Glu Val Met Leu Gly Glu
171                 176                 181                 186

gaa ttt ctt agc ctg agt ctg gac cag gtg tgc agc ttg ata tcc agc     1046
Glu Phe Leu Ser Leu Ser Leu Asp Gln Val Cys Ser Leu Ile Ser Ser
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187                 192                 197                 202

gac aag ctg acc gtt tct tca gaa gag aag gtg ttt gaa gct gtg atc     1094
Asp Lys Leu Thr Val Ser Ser Glu Glu Lys Val Phe Glu Ala Val Ile
203                 208                 213                 218

tca tgg atc aat tat gag aaa gaa aac cgt tta gag cac atg gca aag     1142
Ser Trp Ile Asn Tyr Glu Lys Glu Asn Arg Leu Glu His Met Ala Lys
219                 224                 229                 234

ctg atg gaa cat gtc cga ctt cct ctc tta cct agg gac tac cta gtc     1190
Leu Met Glu His Val Arg Leu Pro Leu Leu Pro Arg Asp Tyr Leu Val
235                 240                 245                 250

caa acg gtt gaa gaa gaa gct ttg ata aag aat aac aac acc tgt aaa     1238
Gln Thr Val Glu Glu Glu Ala Leu Ile Lys Asn Asn Asn Thr Cys Lys
251                 256                 261                 266

gac ttc ctc att gag gcc atg aaa tac cat ctc ctc cct ctg gat cag     1286
Asp Phe Leu Ile Glu Ala Met Lys Tyr His Leu Leu Pro Leu Asp Gln
267                 272                 277                 282

aga cta ttg att aag aac cca agg acc aag ccc agg act cca gtc agc     1334
Arg Leu Leu Ile Lys Asn Pro Arg Thr Lys Pro Arg Thr Pro Val Ser
283                 288                 293                 298

ctt ccc aag gtc atg att gtg gtt ggc ggc cag gca ccc aag gca atc     1382
Leu Pro Lys Val Met Ile Val Val Gly Gly Gln Ala Pro Lys Ala Ile
299                 304                 309                 314

cgc agt gtg gag tgc tat gat ttc gag gag gac cgg tgg gat cag att     1430
Arg Ser Val Glu Cys Tyr Asp Phe Glu Glu Asp Arg Trp Asp Gln Ile
315                 320                 325                 330

gct gag ctt cct tcc aga aga tgc aga gca ggt gtg gtg ttc atg gct     1478
Ala Glu Leu Pro Ser Arg Arg Cys Arg Ala Gly Val Val Phe Met Ala
331                 336                 341                 346

ggc cac gtg tat gcc gtg gga ggg ttt aat ggc tca ctg cgg gtg cgg     1526
Gly His Val Tyr Ala Val Gly Gly Phe Asn Gly Ser Leu Arg Val Arg
347                 352                 357                 362

aca gtg gat gtg tat gac ggc gtg aag gac cag tgg acg tcc att gcc     1574
Thr Val Asp Val Tyr Asp Gly Val Lys Asp Gln Trp Thr Ser Ile Ala
363                 368                 373                 378

agc atg cag gag cgc cgg agc aca ctg ggc gca gcg gtg ctc aat gac     1622
Ser Met Gln Glu Arg Arg Ser Thr Leu Gly Ala Ala Val Leu Asn Asp
379                 384                 389                 394

ttg ctc tac gca gtg gga ggc ttt gat ggc agt act ggc cta gca tcg     1670
Leu Leu Tyr Ala Val Gly Gly Phe Asp Gly Ser Thr Gly Leu Ala Ser
395                 400                 405                 410

gtg gaa gcc tac agc tac aag acc aac gag tgg ttc ttt gtg gcc ccg     1718
Val Glu Ala Tyr Ser Tyr Lys Thr Asn Glu Trp Phe Phe Val Ala Pro
411                 416                 421                 426
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atg aac acg cgg cag agc agt gtg ggt gtg ggc gtt gtg gag ggg aag     1766
Met Asn Thr Arg Gln Ser Ser Val Gly Val Gly Val Val Glu Gly Lys
427                 432                 437                 442

cta tat gct gtt ggg ggt tat gat gga gct tcc cgc cag tgt ctg agc     1814
Leu Tyr Ala Val Gly Gly Tyr Asp Gly Ala Ser Arg Gln Cys Leu Ser
443                 448                 453                 458

act gtg gaa cag tac aac cca gcg acc aat gaa tgg ata tac gtg gcg     1862
Thr Val Glu Gln Tyr Asn Pro Ala Thr Asn Glu Trp Ile Tyr Val Ala
459                 464                 469                 474

gac atg agc acc cgc cgc agt ggc gca ggg gtt gga gtg ctt agc gga     1910
Asp Met Ser Thr Arg Arg Ser Gly Ala Gly Val Gly Val Leu Ser Gly
475                 480                 485                 490

cag ctg tac gcc aca ggt ggg cat gat ggg cct ttg gtg agg aag agc     1958
Gln Leu Tyr Ala Thr Gly Gly His Asp Gly Pro Leu Val Arg Lys Ser
491                 496                 501                 506

gtt gag gtt tac gat cct gga aca aat acc tgg aag caa gtg gca gac     2006
Val Glu Val Tyr Asp Pro Gly Thr Asn Thr Trp Lys Gln Val Ala Asp
507                 512                 517                 522

atg aac atg tgc cgg cgc aac gca ggg gtc tgt gca gta aat ggg ctc     2054
Met Asn Met Cys Arg Arg Asn Ala Gly Val Cys Ala Val Asn Gly Leu
523                 528                 533                 538

ctg tat gtg gtt gga ggg gat gat gga tcc tgc aac ttg gct tcg gtg     2102
Leu Tyr Val Val Gly Gly Asp Asp Gly Ser Cys Asn Leu Ala Ser Val
539                 544                 549                 554

gag tac tac aat cct gtc act gac aaa tgg acg ctg ctt cca acg aac     2150
Glu Tyr Tyr Asn Pro Val Thr Asp Lys Trp Thr Leu Leu Pro Thr Asn
555                 560                 565                 570

atg agc acg ggg cgg agc tat gca ggt gtt gcc gtg att cac aag tcc     2198
Met Ser Thr Gly Arg Ser Tyr Ala Gly Val Ala Val Ile His Lys Ser
571                 576                 581                 586

ttg tga cccaaactcc tactgccagg aggtggagga aggagcaggt gctgcctgtg      2254
Leu  *
587

actctgaaca gcaggacctt ggtgactgga ttcaacttgc ttgggagggt ctgtgctgct   2314

gtgagaaccg ctctcctctg acttggcaga ctggtgttgt tcatcgcagt gtggacacca   2374

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                                   1               5

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Val Leu Ser Gly Phe Val Leu Gly Ala Leu Ala Phe Gln His Leu Asn
  9                  14                  19                  24

acg gac tcg gac acg gaa ggt ttt ctt ctt ggg gaa gta aaa ggt gaa      148
Thr Asp Ser Asp Thr Glu Gly Phe Leu Leu Gly Glu Val Lys Gly Glu
 25                  30                  35                  40

gcc aag aac agc att act gat tcc caa atg gat gat gtt gaa gtt gtt      196
Ala Lys Asn Ser Ile Thr Asp Ser Gln Met Asp Asp Val Glu Val Val
 41                  46                  51                  56

tat aca att gac att cag aaa tat att cca tgc tat cag ctt ttt agc      244
Tyr Thr Ile Asp Ile Gln Lys Tyr Ile Pro Cys Tyr Gln Leu Phe Ser
 57                  62                  67                  72

ttt tat aat tct tca ggc gaa gta aat gag caa gca ctg aag aaa ata      292
Phe Tyr Asn Ser Ser Gly Glu Val Asn Glu Gln Ala Leu Lys Lys Ile
 73                  78                  83                  88

tta tca aat gtc aaa aag aat gtg gta ggt tgg tac aaa ttc cgt cgt      340
Leu Ser Asn Val Lys Lys Asn Val Val Gly Trp Tyr Lys Phe Arg Arg
 89                  94                  99                 104

cat tca gat cag atc atg acg ttt aga gag agg ctg ctt cac aaa aac      388
His Ser Asp Gln Ile Met Thr Phe Arg Glu Arg Leu Leu His Lys Asn
105                 110                 115                 120

ttg cag gag cat ttt tca aac caa gac ctt gtt ttt ctg cta tta aca      436
Leu Gln Glu His Phe Ser Asn Gln Asp Leu Val Phe Leu Leu Leu Thr
121                 126                 131                 136

cca agt ata ata aca gaa agc tgc tct act cat cga ctg gaa cat tcc      484
Pro Ser Ile Ile Thr Glu Ser Cys Ser Thr His Arg Leu Glu His Ser
137                 142                 147                 152

tta tat aaa cct caa aaa gga ctt ttt cac agg gta cct tta gtg gtt      532
Leu Tyr Lys Pro Gln Lys Gly Leu Phe His Arg Val Pro Leu Val Val
153                 158                 163                 168

gcc aat ctg ggc atg tct gaa caa ctg ggt tat aaa act gta tca ggt      580
Ala Asn Leu Gly Met Ser Glu Gln Leu Gly Tyr Lys Thr Val Ser Gly
169                 174                 179                 184

tcc tgt atg tcc act ggt ttt agc cga gca gta caa aca cac agc tct      628
Ser Cys Met Ser Thr Gly Phe Ser Arg Ala Val Gln Thr His Ser Ser
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185                 190                 195                 200

aaa ttt ttt gaa gaa gat gga tcc tta aag gag gta cat aag ata aat      676
Lys Phe Phe Glu Glu Asp Gly Ser Leu Lys Glu Val His Lys Ile Asn
201                 206                 211                 216

gaa atg tat gct tca tta caa gag gaa tta aag ctc tac tcc ttt tct      724
Glu Met Tyr Ala Ser Leu Gln Glu Glu Leu Lys Leu Tyr Ser Phe Ser
217                 222                 227                 232

gaa tgt cat ctt cat cca gga tcc agg ctg aag gag cag ccc tta ttt      772
Glu Cys His Leu His Pro Gly Ser Arg Leu Lys Glu Gln Pro Leu Phe
233                 238                 243                 248

ggg aca tgt cct cat ggc ata agg caa aga gca aga aag cta gtg gag      820
Gly Thr Cys Pro His Gly Ile Arg Gln Arg Ala Arg Lys Leu Val Glu
249                 254                 259                 264

cca ggc gcg gtg gct cgc gcc tgt ggt ccc agc gct ttg gga ggc cga      868
Pro Gly Ala Val Ala Arg Ala Cys Gly Pro Ser Ala Leu Gly Gly Arg
265                 270                 275                 280

ggt ggg cgg atc gcg agg tca ggg ggt cga gac cat cct ggc tag cac      916
Gly Gly Arg Ile Ala Arg Ser Gly Gly Arg Asp His Pro Gly  *
281                 286                 291

ggtgaggccc cgtctctact agaagtgcag aaaaaattgg ccgggcgtgg tggtgggcgc    976

ctgtggtccc ggctactcgg gtggctgggg caggggaatg gcgtgagccc gggggatgga   1036

gcttgcggtg ggccgggatc gtgccgctgc actccagcct gggcgacagg gcgggactcc   1096

gtctcaaaaa aaaaaaaa                                                1114
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<210> 321
<211> 936
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(933)

<400> 321

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atg ttc agt ctg atg gcc agt tgc tgc ggc tgg ttc aag cgg tgg cgg      48
Met Phe Ser Leu Met Ala Ser Cys Cys Gly Trp Phe Lys Arg Trp Arg
  1               5                  10

gag cct gtc aga aag gtg act ctt ttg atg gtg gga ctt gat aat gct       96
Glu Pro Val Arg Lys Val Thr Leu Leu Met Val Gly Leu Asp Asn Ala
 17                  22                  27                  32

ggt aaa acc gca aca gca aag gga atc caa gga gaa tac cct gaa gat      144
Gly Lys Thr Ala Thr Ala Lys Gly Ile Gln Gly Glu Tyr Pro Glu Asp
```

```
 33                  38                  43                  48

gta gct cct act gtt gga ttt tca aaa att aac ctt aga caa gga aag      192
Val Ala Pro Thr Val Gly Phe Ser Lys Ile Asn Leu Arg Gln Gly Lys
 49                  54                  59                  64

ttt gaa gtc acc atc ttt gac ttg gga ggt gga ata aga att cgg gga      240
Phe Glu Val Thr Ile Phe Asp Leu Gly Gly Gly Ile Arg Ile Arg Gly
 65                  70                  75                  80

atc tgg aag aat tac tat gct gaa tcc tat ggg gta ata ttt gtt gtg      288
Ile Trp Lys Asn Tyr Tyr Ala Glu Ser Tyr Gly Val Ile Phe Val Val
 81                  86                  91                  96

gat tcc agt gat gaa gag aga atg gaa gag aca aaa gag gct atg tca      336
Asp Ser Ser Asp Glu Glu Arg Met Glu Glu Thr Lys Glu Ala Met Ser
 97                 102                 107                 112

gaa atg cta aga cat cct agg ata tcg gga aag cct ata ttg gtg ttg      384
Glu Met Leu Arg His Pro Arg Ile Ser Gly Lys Pro Ile Leu Val Leu
113                 118                 123                 128

gca aat aaa caa gat aaa gaa gga gct tta gga gaa gct gat gtc att      432
Ala Asn Lys Gln Asp Lys Glu Gly Ala Leu Gly Glu Ala Asp Val Ile
129                 134                 139                 144

gaa tgt cta tct ctg gaa aaa ttg gtc aat gag cac aag tgc ctg tgt      480
Glu Cys Leu Ser Leu Glu Lys Leu Val Asn Glu His Lys Cys Leu Cys
145                 150                 155                 160

cag ata gaa cca tgt tca gca atc tcg ggg tat gga aag aaa att gac      528
Gln Ile Glu Pro Cys Ser Ala Ile Ser Gly Tyr Gly Lys Lys Ile Asp
161                 166                 171                 176

aag tcc att aaa aaa ggc ctt tat tgg ctg cta cat gtt att gca aga      576
Lys Ser Ile Lys Lys Gly Leu Tyr Trp Leu Leu His Val Ile Ala Arg
177                 182                 187                 192

gac ttt gat gcc tta aat gaa cgc atc caa aaa gag aca aca gag cag      624
Asp Phe Asp Ala Leu Asn Glu Arg Ile Gln Lys Glu Thr Thr Glu Gln
193                 198                 203                 208

cgt gct ctt gag gaa caa gag aaa caa gaa aga gct gaa cga gtg cga      672
Arg Ala Leu Glu Glu Gln Glu Lys Gln Glu Arg Ala Glu Arg Val Arg
209                 214                 219                 224

ata tta cga gaa gaa aga aaa caa aat gaa cag gag cag gct gaa ctc      720
Ile Leu Arg Glu Glu Arg Lys Gln Asn Glu Gln Glu Gln Ala Glu Leu
225                 230                 235                 240

gat gga acc agt ggt ctg gct gag ttg gac cca gaa cca acg aat cct      768
Asp Gly Thr Ser Gly Leu Ala Glu Leu Asp Pro Glu Pro Thr Asn Pro
241                 246                 251                 256

ttc cag cca ata gca tct gta atc att gag aat gaa gga aaa ctt gaa      816
Phe Gln Pro Ile Ala Ser Val Ile Ile Glu Asn Glu Gly Lys Leu Glu
257                 262                 267                 272
```

```
aga gag aaa aaa aac caa aaa atg gag aaa gac agt gat ggc tgc cac      864
Arg Glu Lys Lys Asn Gln Lys Met Glu Lys Asp Ser Asp Gly Cys His
273                 278                 283                 288

ctg aaa cat aaa atg gag cat gag caa ata gag aca caa ggc cag gtt      912
Leu Lys His Lys Met Glu His Glu Gln Ile Glu Thr Gln Gly Gln Val
289                 294                 299                 304

aat cac aat ggc caa aaa aaa taa                                     936
Asn His Asn Gly Gln Lys Lys
305                 310
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<210> 322
<211> 1488
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(1485)

<400> 322

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atg agg tct ccg gtt cga gac ctg gcc cgg aac gat ggc gag gag agc      48
Met Arg Ser Pro Val Arg Asp Leu Ala Arg Asn Asp Gly Glu Glu Ser
  1               5                  10

acg gac cgc acg cct ctt cta ccg ggc gcc cca cgg gcc gaa gcc gct      96
Thr Asp Arg Thr Pro Leu Leu Pro Gly Ala Pro Arg Ala Glu Ala Ala
 17                  22                  27                  32

cca gtg tgc tgc tct gct cgt tac aac tta gca att ttg gcc ttt ttt     144
Pro Val Cys Cys Ser Ala Arg Tyr Asn Leu Ala Ile Leu Ala Phe Phe
 33                  38                  43                  48

ggt ttc ttc att gtg tat gca tta cgt gtg aat ctg agt gtt gcg tta     192
Gly Phe Phe Ile Val Tyr Ala Leu Arg Val Asn Leu Ser Val Ala Leu
 49                  54                  59                  64

gtg gat atg gta gat tca aat aca act tta gaa gat aat aga act tcc     240
Val Asp Met Val Asp Ser Asn Thr Thr Leu Glu Asp Asn Arg Thr Ser
 65                  70                  75                  80

aag gcg tgt cca gag cat tct gct ccc ata aaa gtt cat cat aat caa     288
Lys Ala Cys Pro Glu His Ser Ala Pro Ile Lys Val His His Asn Gln
 81                  86                  91                  96

acg ggt aag aag tac caa tgg gat gca gaa act caa gga tgg att ctc     336
Thr Gly Lys Lys Tyr Gln Trp Asp Ala Glu Thr Gln Gly Trp Ile Leu
 97                 102                 107                 112

ggt tcc ttt ttt tat ggc tac atc atc aca cag att cct gga gga tat     384
Gly Ser Phe Phe Tyr Gly Tyr Ile Ile Thr Gln Ile Pro Gly Gly Tyr
```

```
113                 118                 123                 128

gtt gcc agc aaa ata ggg ggg aaa atg ctg cta gga ttt ggg atc ctt      432
Val Ala Ser Lys Ile Gly Gly Lys Met Leu Leu Gly Phe Gly Ile Leu
129                 134                 139                 144

ggc act gct gtc ctc acc ctg ttc act ccc att gct gca gat tta gga      480
Gly Thr Ala Val Leu Thr Leu Phe Thr Pro Ile Ala Ala Asp Leu Gly
145                 150                 155                 160

gtt gga cca ctc att gta ctc aga gca cta gaa gga cta gga gag ggt      528
Val Gly Pro Leu Ile Val Leu Arg Ala Leu Glu Gly Leu Gly Glu Gly
161                 166                 171                 176

gtt aca ttt cca gcc atg cat gcc atg tgg tct tct tgg gct ccc cct      576
Val Thr Phe Pro Ala Met His Ala Met Trp Ser Ser Trp Ala Pro Pro
177                 182                 187                 192

ctt gaa aga agc aaa ctt ctt agc att tca tat gca gga gca cag ctt      624
Leu Glu Arg Ser Lys Leu Leu Ser Ile Ser Tyr Ala Gly Ala Gln Leu
193                 198                 203                 208

ggg aca gta att tct ctt cct ctt tct gga ata att tgc tac tat atg      672
Gly Thr Val Ile Ser Leu Pro Leu Ser Gly Ile Ile Cys Tyr Tyr Met
209                 214                 219                 224

aat tgg act tat gtc ttc tac ttt ttt ggt act att gga ata ttt tgg      720
Asn Trp Thr Tyr Val Phe Tyr Phe Phe Gly Thr Ile Gly Ile Phe Trp
225                 230                 235                 240

ttt ctt ttg tgg atc tgg tta gtt agt gac aca cca caa aaa cac aag      768
Phe Leu Leu Trp Ile Trp Leu Val Ser Asp Thr Pro Gln Lys His Lys
241                 246                 251                 256

aga att tcc cat tat gaa aag gaa tac att ctt tca tca tta aga aat      816
Arg Ile Ser His Tyr Glu Lys Glu Tyr Ile Leu Ser Ser Leu Arg Asn
257                 262                 267                 272

cag ctt tct tca cag aag tca ggg ccg tgg gta ccc att tta aaa tcc      864
Gln Leu Ser Ser Gln Lys Ser Gly Pro Trp Val Pro Ile Leu Lys Ser
273                 278                 283                 288

ctg cca ctt tgg gct atc gta gtt gca cac ttt tct tac aac tgg act      912
Leu Pro Leu Trp Ala Ile Val Val Ala His Phe Ser Tyr Asn Trp Thr
289                 294                 299                 304

ttt tat act tta ttg aca tta ttg cct act tat atg aag gag atc cta      960
Phe Tyr Thr Leu Leu Thr Leu Leu Pro Thr Tyr Met Lys Glu Ile Leu
305                 310                 315                 320

agg ttc aat gtt caa gag aat ggg ttt tta tct tca ttg cct tat tta     1008
Arg Phe Asn Val Gln Glu Asn Gly Phe Leu Ser Ser Leu Pro Tyr Leu
321                 326                 331                 336

ggc tct tgg tta tgt atg atc ctg tct ggt caa gct gct gac aat tta     1056
Gly Ser Trp Leu Cys Met Ile Leu Ser Gly Gln Ala Ala Asp Asn Leu
337                 342                 347                 352
```

```
agg gca aaa tgg aat ttt tca act tta tgt gtt cgc aga att ttt agc     1104
Arg Ala Lys Trp Asn Phe Ser Thr Leu Cys Val Arg Arg Ile Phe Ser
353                 358                 363                 368

ctt ata gga atg att gga cct gca gta ttc ctg gta gct gct ggc ttc     1152
Leu Ile Gly Met Ile Gly Pro Ala Val Phe Leu Val Ala Ala Gly Phe
369                 374                 379                 384

att ggc tgt gat tat tct ttg gcc gtt gct ttc cta act ata tca aca     1200
Ile Gly Cys Asp Tyr Ser Leu Ala Val Ala Phe Leu Thr Ile Ser Thr
385                 390                 395                 400

aca ctg gga ggc ttt tgc tct tct gga ttt agc atc aac cat ctg gat     1248
Thr Leu Gly Gly Phe Cys Ser Ser Gly Phe Ser Ile Asn His Leu Asp
401                 406                 411                 416

att gct cct tcg tat gct ggt atc ctc ctg ggc atc aca aat aca ttt     1296
Ile Ala Pro Ser Tyr Ala Gly Ile Leu Leu Gly Ile Thr Asn Thr Phe
417                 422                 427                 432

gcc act att cca gga atg gtt ggg ccc gtc att gct aaa agt ctg acc     1344
Ala Thr Ile Pro Gly Met Val Gly Pro Val Ile Ala Lys Ser Leu Thr
433                 438                 443                 448

cct gat aac act gtt gga gaa tgg caa acc gtg ttc tat att gct gct     1392
Pro Asp Asn Thr Val Gly Glu Trp Gln Thr Val Phe Tyr Ile Ala Ala
449                 454                 459                 464

gct att aat gtt ttt ggt gcc att ttc ttt aca cta ttc gcc aaa ggt     1440
Ala Ile Asn Val Phe Gly Ala Ile Phe Phe Thr Leu Phe Ala Lys Gly
465                 470                 475                 480

gaa gta caa aac tgg gct ctc aat gat cac cat gga cac aga cac tga     1488
Glu Val Gln Asn Trp Ala Leu Asn Asp His His Gly His Arg His
481                 486                 491
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<210> 323
<211> 1606
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (351)..(1331)

<220>
<221> misc_feature
<222> (1)...(1606)
<223> n = a,t,c or g

<400> 323
agagcccgcc taaaatttac cctcactaaa gggaataagc ttgcggccgc cgcctccaaa 60

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gggacggttt tctagagctc cgacgcctct cggtgcccct ctgctccggc ccttgccctt    120

tgacctcgct ctcgcggcag ggtgagaggt cgggtggcca tcttgtggcg gcggcgcggg    180

cggctgttac tgcggagacc catcccctcc cccttctcgc acccctggca gtctgtcagt    240

cggtaaaaag tcccgcagcc tgtcaggtga ggccccggcc tcgtgccgtc gctcttcccg    300

ccgcactggg cggcccaggc cgctccctgc cgggcctcac tgccgccacc   atg tcc     356
                                                          Met Ser
                                                            1

tcc ttc tct gag tcg gcg ctg gag aag aag ctc tcg gag ctg agc aac      404
Ser Phe Ser Glu Ser Ala Leu Glu Lys Lys Leu Ser Glu Leu Ser Asn
  3                   8                  13                  18

tct cag cag agc gtg cag acc ctg tcc ctt tgg ctc atc cac cac cgc      452
Ser Gln Gln Ser Val Gln Thr Leu Ser Leu Trp Leu Ile His His Arg
 19                  24                  29                  34

aag cac gcg gga ccc atc gtc tcc gtg tgg cac cgc gag ctc cgc aaa      500
Lys His Ala Gly Pro Ile Val Ser Val Trp His Arg Glu Leu Arg Lys
 35                  40                  45                  50

gcc aaa tca aat aga aag ctt act ttt ctg tat tta gcg aat gat gtc      548
Ala Lys Ser Asn Arg Lys Leu Thr Phe Leu Tyr Leu Ala Asn Asp Val
 51                  56                  61                  66

atc caa aac agt aaa agg aaa gga cct gaa ttc act aga gaa ttt gaa      596
Ile Gln Asn Ser Lys Arg Lys Gly Pro Glu Phe Thr Arg Glu Phe Glu
 67                  72                  77                  82

tct gtc ctt gtg gat gct ttt tct cat gtt gcc aga gag gca gat gaa      644
Ser Val Leu Val Asp Ala Phe Ser His Val Ala Arg Glu Ala Asp Glu
 83                  88                  93                  98

ggc tgt aaa aaa cct tta gaa aga ttg ctg aac atc tgg caa gaa cga      692
Gly Cys Lys Lys Pro Leu Glu Arg Leu Leu Asn Ile Trp Gln Glu Arg
 99                 104                 109                 114

agt gtg tat ggc ggc gag ttc ata cag cag ctg aag ctg tct atg gag      740
Ser Val Tyr Gly Gly Glu Phe Ile Gln Gln Leu Lys Leu Ser Met Glu
115                 120                 125                 130

gac tcc aag agc cct ccc ccc aaa gca aca gaa gag aag aaa tct ctg      788
Asp Ser Lys Ser Pro Pro Pro Lys Ala Thr Glu Glu Lys Lys Ser Leu
131                 136                 141                 146

aaa cga act ttt cag caa att cag gag gag gag gat gac gac tac cct      836
Lys Arg Thr Phe Gln Gln Ile Gln Glu Glu Glu Asp Asp Asp Tyr Pro
147                 152                 157                 162

ggc agc tac tct cct cag gat cct tct gca gga ccc ctc ttg act gag      884
Gly Ser Tyr Ser Pro Gln Asp Pro Ser Ala Gly Pro Leu Leu Thr Glu
163                 168                 173                 178
```

```
gaa cta atc aaa gct ttg cag gat ctg gaa aat gcc gca tca ggg gat      932
Glu Leu Ile Lys Ala Leu Gln Asp Leu Glu Asn Ala Ala Ser Gly Asp
179                 184                 189                 194

gct act gtc cga cag aaa att gct tct ctg ccc cag gaa gtg caa gat      980
Ala Thr Val Arg Gln Lys Ile Ala Ser Leu Pro Gln Glu Val Gln Asp
195                 200                 205                 210

gtt tct cta ttg gaa aaa ata aca gac aaa gag gca gct gaa cgt ctt     1028
Val Ser Leu Leu Glu Lys Ile Thr Asp Lys Glu Ala Ala Glu Arg Leu
211                 216                 221                 226

tca aaa aca gta gat gaa gca tgt ctg tta cta gca gaa tat aac ggg     1076
Ser Lys Thr Val Asp Glu Ala Cys Leu Leu Leu Ala Glu Tyr Asn Gly
227                 232                 237                 242

cgc ctg gca gca gaa ctg gag gac cgt cgc cag ctg gct cgg atg ttg     1124
Arg Leu Ala Ala Glu Leu Glu Asp Arg Arg Gln Leu Ala Arg Met Leu
243                 248                 253                 258

gtg gag tat acc cag aat cag aaa gat gtt ttg tcg gag aag gag aaa     1172
Val Glu Tyr Thr Gln Asn Gln Lys Asp Val Leu Ser Glu Lys Glu Lys
259                 264                 269                 274

aaa cta gag gaa tac aaa cag aag ctt gca cga gta acc cag gtc cgc     1220
Lys Leu Glu Glu Tyr Lys Gln Lys Leu Ala Arg Val Thr Gln Val Arg
275                 280                 285                 290

aag gaa ctg aaa tcc cat att cag agc ttg cca gac ctc tca ctg ctg     1268
Lys Glu Leu Lys Ser His Ile Gln Ser Leu Pro Asp Leu Ser Leu Leu
291                 296                 301                 306

ccc aac gtc aca ggg ggc tta gcc ccc ctg ccc tct gct ggg gac ctg     1316
Pro Asn Val Thr Gly Gly Leu Ala Pro Leu Pro Ser Ala Gly Asp Leu
307                 312                 317                 322

ttt tca act gac tag gatgggtgtc atgtcccaga tttctgtttg taccagcaga     1371
Phe Ser Thr Asp  *
323

aagaagaggg caagtcatgg ttggaaataa ccttctagcc cctggttcta tcccttcttc   1431

cgcccagccc cccagcctca agaaagaacc tcagactctg attctcctct tcagcctctc   1491

atcttgagca cagttcagaa cagtggcgac tggaatctgg tttatattca tatttgcaaa   1551

gactacagac tttttctccc acctcgtgcc gaattnnctg cctcgagggc caaat        1606
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<210> 324
<211> 2580
<212> DNA
<213> Homo sapiens

<220>

Confidential - Filed Under Seal

<221> CDS
<222> (367)..(1674)

<400> 324

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ggtaccgcgc cggaattccc gggtcgacga tttcgtctcc tcctcctcct ccctcctctt     60

ccccaccttc ctccactccc tcccttcccc tccccttcta cctcctcctc ggccagctca    120

ggttgcagct tctctgggga actgctcacc tttccggagc aggggaagct gccccgtgcc    180

cgggagggag cgggcgcacc gcggccccca ggacacgcgc tgacccggct gcccagtccc    240

tcatgatcat gaacaagatg aagaacttta agcgccgttt ctccctgtca gtgccccgca    300

ctgagaccat tgaagaatcc ttggctgaat tcacggagca attcaaccag ctccacaacc    360

ggcgga   atg aga gtg agg gac ttg cag ctc ggt cct ctt ggc aga gac      408
         Met Arg Val Arg Asp Leu Gln Leu Gly Pro Leu Gly Arg Asp
           1               5                  10

ccc ccg cag gag tgc agc acc ttc tcc cca aca gac agc ggg gag gag      456
Pro Pro Gln Glu Cys Ser Thr Phe Ser Pro Thr Asp Ser Gly Glu Glu
 15                  20                  25                  30

ccg ggg cag ctc tcc cct ggc gtg cag ttc cag cgg cgg cag aac cag      504
Pro Gly Gln Leu Ser Pro Gly Val Gln Phe Gln Arg Arg Gln Asn Gln
 31                  36                  41                  46

cgc cgc ttc tcc atg gag gac gtc agc aag agg ctc tct ctg ccc atg      552
Arg Arg Phe Ser Met Glu Asp Val Ser Lys Arg Leu Ser Leu Pro Met
 47                  52                  57                  62

gat atc cgc ctg ccc cag gaa ttc cta cag aag cta cag atg gag agc      600
Asp Ile Arg Leu Pro Gln Glu Phe Leu Gln Lys Leu Gln Met Glu Ser
 63                  68                  73                  78

cca gat ctg ccc aag ccg ctc agc cgc atg tcc cgc cgg gcc tcc ctg      648
Pro Asp Leu Pro Lys Pro Leu Ser Arg Met Ser Arg Arg Ala Ser Leu
 79                  84                  89                  94

tca gac att ggc ttt ggg aaa ctg gaa aca tac gtg aaa ctg gac aaa      696
Ser Asp Ile Gly Phe Gly Lys Leu Glu Thr Tyr Val Lys Leu Asp Lys
 95                 100                 105                 110

ctg gga gag ggc acc tat gcc aca gtc ttc aaa ggg cgc agc aaa ctg      744
Leu Gly Glu Gly Thr Tyr Ala Thr Val Phe Lys Gly Arg Ser Lys Leu
111                 116                 121                 126

acg gag aac ctt gtg gcc ctg aaa gag atc cgg ctg gag cac gag gag      792
Thr Glu Asn Leu Val Ala Leu Lys Glu Ile Arg Leu Glu His Glu Glu
127                 132                 137                 142

gga gcg ccc tgc act gcc atc cga gag gtg tct ctg ctg aag aac ctg      840
Gly Ala Pro Cys Thr Ala Ile Arg Glu Val Ser Leu Leu Lys Asn Leu
143                 148                 153                 158

aag cac gcc aat att gtg acc ctg cat gac ctc atc cac aca gat cgg      888
```

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Lys His Ala Asn Ile Val Thr Leu His Asp Leu Ile His Thr Asp Arg
159                 164                 169                 174

tcc ctc acc ctg gtg ttt gag tac ctg gac agt gac ctg aag cag tat      936
Ser Leu Thr Leu Val Phe Glu Tyr Leu Asp Ser Asp Leu Lys Gln Tyr
175                 180                 185                 190

ctg gac cac tgt ggg aac ctc atg agc atg cac aac gtc aag att ttc      984
Leu Asp His Cys Gly Asn Leu Met Ser Met His Asn Val Lys Ile Phe
191                 196                 201                 206

atg ttc cag ctg ctc cgg ggc ctc gcc tac tgt cac cac cgc aag atc     1032
Met Phe Gln Leu Leu Arg Gly Leu Ala Tyr Cys His His Arg Lys Ile
207                 212                 217                 222

ctg cac cgg gac ctg aag ccc cag aac ctg ctc atc aac gag agg ggg     1080
Leu His Arg Asp Leu Lys Pro Gln Asn Leu Leu Ile Asn Glu Arg Gly
223                 228                 233                 238

gag ctg aag ctg gcc gac ttt gga ctg gcc agg gcc aag tca gtg ccc     1128
Glu Leu Lys Leu Ala Asp Phe Gly Leu Ala Arg Ala Lys Ser Val Pro
239                 244                 249                 254

aca aag act tac tcc aat gag gtg gtg acc ctg tgg tac agg ccc ccc     1176
Thr Lys Thr Tyr Ser Asn Glu Val Val Thr Leu Trp Tyr Arg Pro Pro
255                 260                 265                 270

gat gtg ctg ctg gga tcc aca gag tac tcc acc ccc att gat atg tgg     1224
Asp Val Leu Leu Gly Ser Thr Glu Tyr Ser Thr Pro Ile Asp Met Trp
271                 276                 281                 286

ggc gtg ggc tgc atc cac tac gag atg gcc aca ggg agg ccc ctc ttc     1272
Gly Val Gly Cys Ile His Tyr Glu Met Ala Thr Gly Arg Pro Leu Phe
287                 292                 297                 302

ccg ggc tcc aca gtc aag gag gag ctg cac ctc atc tct cgc ctc ctc     1320
Pro Gly Ser Thr Val Lys Glu Glu Leu His Leu Ile Ser Arg Leu Leu
303                 308                 313                 318

ggg acc ccc aca gaa gag acg tgg ccc ggc gtg acc gcc ttc tct gag     1368
Gly Thr Pro Thr Glu Glu Thr Trp Pro Gly Val Thr Ala Phe Ser Glu
319                 324                 329                 334

ttc cgc acc tac agc ttc ccc tgc tac ctc ccg cag ccg ctc atc aac     1416
Phe Arg Thr Tyr Ser Phe Pro Cys Tyr Leu Pro Gln Pro Leu Ile Asn
335                 340                 345                 350

cac gcg ccc agg ttg gat acg gat ggc atc cac ctc ctg agc agc ctg     1464
His Ala Pro Arg Leu Asp Thr Asp Gly Ile His Leu Leu Ser Ser Leu
351                 356                 361                 366

ctc ctg tat gaa tcc aag agt cgc atg tca gca gag gct gcc ctg agt     1512
Leu Leu Tyr Glu Ser Lys Ser Arg Met Ser Ala Glu Ala Ala Leu Ser
367                 372                 377                 382

cac tcc tac ttc cgg tct ctg gga gag cgt gtg cac cag ctt gaa gac     1560
His Ser Tyr Phe Arg Ser Leu Gly Glu Arg Val His Gln Leu Glu Asp
```

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383                 388                 393                 398

act gcc tcc atc ttc tcc ctg aag gag atc cag ctc cag aag gac cca     1608
Thr Ala Ser Ile Phe Ser Leu Lys Glu Ile Gln Leu Gln Lys Asp Pro
399                 404                 409                 414

ggc tac cga ggc ttg gcc ttc cag cag cca gga cga ggg aag aac agg     1656
Gly Tyr Arg Gly Leu Ala Phe Gln Gln Pro Gly Arg Gly Lys Asn Arg
415                 420                 425                 430

cgg cag agc atc ttc tga gccacg cccaccttgc tgtggccaag ggacaagaga     1710
Arg Gln Ser Ile Phe  *
431                 436

tcacatggag cacaaattcg ggtaggatgg agcctgtgtg gccctcggag gactgaagaa   1770

cgagggctga cagccagcct ggaagaccgc ttggcagccc ttctggccac ggctgtttct   1830

tctttgtgct tcccgtgtgc ctccccagta gccctcacct gcataccaac ccctccttta   1890

cccacgttgg ggctggcata agctgcttcc ctgagaggac atgaggggggg ggcggtcctc   1950

gtaccctctc ccaccctggt gtttgggcac ctgcgtggga tgcacacgga tgacagaatc   2010

aaggcgccag gatgggcact ctgccctgga tacaggctct accctcctcc cccaggacct   2070

gcctagtgcc agtttggtag tccccctttc tggccccttg gagcccacac acgtttcatc   2130

tttttccccct ctgagagcaa gaagagacat ggcatgttct ctgggaccct ggaatcctag   2190

gtacccacat gtgtgccaaa gcctacccca cctggcaggt gtcccacagc aacagaagga   2250

atagtagtcc ccactctttc catcagccct accctaccct cattccccga caccctctgg   2310

cttgaaccat ggctgagcag tgccggcata cgctttgctg gcatgcttgg atgcccagct   2370

gtgtccagag gtggcctggg accgccagtt gcacgcctgc cacctcagcc agcccccgcc   2430

cagctcatca gtctgaatgg agttgcctta aattggcagg tggtaccgta ctcactgccc   2490

ttggagctgt gaccggctcc tgcctgtcca ccccttcccg aggtggctcc tgcttacctt   2550

atcatcccag ggctctgatt agccaggcct                                    2580
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<400> 325

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aaaagcaggc tggtaccggt ccggaattcc cgggatcggg ggccgtgccg ggcgccatc   119

atg gac gag gac tac tac ggg agc gcg gcc gag tgg ggc gac gag gct      167
Met Asp Glu Asp Tyr Tyr Gly Ser Ala Ala Glu Trp Gly Asp Glu Ala
  1               5                  10                  15

gac ggc ggc cag cag gag gat gat tct gga gaa gga gag gat gat gcg      215
Asp Gly Gly Gln Gln Glu Asp Asp Ser Gly Glu Gly Glu Asp Asp Ala
 17                  22                  27                  32

gag gtt cag caa gaa tgc ctg cat aaa ttt tcc acc cgg gat tat atc      263
Glu Val Gln Gln Glu Cys Leu His Lys Phe Ser Thr Arg Asp Tyr Ile
 33                  38                  43                  48

atg gaa ccc tcc atc ttc aac act ctg aag agg tat ttt cag gca gga      311
Met Glu Pro Ser Ile Phe Asn Thr Leu Lys Arg Tyr Phe Gln Ala Gly
 49                  54                  59                  64

ggg tct cca gag aat gtt atc cag ctc tta tct gaa aac tac acc gct      359
Gly Ser Pro Glu Asn Val Ile Gln Leu Leu Ser Glu Asn Tyr Thr Ala
 65                  70                  75                  80

gtg gcc cag act gtg aac ctg ctg gcc gag tgg ctc att cag aca ggt      407
Val Ala Gln Thr Val Asn Leu Leu Ala Glu Trp Leu Ile Gln Thr Gly
 81                  86                  91                  96

gtt gag cca gtg cag gtt cag gaa act gtg gaa aat cac ttg aag agt      455
Val Glu Pro Val Gln Val Gln Glu Thr Val Glu Asn His Leu Lys Ser
 97                 102                 107                 112

ttg ctg atc aaa cat ttt gac ccc cgc aaa gca gat tct att ttt act      503
Leu Leu Ile Lys His Phe Asp Pro Arg Lys Ala Asp Ser Ile Phe Thr
113                 118                 123                 128

gaa gaa gga gag acc cca gcg tgg ctg gaa cag atg att gca cat acc      551
Glu Glu Gly Glu Thr Pro Ala Trp Leu Glu Gln Met Ile Ala His Thr
129                 134                 139                 144

acg tgg cgg gac ctt ttt tat aaa ctg gct gaa gcc cat cca gac tgt      599
Thr Trp Arg Asp Leu Phe Tyr Lys Leu Ala Glu Ala His Pro Asp Cys
145                 150                 155                 160

ttg atg ctg aac ttc acc gtt aag ctt att tct gac gca ggg tac cag      647
Leu Met Leu Asn Phe Thr Val Lys Leu Ile Ser Asp Ala Gly Tyr Gln
161                 166                 171                 176

ggg gag atc acc agt gtg tcc aca gca tgc cag cag cta gaa gtg ttc      695
Gly Glu Ile Thr Ser Val Ser Thr Ala Cys Gln Gln Leu Glu Val Phe
177                 182                 187                 192

tcg aga gtg ctc cgg acc tct cta gct aca att tta gat gga gga gaa      743
Ser Arg Val Leu Arg Thr Ser Leu Ala Thr Ile Leu Asp Gly Gly Glu
193                 198                 203                 208

gaa aac ctt gaa aaa aat ctc cct gag ttt gcc aag atg gtg tgc cac      791
```

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Glu Asn Leu Glu Lys Asn Leu Pro Glu Phe Ala Lys Met Val Cys His
209                 214                 219                 224

ggg gag cac acg tac ctg ttt gcc cag gcc atg atg tcc gtg ctg gcc      839
Gly Glu His Thr Tyr Leu Phe Ala Gln Ala Met Met Ser Val Leu Ala
225                 230                 235                 240

cag gag gag cag ggg ggc tcc gct gtg cgc agg atc gcc cag gaa gtg      887
Gln Glu Glu Gln Gly Gly Ser Ala Val Arg Arg Ile Ala Gln Glu Val
241                 246                 251                 256

cag cgc ttt gcc cag gag aaa ggt cat gac gcc agt cag atc aca cta      935
Gln Arg Phe Ala Gln Glu Lys Gly His Asp Ala Ser Gln Ile Thr Leu
257                 262                 267                 272

gcc ttg ggc aca gct gcc tcc tac ccc agg gcc tgc cag gct ctc ggg      983
Ala Leu Gly Thr Ala Ala Ser Tyr Pro Arg Ala Cys Gln Ala Leu Gly
273                 278                 283                 288

gcc atg ctg tcc aaa gga gcc ctg aac cct gct gac atc acc gtc ctg     1031
Ala Met Leu Ser Lys Gly Ala Leu Asn Pro Ala Asp Ile Thr Val Leu
289                 294                 299                 304

ttc aag atg ttc aca agc atg gac cct cct ccg gtt gaa ctt atc cgc     1079
Phe Lys Met Phe Thr Ser Met Asp Pro Pro Pro Val Glu Leu Ile Arg
305                 310                 315                 320

gtt cca gcc ttc ctg gac ctg ttc atg cag tca ctc ttt aaa cca ggg     1127
Val Pro Ala Phe Leu Asp Leu Phe Met Gln Ser Leu Phe Lys Pro Gly
321                 326                 331                 336

gct cgg atc aac cag gac cac aag cac aaa tac atc cac atc ttg gcg     1175
Ala Arg Ile Asn Gln Asp His Lys His Lys Tyr Ile His Ile Leu Ala
337                 342                 347                 352

tac gca gca agc gtg gtt gag acc tgg aag aag aac aag cga gtg agc     1223
Tyr Ala Ala Ser Val Val Glu Thr Trp Lys Lys Asn Lys Arg Val Ser
353                 358                 363                 368

atc aat aaa gat gag ctg aag tca acg tca aaa gct gtc gaa acc gtt     1271
Ile Asn Lys Asp Glu Leu Lys Ser Thr Ser Lys Ala Val Glu Thr Val
369                 374                 379                 384

cac aat ttg tgt tgc aac gag aac aaa ggg gcc tct gaa cta gtg gca     1319
His Asn Leu Cys Cys Asn Glu Asn Lys Gly Ala Ser Glu Leu Val Ala
385                 390                 395                 400

gaa ttg agc aca ctt tat cag tgt att agg ttt cca gtg gta gca atg     1367
Glu Leu Ser Thr Leu Tyr Gln Cys Ile Arg Phe Pro Val Val Ala Met
401                 406                 411                 416

ggt gtg ctg aag tgg gtg gat tgg act gta tca gaa cca agg tac ttt     1415
Gly Val Leu Lys Trp Val Asp Trp Thr Val Ser Glu Pro Arg Tyr Phe
417                 422                 427                 432

cag ctg cag act gac cat acc cct gtc cac ctg gcg ttg ctg gat gag     1463
Gln Leu Gln Thr Asp His Thr Pro Val His Leu Ala Leu Leu Asp Glu
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433                 438                 443                 448

atc agc acc tgc cac cag ctc ctg cac ccc cag gtc ctg cag ctg ctt     1511
Ile Ser Thr Cys His Gln Leu Leu His Pro Gln Val Leu Gln Leu Leu
449                 454                 459                 464

gtt aag ctt ttt gag act gag cac tcc cag ctg gac gtg atg gag cag     1559
Val Lys Leu Phe Glu Thr Glu His Ser Gln Leu Asp Val Met Glu Gln
465                 470                 475                 480

ctt gag ttg aag aag aca ctg ctg gac agg atg gtt cac ctg ctg agt     1607
Leu Glu Leu Lys Lys Thr Leu Leu Asp Arg Met Val His Leu Leu Ser
481                 486                 491                 496

cga ggt tat gta ctt cct gtt gtc agt tac atc cga aag tgt ctg gag     1655
Arg Gly Tyr Val Leu Pro Val Val Ser Tyr Ile Arg Lys Cys Leu Glu
497                 502                 507                 512

aag ctg gac act gac att tca ctc att cgc tat ttt gtc act gag gtg     1703
Lys Leu Asp Thr Asp Ile Ser Leu Ile Arg Tyr Phe Val Thr Glu Val
513                 518                 523                 528

ctg gac gtc att gct cct cct tat acc tct gac ttc gtg caa ctt ttc     1751
Leu Asp Val Ile Ala Pro Pro Tyr Thr Ser Asp Phe Val Gln Leu Phe
529                 534                 539                 544

ctc ccc atc ctg gag aat gac agc atc gca ggt acc atc aaa acg gaa     1799
Leu Pro Ile Leu Glu Asn Asp Ser Ile Ala Gly Thr Ile Lys Thr Glu
545                 550                 555                 560

ggc gag cat gac cct gtg acg gag ttt ata gct cac tgc aaa tct aac     1847
Gly Glu His Asp Pro Val Thr Glu Phe Ile Ala His Cys Lys Ser Asn
561                 566                 571                 576

ttc atc atg gtg aac taa tttaga gcatcctcca gagctgaagc agaacattcc     1901
Phe Ile Met Val Asn  *
577                 582

agaacccgtt gtggaaaaac cctttcaaga agctgtttta agaggctctg gcagcgtctt   1961

gaaaatgggc accgctggga ggaggtggat gacttcttta caaaggaaaa tggtagcagc   2021

ttcagtgaga aactgccctt acaaacagtc ccttctctgc tgtcaatcca atactgctcc   2081

caaatcctgt tttcagtgtt catttccctc aaggcaggcg ctgggctccc acgacccctc   2141

aggacagatc tggccgtcag ccgcgggccg ctgggaactc cactcgggga actcctttcc   2201

aagctgacct cagttttctc acaagaaccc agttagctga tgttttattg taattgtctt   2261

aatttgctaa gaacaagtaa taagtaaatt tttaaaaagc caaaaaaaaa a            2312
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agaccgggaa catggcgctg ggagcgctgt agcagctgag aaggggctga ggcaccgccg 120

cttcgctgac agccggccac cagaaataca ctgtggtgaa atgcttccac ctcttgctaa 180

aatgaacact gagaaaaaat gaagaagact gacaagcacc agcgaaaagt tgcagaatag 240

aaatagccac actcctctgg agtctttaat tcatccacag ccatcatata aaggttttgg 300

catc atg ttt ggg aag aaa aag aaa aag att gaa ata tct ggc ccg tcc 349
Met Phe Gly Lys Lys Lys Lys Lys Ile Glu Ile Ser Gly Pro Ser
1 5 10

aac ttt gaa cac agg gtt cat act ggg ttt gat cca caa gag cag aag 397
Asn Phe Glu His Arg Val His Thr Gly Phe Asp Pro Gln Glu Gln Lys
16 21 26 31

ttt acc ggc ctt ccc cag cag tgg cac agc ctg tta gca gat acg gcc 445
Phe Thr Gly Leu Pro Gln Gln Trp His Ser Leu Leu Ala Asp Thr Ala
32 37 42 47

aac agg cca aag cct atg gtg gac cct tca tgc atc aca ccc atc cag 493
Asn Arg Pro Lys Pro Met Val Asp Pro Ser Cys Ile Thr Pro Ile Gln
48 53 58 63

ctg gct cct atg aag aca atc gtt aga gga aac aaa ccc tgc aag gaa 541
Leu Ala Pro Met Lys Thr Ile Val Arg Gly Asn Lys Pro Cys Lys Glu
64 69 74 79

acc tcc atc aac ggc ctg cta gag gat ttt gac aac atc tcg gtg act 589
Thr Ser Ile Asn Gly Leu Leu Glu Asp Phe Asp Asn Ile Ser Val Thr
80 85 90 95

cgc tcc aac tcc cta agg aaa gaa agc cca ccc acc cca gat cag gga 637
Arg Ser Asn Ser Leu Arg Lys Glu Ser Pro Pro Thr Pro Asp Gln Gly
96 101 106 111

gcc tcc agc cac ggt cca ggc cac gcg gaa gaa aat ggc ttc atc acc 685
Ala Ser Ser His Gly Pro Gly His Ala Glu Glu Asn Gly Phe Ile Thr
112 117 122 127

ttc tcc cag tat tcc agc gaa tcc gat act act gct gac tac acg acc 733
Phe Ser Gln Tyr Ser Ser Glu Ser Asp Thr Thr Ala Asp Tyr Thr Thr
128 133 138 143

gaa aag tac agg gag aag agt ctc tat gga gat gat ctg gat ccg tat 781
Glu Lys Tyr Arg Glu Lys Ser Leu Tyr Gly Asp Asp Leu Asp Pro Tyr
144 149 154 159

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tat aga ggc agc cac gca gcc aag caa aat ggg cac gta atg aaa atg      829
Tyr Arg Gly Ser His Ala Ala Lys Gln Asn Gly His Val Met Lys Met
160                 165                 170                 175

aag cac ggg gag gcc tac tat tct gag gtg aag cct ttg aaa tcc gat      877
Lys His Gly Glu Ala Tyr Tyr Ser Glu Val Lys Pro Leu Lys Ser Asp
176                 181                 186                 191

ttt gcc aga ttt tct gcc gat tat cac tca cat ttg gac tca ctg agc      925
Phe Ala Arg Phe Ser Ala Asp Tyr His Ser His Leu Asp Ser Leu Ser
192                 197                 202                 207

aaa cca agt gaa tac agt gac ctc aag tgg gag tat cag aga gcc tcg      973
Lys Pro Ser Glu Tyr Ser Asp Leu Lys Trp Glu Tyr Gln Arg Ala Ser
208                 213                 218                 223

agt agc tcc cct ctg gat tat tca ttc caa ttc aca cct tct aga act     1021
Ser Ser Ser Pro Leu Asp Tyr Ser Phe Gln Phe Thr Pro Ser Arg Thr
224                 229                 234                 239

gca ggg acc agc ggg tgc tcc aag gag agc ctg gcg tac agt gaa agt     1069
Ala Gly Thr Ser Gly Cys Ser Lys Glu Ser Leu Ala Tyr Ser Glu Ser
240                 245                 250                 255

gaa tgg gga ccc agc ctg gat gac tat gac agg agg cca aag tct tcg     1117
Glu Trp Gly Pro Ser Leu Asp Asp Tyr Asp Arg Arg Pro Lys Ser Ser
256                 261                 266                 271

tac ctg aat cag aca agc cct cag ccc acc atg cgg cag agg tcc agg     1165
Tyr Leu Asn Gln Thr Ser Pro Gln Pro Thr Met Arg Gln Arg Ser Arg
272                 277                 282                 287

tca ggc tcg gga ctc cag gaa ccg atg atg tca ttt gga gca agt gca     1213
Ser Gly Ser Gly Leu Gln Glu Pro Met Met Ser Phe Gly Ala Ser Ala
288                 293                 298                 303

ttt aaa acc cat ccc caa gga cac tcc tac aac tcc tac acc tac cct     1261
Phe Lys Thr His Pro Gln Gly His Ser Tyr Asn Ser Tyr Thr Tyr Pro
304                 309                 314                 319

cgc ttg tcc gag ccc aca atg tgc att cca aag gtg gat tac gat cga     1309
Arg Leu Ser Glu Pro Thr Met Cys Ile Pro Lys Val Asp Tyr Asp Arg
320                 325                 330                 335

gca cag atg gtc ctc agc cct cca ctg tca ggg tct gac acc tac ccc     1357
Ala Gln Met Val Leu Ser Pro Pro Leu Ser Gly Ser Asp Thr Tyr Pro
336                 341                 346                 351

agg ggc cct gcc aaa cta cct caa agt caa agc aaa tcg ggc tat tcc     1405
Arg Gly Pro Ala Lys Leu Pro Gln Ser Gln Ser Lys Ser Gly Tyr Ser
352                 357                 362                 367

tca agc agt cac cag tac ccg tct ggg tac cac aaa gcc acc ttg tac     1453
Ser Ser Ser His Gln Tyr Pro Ser Gly Tyr His Lys Ala Thr Leu Tyr
368                 373                 378                 383
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cat cac ccc tcc ctg cag agc agt tcg cag tac atc tcc acg gct tcc     1501
His His Pro Ser Leu Gln Ser Ser Ser Gln Tyr Ile Ser Thr Ala Ser
384                 389                 394                 399

tac ctg agc tcc ctc agc ctc tca tcc agc acc tac ccg ccg ccc agc     1549
Tyr Leu Ser Ser Leu Ser Leu Ser Ser Ser Thr Tyr Pro Pro Pro Ser
400                 405                 410                 415

tgg ggc tcc tcc tcc gac cag cag ccc tcc agg gtg tcc cat gaa cag     1597
Trp Gly Ser Ser Ser Asp Gln Gln Pro Ser Arg Val Ser His Glu Gln
416                 421                 426                 431

ttt cgg gcg gcc ctg cag ctg gtg gtc agc cca gga gac ccc agg gaa     1645
Phe Arg Ala Ala Leu Gln Leu Val Val Ser Pro Gly Asp Pro Arg Glu
432                 437                 442                 447

tac ttg gcc aac ttt atc aaa atc ggg gaa ggc tca acc ggc atc gta     1693
Tyr Leu Ala Asn Phe Ile Lys Ile Gly Glu Gly Ser Thr Gly Ile Val
448                 453                 458                 463

tgc atc gcc acc gag aaa cac aca ggg aaa caa gtt gca gtg aag aaa     1741
Cys Ile Ala Thr Glu Lys His Thr Gly Lys Gln Val Ala Val Lys Lys
464                 469                 474                 479

atg gac ctc cgg aag caa cag aga cga gaa ctg ctt ttc aat gag gtc     1789
Met Asp Leu Arg Lys Gln Gln Arg Arg Glu Leu Leu Phe Asn Glu Val
480                 485                 490                 495

gtg atc atg cgg gat tac cac cat gac aat gtg gtt gac atg tac aac     1837
Val Ile Met Arg Asp Tyr His His Asp Asn Val Val Asp Met Tyr Asn
496                 501                 506                 511

agc tac ctt gtc ggc gat gag ctc tgg gtg gtc atg gag ttt cta gaa     1885
Ser Tyr Leu Val Gly Asp Glu Leu Trp Val Val Met Glu Phe Leu Glu
512                 517                 522                 527

ggt ggt gcc ttg aca gac att gtg act cac acc aga atg aat gaa gaa     1933
Gly Gly Ala Leu Thr Asp Ile Val Thr His Thr Arg Met Asn Glu Glu
528                 533                 538                 543

cag ata gct act gtc tgc ctg tca gtt ctg aga gct ctc tcc tac ctt     1981
Gln Ile Ala Thr Val Cys Leu Ser Val Leu Arg Ala Leu Ser Tyr Leu
544                 549                 554                 559

cat aac caa gga gtg att cac agg gac ata aaa agt gac tcc atc ctc     2029
His Asn Gln Gly Val Ile His Arg Asp Ile Lys Ser Asp Ser Ile Leu
560                 565                 570                 575

ctg aca agc gat ggc cgg ata aag ttg tct gat ttt ggt ttc tgt gct     2077
Leu Thr Ser Asp Gly Arg Ile Lys Leu Ser Asp Phe Gly Phe Cys Ala
576                 581                 586                 591

caa gtt tcc aaa gag gtg ccg aag agg aaa tca ttg gtt ggc act ccc     2125
Gln Val Ser Lys Glu Val Pro Lys Arg Lys Ser Leu Val Gly Thr Pro
592                 597                 602                 607

tac tgg atg gcc cct gag gtg att tct agg cta cct tat ggg aca gag     2173
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Tyr Trp Met Ala Pro Glu Val Ile Ser Arg Leu Pro Tyr Gly Thr Glu
608                 613                 618                 623

gtg gac atc tgg tcc ctc ggg atc atg gtg ata gaa atg att gat ggc     2221
Val Asp Ile Trp Ser Leu Gly Ile Met Val Ile Glu Met Ile Asp Gly
624                 629                 634                 639

gag ccc ccc tac ttc aat gag cct ccc ctc cag gcg atg cgg agg atc     2269
Glu Pro Pro Tyr Phe Asn Glu Pro Pro Leu Gln Ala Met Arg Arg Ile
640                 645                 650                 655

cgg gac agt tta cct cca aga gtg aag gac cta cac aag gtt tct tca     2317
Arg Asp Ser Leu Pro Pro Arg Val Lys Asp Leu His Lys Val Ser Ser
656                 661                 666                 671

gtg ctc cgg gga ttc cta gac ttg atg ttg gtg agg gag ccc tct cag     2365
Val Leu Arg Gly Phe Leu Asp Leu Met Leu Val Arg Glu Pro Ser Gln
672                 677                 682                 687

aga gca aca gcc cag gaa ctc ctc gga cat cca ttc tta aaa cta gca     2413
Arg Ala Thr Ala Gln Glu Leu Leu Gly His Pro Phe Leu Lys Leu Ala
688                 693                 698                 703

ggt cca ccg tct tgc atc gtc ccc ctc atg aga caa tac agg cat cac     2461
Gly Pro Pro Ser Cys Ile Val Pro Leu Met Arg Gln Tyr Arg His His
704                 709                 714                 719

tga gcag aggattcgtg taggtggcaa agctagatga ggacatgaga ataattcagg     2518
 *
720

agaacaaaag gaaacacaga acatgcaaaa ggcctgtgca ttctagacca gccaattggt   2578

gggacagcgt gatgaccggc agggttcaac agaccagggc atcttcttgt gtcttaaaca   2638

ggcatctctc cactgacagc cggtgtggtc acttggagca cggctttaat aagtcattat   2698

tatatttttc agcccttcat ccagcaaatc agaaggactc agtacaaact ccgttatgat   2758

atatcctagc cacatgcagg gtaacatgta ggattttcta tattgaaaga atacttttct   2818

ggcaaaaaaa aaa                                                      2831
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<222> (97)..(846)

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tttcgtgccc cgccgcacca gagcagtggt acaggc  atg gat ggg aag aaa tgc     114
                                         Met Asp Gly Lys Lys Cys
                                           1

agc gta tgg atg ttc cta cct ctt gta ttt act ttg ttt act tca gct     162
Ser Val Trp Met Phe Leu Pro Leu Val Phe Thr Leu Phe Thr Ser Ala
  7                  12                  17                  22

gga ttg tgg ata gta tac ttc ata gct gtg gaa gat gac aaa att tta     210
Gly Leu Trp Ile Val Tyr Phe Ile Ala Val Glu Asp Asp Lys Ile Leu
 23                  28                  33                  38

cca tta aat tca gct gaa agg aaa cct ggt gtg aag cat gca cca tat     258
Pro Leu Asn Ser Ala Glu Arg Lys Pro Gly Val Lys His Ala Pro Tyr
 39                  44                  49                  54

ata agc att gca ggt gat gat cct cct gca agc tgt gtg ttt agt caa     306
Ile Ser Ile Ala Gly Asp Asp Pro Pro Ala Ser Cys Val Phe Ser Gln
 55                  60                  65                  70

gtt atg aac atg gca gcc ttc cta gcc ctt gtg gta gct gtt ctg cgc     354
Val Met Asn Met Ala Ala Phe Leu Ala Leu Val Val Ala Val Leu Arg
 71                  76                  81                  86

ttc ata caa ctg aaa ccg aag gtt tta aac ccg tgg ctg aat att agt     402
Phe Ile Gln Leu Lys Pro Lys Val Leu Asn Pro Trp Leu Asn Ile Ser
 87                  92                  97                 102

gga ttg gtg gct ctg tgt ctg gct tcc ttc gga atg acc tta ctt ggt     450
Gly Leu Val Ala Leu Cys Leu Ala Ser Phe Gly Met Thr Leu Leu Gly
103                 108                 113                 118

aat ttt cag ctc aca aat gat gaa gaa atc cat aac gtc gga act tcc     498
Asn Phe Gln Leu Thr Asn Asp Glu Glu Ile His Asn Val Gly Thr Ser
119                 124                 129                 134

ttg acc ttt gga ttt ggc aca ttg acc tgc tgg atc cag gct gcg ctg     546
Leu Thr Phe Gly Phe Gly Thr Leu Thr Cys Trp Ile Gln Ala Ala Leu
135                 140                 145                 150

aca ctc aag gtc aac atc aag aat gaa gga cgg aga gtt gga att cca     594
Thr Leu Lys Val Asn Ile Lys Asn Glu Gly Arg Arg Val Gly Ile Pro
151                 156                 161                 166

cgg gtt att ctg tcg gca tct atc act ctc tgt gtg gtc ctc tac ttc     642
Arg Val Ile Leu Ser Ala Ser Ile Thr Leu Cys Val Val Leu Tyr Phe
167                 172                 177                 182

atc ctc atg gcc caa agc atc cac atg tat gca gcc agg gtc cag tgg     690
Ile Leu Met Ala Gln Ser Ile His Met Tyr Ala Ala Arg Val Gln Trp
183                 188                 193                 198

ggc ctg gtc atg tgc ttc ctg tct tat ttt ggc acc ttt gcc gtg gag     738
Gly Leu Val Met Cys Phe Leu Ser Tyr Phe Gly Thr Phe Ala Val Glu
199                 204                 209                 214
```

```
ttc cgg cat tac cgc tat gag att gtt tgc tct gag tac cag gag aat      786
Phe Arg His Tyr Arg Tyr Glu Ile Val Cys Ser Glu Tyr Gln Glu Asn
215                 220                 225                 230

ttc cta agc ttc tca gaa agc ctg tca gaa gct tct gaa tat cag act      834
Phe Leu Ser Phe Ser Glu Ser Leu Ser Glu Ala Ser Glu Tyr Gln Thr
231                 236                 241                 246

gac cag gtg taa acc atcagttttt ccttgctggt gaggtgggtg tgacagtggg      889
Asp Gln Val  *
247

ggaggggcca gtaggacaca ctcacaggac ttgacataga acctcatttc acacacacac    949

acacacacac attcatggcc acatttgcca aatgagcttt tcagggcgag ttatttcttt   1009

aatgaaaaag cacaagccct tatgtgtcga aatacacgct gttacactga aaatatatgc   1069

acgacagagc aagaagcttg tgcatgatca cttcttatcc gtccccttcc cagcactccc   1129

tcctcttccc attctctcca catgtctcaa gcaccctg                           1167
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US 9,650,450 B2

<210> 328
<211> 1365
<212> DNA
<213> Homo sapiens

<220>
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<222> (138)..(1220)

<400> 328

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ctctagccgt cgaggagctg cctggggacg tttgccctgg ggccccagcc tggcccgggt    120

caccctggca tgaggag   atg ggc ctg ttg ctc ctg gtc cca ttg ctc ctg     170
                     Met Gly Leu Leu Leu Leu Val Pro Leu Leu Leu
                       1               5

ctg ccc ggc tcc tac gga ctg ccc ttc tac aac ggc ttc tac tac tcc      218
Leu Pro Gly Ser Tyr Gly Leu Pro Phe Tyr Asn Gly Phe Tyr Tyr Ser
 12                  17                  22                  27

aac agc gcc aac gac cag aac cta ggc aac ggt cat ggc aaa gac ctc      266
Asn Ser Ala Asn Asp Gln Asn Leu Gly Asn Gly His Gly Lys Asp Leu
 28                  33                  38                  43

ctt aat gga gtg aag ctg gtg gtg gag aca ccc gag gag acc ctg ttc      314
Leu Asn Gly Val Lys Leu Val Val Glu Thr Pro Glu Glu Thr Leu Phe
 44                  49                  54                  59

acc tac caa ggg gcc agt gtg atc ctg ccc tgc cgc tac cgc tac gag      362
Thr Tyr Gln Gly Ala Ser Val Ile Leu Pro Cys Arg Tyr Arg Tyr Glu
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 60                  65                  70                  75

ccg gcc ctg gtc tcc ccg cgg cgt gtg cgt gtc aaa tgg tgg aag ctg      410
Pro Ala Leu Val Ser Pro Arg Arg Val Arg Val Lys Trp Trp Lys Leu
 76                  81                  86                  91

tcg gag aac ggg gcc cca gag aag gac gtg ctg gtg gcc atc ggg ctg      458
Ser Glu Asn Gly Ala Pro Glu Lys Asp Val Leu Val Ala Ile Gly Leu
 92                  97                 102                 107

agg cac cgc tcc ttt ggg gac tac caa ggc cgc gtg cac ctg cgg cag      506
Arg His Arg Ser Phe Gly Asp Tyr Gln Gly Arg Val His Leu Arg Gln
108                 113                 118                 123

gac aaa gag cat gac gtc tcg ctg gag atc cag gat ctg cgg ctg gag      554
Asp Lys Glu His Asp Val Ser Leu Glu Ile Gln Asp Leu Arg Leu Glu
124                 129                 134                 139

gac tat ggg cgt tac cgc tgt gag gtc att gac ggg ctg gag gat gaa      602
Asp Tyr Gly Arg Tyr Arg Cys Glu Val Ile Asp Gly Leu Glu Asp Glu
140                 145                 150                 155

agc ggt ctg gtg gag ctg gag ctg cgg ggt gtg gtc ttt cct tac cag      650
Ser Gly Leu Val Glu Leu Glu Leu Arg Gly Val Val Phe Pro Tyr Gln
156                 161                 166                 171

tcc ccc aac ggg cgc tac cag ttc aac ttc cac gag ggc cag cag gtc      698
Ser Pro Asn Gly Arg Tyr Gln Phe Asn Phe His Glu Gly Gln Gln Val
172                 177                 182                 187

tgt gca gag cag gct gcg gtg gtg gcc tcc ttt gag cag ctc ttc cgg      746
Cys Ala Glu Gln Ala Ala Val Val Ala Ser Phe Glu Gln Leu Phe Arg
188                 193                 198                 203

gcc tgg gag gag ggc ctg gac tgg tgc aac gcg ggc tgg ctg cag gat      794
Ala Trp Glu Glu Gly Leu Asp Trp Cys Asn Ala Gly Trp Leu Gln Asp
204                 209                 214                 219

gcc acg gtg cag tac ccc atc atg ttg ccc cgg cag ccc tgc ggt ggc      842
Ala Thr Val Gln Tyr Pro Ile Met Leu Pro Arg Gln Pro Cys Gly Gly
220                 225                 230                 235

ccg ggc ctg gca cct ggc gtg cga agc tac ggc ccc cgc cac cgc cgc      890
Pro Gly Leu Ala Pro Gly Val Arg Ser Tyr Gly Pro Arg His Arg Arg
236                 241                 246                 251

ctg cac cgc tat gat gta ttc tgc ttc gct act gcc ctc aag ggg cgg      938
Leu His Arg Tyr Asp Val Phe Cys Phe Ala Thr Ala Leu Lys Gly Arg
252                 257                 262                 267

gtg tac tac ctg gag cac cct gag aag ctg acg ctg aca gag gca agg      986
Val Tyr Tyr Leu Glu His Pro Glu Lys Leu Thr Leu Thr Glu Ala Arg
268                 273                 278                 283

gag gcc tgc cag gaa gat gat gcc acg atc gcc aag gtg gga cag ctc     1034
Glu Ala Cys Gln Glu Asp Asp Ala Thr Ile Ala Lys Val Gly Gln Leu
284                 289                 294                 299
```

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ttt gcc gcc tgg aag ttc cat ggc ctg gac cgc tgc gac gct ggc tgg     1082
Phe Ala Ala Trp Lys Phe His Gly Leu Asp Arg Cys Asp Ala Gly Trp
300                 305                 310                 315

ctg gca gat ggt agc gtc cgc tac cct gtg gtt cac ccg cat cct aac     1130
Leu Ala Asp Gly Ser Val Arg Tyr Pro Val Val His Pro His Pro Asn
316                 321                 326                 331

tgt ggg ccc cca gag cct ggg gtc cga agc ttt ggc ttc ccc gac ccg     1178
Cys Gly Pro Pro Glu Pro Gly Val Arg Ser Phe Gly Phe Pro Asp Pro
332                 337                 342                 347

cag agc cgc ttg tac ggt gtt tac tgc tac cgc cag cac tag gacctgg     1227
Gln Ser Arg Leu Tyr Gly Val Tyr Cys Tyr Arg Gln His  *
348                 353                 358

ggccctcccc tgccgcattc cctcactggc tgtgtattta ttgagtggtt cgttttccct   1287

tgtgggttgg agccatttta actgttttta tacttctcaa tttaaatttt ctttaaacat   1347

ttttttacta ttttttgg                                                 1365
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<210> 329
<211> 1700
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (120)..(1553)

<400> 329

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gcacgaggtc gagtggctct tcctggctgc tgaggcgggt taaggtctga gggtcttgtg     60

gggccacggc gctgatcacc aggtgtttgg cttggtcggt tcttatttct cgcctggca   119

atg gcg acg tac acc tgc ata act tgc cgg gtg gcg ttc cgc gac gcg      167
Met Ala Thr Tyr Thr Cys Ile Thr Cys Arg Val Ala Phe Arg Asp Ala
  1               5                  10                  15

gac atg cag cgg gcc cac tat aag acg gac tgg cac cgc tac aac ctg      215
Asp Met Gln Arg Ala His Tyr Lys Thr Asp Trp His Arg Tyr Asn Leu
 17                  22                  27                  32

cgg cgg aag gtg gcc agc atg gcc cca gtg acc gcc gag ggc ttc cag      263
Arg Arg Lys Val Ala Ser Met Ala Pro Val Thr Ala Glu Gly Phe Gln
 33                  38                  43                  48

gag cga gtg cgg gcg cag cgg gcc gtc gcg gag gag gag agc aag ggc      311
Glu Arg Val Arg Ala Gln Arg Ala Val Ala Glu Glu Glu Ser Lys Gly
 49                  54                  59                  64

tcg gcc acc tac tgc acc gtt tgc agt aag aag ttt gcc tct ttc aac      359
```

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Ser Ala Thr Tyr Cys Thr Val Cys Ser Lys Lys Phe Ala Ser Phe Asn
 65                  70                  75                  80

gcc tac gag aac cac ctc aag tcc cgg cgt cac gtt gag ctg gag aag      407
Ala Tyr Glu Asn His Leu Lys Ser Arg Arg His Val Glu Leu Glu Lys
 81                  86                  91                  96

aag gcc gtg cag gca gtg aat cgg aaa gtg gag atg atg aat gaa aag      455
Lys Ala Val Gln Ala Val Asn Arg Lys Val Glu Met Met Asn Glu Lys
 97                 102                 107                 112

aac ttg gag aaa gga ctg ggc gtg gac agt gtg gac aag gat gcc atg      503
Asn Leu Glu Lys Gly Leu Gly Val Asp Ser Val Asp Lys Asp Ala Met
113                 118                 123                 128

aac gcg gcc atc cag cag gcc atc aag gcc cag ccg tcc atg tct ccc      551
Asn Ala Ala Ile Gln Gln Ala Ile Lys Ala Gln Pro Ser Met Ser Pro
129                 134                 139                 144

aag aag gcg ccc cca gcg cct gca aag gag gcc agg aat gtc gtg gcc      599
Lys Lys Ala Pro Pro Ala Pro Ala Lys Glu Ala Arg Asn Val Val Ala
145                 150                 155                 160

gtg ggt act ggt ggc cgt ggg acc cac gac cga gac ccg agt gag aaa      647
Val Gly Thr Gly Gly Arg Gly Thr His Asp Arg Asp Pro Ser Glu Lys
161                 166                 171                 176

cca ccc cgg ctc cag tgg ttt gaa cag cag gcg aag aag ttg gca aag      695
Pro Pro Arg Leu Gln Trp Phe Glu Gln Gln Ala Lys Lys Leu Ala Lys
177                 182                 187                 192

cag cag gag gag gac agc gag gag gag gaa gag gac ctg gat gga gac      743
Gln Gln Glu Glu Asp Ser Glu Glu Glu Glu Glu Asp Leu Asp Gly Asp
193                 198                 203                 208

gat tgg gaa gat att gat tct gat gaa gaa ttg gaa tgt gag gat act      791
Asp Trp Glu Asp Ile Asp Ser Asp Glu Glu Leu Glu Cys Glu Asp Thr
209                 214                 219                 224

gaa gca atg gac gat gtg gtg gag cag gat gca gag gag gaa gag gct      839
Glu Ala Met Asp Asp Val Val Glu Gln Asp Ala Glu Glu Glu Glu Ala
225                 230                 235                 240

gag gaa ggc cca ccc ctt ggt gcc atc cct atc acg gac tgc tta ttt      887
Glu Glu Gly Pro Pro Leu Gly Ala Ile Pro Ile Thr Asp Cys Leu Phe
241                 246                 251                 256

tgt tcc cat cat tcc agc tcg ctg atg aag aat gtg gct cac atg acc      935
Cys Ser His His Ser Ser Ser Leu Met Lys Asn Val Ala His Met Thr
257                 262                 267                 272

aaa gac cac agt ttc ttt att cct gat ata gaa tat ctt tca gat att      983
Lys Asp His Ser Phe Phe Ile Pro Asp Ile Glu Tyr Leu Ser Asp Ile
273                 278                 283                 288

aag gga ctg att aaa tac ttg gga gag aaa gtt ggt gtt ggc aag att     1031
Lys Gly Leu Ile Lys Tyr Leu Gly Glu Lys Val Gly Val Gly Lys Ile
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289                 294                 299                 304

tgc ttg tgg tgc aac gag aaa ggg aag tcc ttc tac tcc aca gaa gct     1079
Cys Leu Trp Cys Asn Glu Lys Gly Lys Ser Phe Tyr Ser Thr Glu Ala
305                 310                 315                 320

gta cag gca cat atg aat gac aaa agc cac tgt aag ctc ttc aca gat     1127
Val Gln Ala His Met Asn Asp Lys Ser His Cys Lys Leu Phe Thr Asp
321                 326                 331                 336

ggc gat gct gct ttg gaa ttt gca gac ttc tat gat ttt agg agt agc     1175
Gly Asp Ala Ala Leu Glu Phe Ala Asp Phe Tyr Asp Phe Arg Ser Ser
337                 342                 347                 352

tat cca gat cac aag gaa ggg gag gac ccc aat aag gct gag gag ttg     1223
Tyr Pro Asp His Lys Glu Gly Glu Asp Pro Asn Lys Ala Glu Glu Leu
353                 358                 363                 368

ccc tca gaa aag aac ttg gaa tat gat gat gaa acc atg gaa ttg att     1271
Pro Ser Glu Lys Asn Leu Glu Tyr Asp Asp Glu Thr Met Glu Leu Ile
369                 374                 379                 384

ctg cct tct ggt gcc aga gtg ggt cat cgc tcc ttg atg aga tac tac     1319
Leu Pro Ser Gly Ala Arg Val Gly His Arg Ser Leu Met Arg Tyr Tyr
385                 390                 395                 400

aaa cag cga ttt ggc ttg tca aga gct gtg gca gtt gcc aaa aat cgg     1367
Lys Gln Arg Phe Gly Leu Ser Arg Ala Val Ala Val Ala Lys Asn Arg
401                 406                 411                 416

aag gcc gtg ggc cga gta ctt cag cag tac aga gcc ctg gga tgg act     1415
Lys Ala Val Gly Arg Val Leu Gln Gln Tyr Arg Ala Leu Gly Trp Thr
417                 422                 427                 432

ggc agc aca gga gcg gct ctt atg cga gag cga gac atg cag tat gtc     1463
Gly Ser Thr Gly Ala Ala Leu Met Arg Glu Arg Asp Met Gln Tyr Val
433                 438                 443                 448

caa agg atg aaa tca aaa tgg atg ctg aag aca gga atg aag aac aat     1511
Gln Arg Met Lys Ser Lys Trp Met Leu Lys Thr Gly Met Lys Asn Asn
449                 454                 459                 464

gcc acc aag cag atg cac ttt cgg gtc caa gtg aga ttc tga gagtctg     1560
Ala Thr Lys Gln Met His Phe Arg Val Gln Val Arg Phe  *
465                 470                 475

ctgggattga gcaatcatct cctgcccaag tttcctcctt gccctgagga ccagtgaaag   1620

acagatcata ggagagaccc ttttgctgct acttcattcg ttctgaccta ataataaaag   1680

ttagaaccat aaaaaaaaaa                                               1700
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<210> 330
<211> 4205

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (267)..(4205)

<400> 330
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ccgccgcggg aggaggagga gccggagcct ctgcctcagc agccgctgga cccgccgccc    120

ttcttcccca tctctccccc gggcctgctg gttttggggg ggagaaggag agaggggact    180

ctggacgtgc cagggtcaga tctcgcctcc gaggaaggtg cagctgaacc tggtgtttta    240

gaggatacct tggtcccaga gtcatc atg aag gcc ctt gat gag cct ccc tat      293
                               Met Lys Ala Leu Asp Glu Pro Pro Tyr
                                 1               5

ttg aca gtg ggc act gat gtg agt gct aaa tac aga gga gcc ttt tgt      341
Leu Thr Val Gly Thr Asp Val Ser Ala Lys Tyr Arg Gly Ala Phe Cys
 10                  15                  20                  25

gaa gcc aag atc aag aca gca aaa aga ctt gtc aaa gtc aag gtg aca      389
Glu Ala Lys Ile Lys Thr Ala Lys Arg Leu Val Lys Val Lys Val Thr
 26                  31                  36                  41

ttt aga cat gat tct tca aca gtg gaa gtt cag gat gac cac ata aag      437
Phe Arg His Asp Ser Ser Thr Val Glu Val Gln Asp Asp His Ile Lys
 42                  47                  52                  57

ggc cca cta aag gta gga gct att gtg gaa gtg aag aat ctt gat ggt      485
Gly Pro Leu Lys Val Gly Ala Ile Val Glu Val Lys Asn Leu Asp Gly
 58                  63                  68                  73

gca tat cag gaa gct gtt atc aat aaa cta aca gat gcg agt tgg tac      533
Ala Tyr Gln Glu Ala Val Ile Asn Lys Leu Thr Asp Ala Ser Trp Tyr
 74                  79                  84                  89

act gta gtt ttt gat gac gga gat gag aag aca ctg aga cga tct tca      581
Thr Val Val Phe Asp Asp Gly Asp Glu Lys Thr Leu Arg Arg Ser Ser
 90                  95                 100                 105

ctg tgc ctg aaa gga gag agg cat ttt gct gaa agt gaa aca tta gac      629
Leu Cys Leu Lys Gly Glu Arg His Phe Ala Glu Ser Glu Thr Leu Asp
106                 111                 116                 121

cag ctc cca ctc acc aac cct gag cat ttt ggc act cca gtc ata gga      677
Gln Leu Pro Leu Thr Asn Pro Glu His Phe Gly Thr Pro Val Ile Gly
122                 127                 132                 137

aag aaa aca aat aga gga aga aga tct aat cat ata cca gag gaa gag      725
Lys Lys Thr Asn Arg Gly Arg Arg Ser Asn His Ile Pro Glu Glu Glu
138                 143                 148                 153

tct tca tca tcc tcc agt gat gaa gat gag gat gat agg aaa cag att      773
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Ser Ser Ser Ser Ser Ser Asp Glu Asp Glu Asp Asp Arg Lys Gln Ile
154                 159                 164                 169

gat gag cta cta ggc aaa gtt gta tgt gta gat tac att agt ttg gat      821
Asp Glu Leu Leu Gly Lys Val Val Cys Val Asp Tyr Ile Ser Leu Asp
170                 175                 180                 185

aaa aag aaa gca ctg tgg ttt cct gca ttg gtg gtt tgt cct gat tgt      869
Lys Lys Lys Ala Leu Trp Phe Pro Ala Leu Val Val Cys Pro Asp Cys
186                 191                 196                 201

agt gat gag att gct gta aaa aag gac aat att ctt gtt cga tct ttc      917
Ser Asp Glu Ile Ala Val Lys Lys Asp Asn Ile Leu Val Arg Ser Phe
202                 207                 212                 217

aaa gat gga aaa ttt act tca gtt cca aga aaa gat gtc cat gaa att      965
Lys Asp Gly Lys Phe Thr Ser Val Pro Arg Lys Asp Val His Glu Ile
218                 223                 228                 233

act agt gac act gca cca aag cct gat gct gtt tta aag caa gcc ttt     1013
Thr Ser Asp Thr Ala Pro Lys Pro Asp Ala Val Leu Lys Gln Ala Phe
234                 239                 244                 249

gaa cag gca ctt gaa ttt cac aaa agt aga act att cct gct aac tgg     1061
Glu Gln Ala Leu Glu Phe His Lys Ser Arg Thr Ile Pro Ala Asn Trp
250                 255                 260                 265

aag act gaa ttg aaa gaa gat agc tct agc agt gaa gca gag gaa gaa     1109
Lys Thr Glu Leu Lys Glu Asp Ser Ser Ser Ser Glu Ala Glu Glu Glu
266                 271                 276                 281

gag gag gag gaa gat gat gaa aaa gaa aag gag gat aat agc agt gaa     1157
Glu Glu Glu Glu Asp Asp Glu Lys Glu Lys Glu Asp Asn Ser Ser Glu
282                 287                 292                 297

gaa gaa gaa gaa ata gaa cca ttt cca gaa gaa agg gag aac ttt ctt     1205
Glu Glu Glu Glu Ile Glu Pro Phe Pro Glu Glu Arg Glu Asn Phe Leu
298                 303                 308                 313

cag caa ttg tac aaa ttt atg gaa gat aga ggt aca cct att aac aaa     1253
Gln Gln Leu Tyr Lys Phe Met Glu Asp Arg Gly Thr Pro Ile Asn Lys
314                 319                 324                 329

cga cct gta ctt gga tat cga aat ttg aat ctc ttt aag tta ttc aga     1301
Arg Pro Val Leu Gly Tyr Arg Asn Leu Asn Leu Phe Lys Leu Phe Arg
330                 335                 340                 345

ctt gta cac aaa ctt gga gga ttt gat aat att gaa agt gga gct gtt     1349
Leu Val His Lys Leu Gly Gly Phe Asp Asn Ile Glu Ser Gly Ala Val
346                 351                 356                 361

tgg aaa caa gtc tac caa gat ctt gga atc cct gtc tta aat tca gct     1397
Trp Lys Gln Val Tyr Gln Asp Leu Gly Ile Pro Val Leu Asn Ser Ala
362                 367                 372                 377

gca gga tac aat gtt aaa tgt gct tat aaa aaa tac tta tat ggt ttt     1445
Ala Gly Tyr Asn Val Lys Cys Ala Tyr Lys Lys Tyr Leu Tyr Gly Phe
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378                 383                 388                 393

gag gag tac tgt aga tca gcc aac att gaa ttt cag atg gca ttg cca     1493
Glu Glu Tyr Cys Arg Ser Ala Asn Ile Glu Phe Gln Met Ala Leu Pro
394                 399                 404                 409

gag aaa gtt gtt aac aag caa tgt aag gag tgt gaa aat gta aaa gaa     1541
Glu Lys Val Val Asn Lys Gln Cys Lys Glu Cys Glu Asn Val Lys Glu
410                 415                 420                 425

ata aaa gtt aag gag gaa aat gaa aca gag atc aaa gaa ata aag atg     1589
Ile Lys Val Lys Glu Glu Asn Glu Thr Glu Ile Lys Glu Ile Lys Met
426                 431                 436                 441

gag gag gag agg aat ata ata cca aga gaa gaa aag cct att gag gat     1637
Glu Glu Glu Arg Asn Ile Ile Pro Arg Glu Glu Lys Pro Ile Glu Asp
442                 447                 452                 457

gaa att gaa aga aaa gaa aat att aag ccc tct ctg gga agt aaa aag     1685
Glu Ile Glu Arg Lys Glu Asn Ile Lys Pro Ser Leu Gly Ser Lys Lys
458                 463                 468                 473

aat tta tta gaa tct ata cct aca cat tct gat cag gaa aaa gaa gtt     1733
Asn Leu Leu Glu Ser Ile Pro Thr His Ser Asp Gln Glu Lys Glu Val
474                 479                 484                 489

aac att aaa aaa cca gaa gac aat gaa aat ctg gat gac aaa gat gat     1781
Asn Ile Lys Lys Pro Glu Asp Asn Glu Asn Leu Asp Asp Lys Asp Asp
490                 495                 500                 505

gac aca act agg gta gat gaa tcc ctc aac ata aag gta gaa gct gag     1829
Asp Thr Thr Arg Val Asp Glu Ser Leu Asn Ile Lys Val Glu Ala Glu
506                 511                 516                 521

gaa gaa aaa gca aaa tct gga gat gaa acg aat aaa gaa gaa gat gaa     1877
Glu Glu Lys Ala Lys Ser Gly Asp Glu Thr Asn Lys Glu Glu Asp Glu
522                 527                 532                 537

gat gat gaa gaa gca gaa gag gag gag gag gag gaa gaa gaa gaa gag     1925
Asp Asp Glu Glu Ala Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu
538                 543                 548                 553

gat gaa gat gat gat gac aac aat gag gaa gag gag ttt gag tgc tat     1973
Asp Glu Asp Asp Asp Asp Asn Asn Glu Glu Glu Glu Phe Glu Cys Tyr
554                 559                 564                 569

cca cca ggc atg aaa gtc caa gtg cgg tat gga cga ggg aaa aat caa     2021
Pro Pro Gly Met Lys Val Gln Val Arg Tyr Gly Arg Gly Lys Asn Gln
570                 575                 580                 585

aaa atg tat gaa gct agt att aaa gat tct gat gtc gaa ggt gga gag     2069
Lys Met Tyr Glu Ala Ser Ile Lys Asp Ser Asp Val Glu Gly Gly Glu
586                 591                 596                 601

gtc ctt tac ttg gtg cat tac tgc gga tgg aat gtg aga tac gat gaa     2117
Val Leu Tyr Leu Val His Tyr Cys Gly Trp Asn Val Arg Tyr Asp Glu
602                 607                 612                 617
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tgg att aaa gca gat aaa ata gta aga cct gct gat aaa aat gtg cca     2165
Trp Ile Lys Ala Asp Lys Ile Val Arg Pro Ala Asp Lys Asn Val Pro
618                 623                 628                 633

aag ata aaa cat cgg aag aaa ata aag aat aaa tta gac aaa gaa aaa     2213
Lys Ile Lys His Arg Lys Lys Ile Lys Asn Lys Leu Asp Lys Glu Lys
634                 639                 644                 649

gac aaa gat gaa aaa tac tct cca aaa aac tgt aaa ctt cgg cgc ttg     2261
Asp Lys Asp Glu Lys Tyr Ser Pro Lys Asn Cys Lys Leu Arg Arg Leu
650                 655                 660                 665

tcc aaa cca cca ttt cag aca aat cca tct cct gaa atg gta tcc aaa     2309
Ser Lys Pro Pro Phe Gln Thr Asn Pro Ser Pro Glu Met Val Ser Lys
666                 671                 676                 681

ctg gat ctc act gat gcc aaa aac tct gat act gct cat att aag tcc     2357
Leu Asp Leu Thr Asp Ala Lys Asn Ser Asp Thr Ala His Ile Lys Ser
682                 687                 692                 697

ata gaa att act tcg atc ctt aat gga ctt caa gct tct gaa agt tct     2405
Ile Glu Ile Thr Ser Ile Leu Asn Gly Leu Gln Ala Ser Glu Ser Ser
698                 703                 708                 713

gct gaa gac agt gag cag gaa gat gag aga ggt gct caa gac atg gat     2453
Ala Glu Asp Ser Glu Gln Glu Asp Glu Arg Gly Ala Gln Asp Met Asp
714                 719                 724                 729

aat aat ggc aaa gaa gaa tct aag att gat cat ttg acc aac aac aga     2501
Asn Asn Gly Lys Glu Glu Ser Lys Ile Asp His Leu Thr Asn Asn Arg
730                 735                 740                 745

aat gat ctt att tca aag gag gaa cag aac agt tca tct ttg cta gaa     2549
Asn Asp Leu Ile Ser Lys Glu Glu Gln Asn Ser Ser Ser Leu Leu Glu
746                 751                 756                 761

gaa aac aaa gtt cat gca gat ttg gta ata tcc aaa cca gtg tca aaa     2597
Glu Asn Lys Val His Ala Asp Leu Val Ile Ser Lys Pro Val Ser Lys
762                 767                 772                 777

tct cca gaa aga tta agg aaa gat ata gaa gta tta tcc gaa gat act     2645
Ser Pro Glu Arg Leu Arg Lys Asp Ile Glu Val Leu Ser Glu Asp Thr
778                 783                 788                 793

gat tat gaa gaa gat gaa gtc aca aaa aag aga aag gat gtc aag aag     2693
Asp Tyr Glu Glu Asp Glu Val Thr Lys Lys Arg Lys Asp Val Lys Lys
794                 799                 804                 809

gac aca aca gat aaa tct tca aaa cca caa ata aaa cgt ggt aaa aga     2741
Asp Thr Thr Asp Lys Ser Ser Lys Pro Gln Ile Lys Arg Gly Lys Arg
810                 815                 820                 825

agg tat tgc aat aca gaa gag tgt cta aaa act gga tca cct ggc aaa     2789
Arg Tyr Cys Asn Thr Glu Glu Cys Leu Lys Thr Gly Ser Pro Gly Lys
826                 831                 836                 841
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aag gaa gag aag gcc aag aac aaa gaa tca ctt tgc atg gaa aac agt     2837
Lys Glu Glu Lys Ala Lys Asn Lys Glu Ser Leu Cys Met Glu Asn Ser
842                 847                 852                 857

agc aac agc tct tca gat gaa gat gaa gaa gaa aca aaa gca aag atg     2885
Ser Asn Ser Ser Ser Asp Glu Asp Glu Glu Glu Thr Lys Ala Lys Met
858                 863                 868                 873

aca cca act aag aaa tac aat ggt ttg gag gaa aaa aga aaa tct cta     2933
Thr Pro Thr Lys Lys Tyr Asn Gly Leu Glu Glu Lys Arg Lys Ser Leu
874                 879                 884                 889

cgg aca act ggt ttc tat tca gga ttt tca gaa gtg gca gaa aaa agg     2981
Arg Thr Thr Gly Phe Tyr Ser Gly Phe Ser Glu Val Ala Glu Lys Arg
890                 895                 900                 905

att aaa ctt tta aat aac tct gat gaa aga ctt caa aac agc agg gcc     3029
Ile Lys Leu Leu Asn Asn Ser Asp Glu Arg Leu Gln Asn Ser Arg Ala
906                 911                 916                 921

aaa gat cga aaa gat gtc tgg tca agt att cag gga cag tgg cct aaa     3077
Lys Asp Arg Lys Asp Val Trp Ser Ser Ile Gln Gly Gln Trp Pro Lys
922                 927                 932                 937

aaa acg ctg aaa gag ctt ttt tca gac tct gat act gag gct gca gct     3125
Lys Thr Leu Lys Glu Leu Phe Ser Asp Ser Asp Thr Glu Ala Ala Ala
938                 943                 948                 953

tcc cca ccg cat cct gcc cca gag gag ggg gtg gca gag gag tca ctg     3173
Ser Pro Pro His Pro Ala Pro Glu Glu Gly Val Ala Glu Glu Ser Leu
954                 959                 964                 969

cag act gtg gct gaa gag gag agt tgt tca ccc agt gta gaa cta gaa     3221
Gln Thr Val Ala Glu Glu Glu Ser Cys Ser Pro Ser Val Glu Leu Glu
970                 975                 980                 985

aaa cca cct cca gtc aat gtc gat agt aaa ccc att gaa gaa gaa aca     3269
Lys Pro Pro Pro Val Asn Val Asp Ser Lys Pro Ile Glu Glu Glu Thr
986                 991                 996                1001

gta gag gtc aat gac aga aaa gca gaa ttt cca agt agt ggc agt aat     3317
Val Glu Val Asn Asp Arg Lys Ala Glu Phe Pro Ser Ser Gly Ser Asn
1002                1007                1012                1017

tca gtg cta aat acc cct cct act aca cct gaa tcg cct tca tca gtc     3365
Ser Val Leu Asn Thr Pro Pro Thr Thr Pro Glu Ser Pro Ser Ser Val
1018                1023                1028                1033

act gta aca gaa ggc agc cgg cag cag tct tct gta aca gta tca gaa     3413
Thr Val Thr Glu Gly Ser Arg Gln Gln Ser Ser Val Thr Val Ser Glu
1034                1039                1044                1049

cca ctg gct cca aac caa gaa gag gtt cga agt atc aag agt gaa act     3461
Pro Leu Ala Pro Asn Gln Glu Glu Val Arg Ser Ile Lys Ser Glu Thr
1050                1055                1060                1065

gat agc aca att gag gtg gat agt gtt gct ggg gag ctc caa gac ctc     3509
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 Asp Ser Thr Ile Glu Val Asp Ser Val Ala Gly Glu Leu Gln Asp Leu
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 Gln Ser Glu Gly Asn Ser Ser Pro Ala Gly Phe Asp Ala Ser Val Ser
1082                1087                1092                1097

 tca agc agt agt aat cag cca gaa cca gaa cat cct gaa aaa gcc tgt     3605
 Ser Ser Ser Ser Asn Gln Pro Glu Pro Glu His Pro Glu Lys Ala Cys
1098                1103                1108                1113

 aca ggt cag aaa aga gtg aaa gat gct cag gga gga gga agt tca tca     3653
 Thr Gly Gln Lys Arg Val Lys Asp Ala Gln Gly Gly Gly Ser Ser Ser
1114                1119                1124                1129

 aaa aag cag aaa aga agc cat aaa gca aca gtg gta aac aac aaa aag     3701
 Lys Lys Gln Lys Arg Ser His Lys Ala Thr Val Val Asn Asn Lys Lys
1130                1135                1140                1145

 aag gga aaa ggc aca aat agt agt gat agt gaa gaa ctt tca gct ggt     3749
 Lys Gly Lys Gly Thr Asn Ser Ser Asp Ser Glu Glu Leu Ser Ala Gly
1146                1151                1156                1161

 gaa agt ata act aag agt cag cca gtc aaa tca gtt tcc act gga atg     3797
 Glu Ser Ile Thr Lys Ser Gln Pro Val Lys Ser Val Ser Thr Gly Met
1162                1167                1172                1177

 aag tct cat agt acc aaa tct ccc gca agg acg cag tct cca gga aaa     3845
 Lys Ser His Ser Thr Lys Ser Pro Ala Arg Thr Gln Ser Pro Gly Lys
1178                1183                1188                1193

 tgt gga aag aat ggt gat aag gat cct gat ctc aag gaa ccc agt aat     3893
 Cys Gly Lys Asn Gly Asp Lys Asp Pro Asp Leu Lys Glu Pro Ser Asn
1194                1199                1204                1209

 cga tta ccc aaa gtt tac aaa tgg agt ttt cag atg tcg gac ctg gaa     3941
 Arg Leu Pro Lys Val Tyr Lys Trp Ser Phe Gln Met Ser Asp Leu Glu
1210                1215                1220                1225

 aat atg aca agt gcc gaa cgc atc aca att ctt caa gaa aaa ctt caa     3989
 Asn Met Thr Ser Ala Glu Arg Ile Thr Ile Leu Gln Glu Lys Leu Gln
1226                1231                1236                1241

 gaa atc aga aaa cat tat ctg tca tta aaa tct gaa gta gct tcc att     4037
 Glu Ile Arg Lys His Tyr Leu Ser Leu Lys Ser Glu Val Ala Ser Ile
1242                1247                1252                1257

 gat cgg agg aga aag cgt tta aag aag aaa gag aga gaa agt gct gct     4085
 Asp Arg Arg Arg Lys Arg Leu Lys Lys Lys Glu Arg Glu Ser Ala Ala
1258                1263                1268                1273

 aca tcc tca tcc tcc tct tca cct tca tcc agc tcc ata aca gct gct     4133
 Thr Ser Ser Ser Ser Ser Ser Pro Ser Ser Ser Ser Ile Thr Ala Ala
1274                1279                1284                1289

 gct atg tta act tta gct gaa ccg tca atg tcc agc gca tca caa aat     4181
 Ala Met Leu Thr Leu Ala Glu Pro Ser Met Ser Ser Ala Ser Gln Asn
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cctcccccac ccttgagtta cccctctgtc tttcctgctg ttgcgcgggt gctcccacag    180

cggagcggag attacagagc cgccggg    atg ccc caa ctc tcc gga gga ggt      231
                                 Met Pro Gln Leu Ser Gly Gly Gly
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ggc ggc ggc ggg ggg gac ccg gaa ctc tgc gcc acg gac gag atg atc      279
Gly Gly Gly Gly Gly Asp Pro Glu Leu Cys Ala Thr Asp Glu Met Ile
  9                  14                  19                  24

ccc ttc aag gac gag ggc gat cct cag aag gaa aag atc ttc gcc gag      327
Pro Phe Lys Asp Glu Gly Asp Pro Gln Lys Glu Lys Ile Phe Ala Glu
 25                  30                  35                  40

atc agt cat ccc gaa gag gaa ggc gat tta gct gac atc aag tct tcc      375
Ile Ser His Pro Glu Glu Glu Gly Asp Leu Ala Asp Ile Lys Ser Ser
 41                  46                  51                  56

ttg gtg aac gag tct gaa atc atc ccg gcc agc aac gga cac gag gtg      423
Leu Val Asn Glu Ser Glu Ile Ile Pro Ala Ser Asn Gly His Glu Val
 57                  62                  67                  72

gcc aga caa gca caa acc tct cag gag ccc tac cac gac aag gcc aga      471
Ala Arg Gln Ala Gln Thr Ser Gln Glu Pro Tyr His Asp Lys Ala Arg
 73                  78                  83                  88

gaa cac ccc gat gac gga aag cat cca gat gga ggc ctc tac aac aag      519
Glu His Pro Asp Asp Gly Lys His Pro Asp Gly Gly Leu Tyr Asn Lys
 89                  94                  99                 104

gga ccc tcc tac tcg agt tat tcc ggg tac ata atg atg cca aat atg      567
Gly Pro Ser Tyr Ser Ser Tyr Ser Gly Tyr Ile Met Met Pro Asn Met
105                 110                 115                 120
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aat aac gac cca tac atg tca aat gga tct ctt tct cca ccc atc ccg      615
Asn Asn Asp Pro Tyr Met Ser Asn Gly Ser Leu Ser Pro Pro Ile Pro
121                 126                 131                 136

aga aca tca aat aaa gtg ccc gtg gtg cag cca tcc cat gcg gtc cat      663
Arg Thr Ser Asn Lys Val Pro Val Val Gln Pro Ser His Ala Val His
137                 142                 147                 152

cct ctc acc ccc ctc atc act tac agt gac gag cac ttt tct cca gga      711
Pro Leu Thr Pro Leu Ile Thr Tyr Ser Asp Glu His Phe Ser Pro Gly
153                 158                 163                 168

tca cac ccg tca cac atc cca tca gat gtc aac tcc aaa caa ggc atg      759
Ser His Pro Ser His Ile Pro Ser Asp Val Asn Ser Lys Gln Gly Met
169                 174                 179                 184

tcc aga cat cct cca gct cct gat atc cct act ttt tat ccc ttg tct      807
Ser Arg His Pro Pro Ala Pro Asp Ile Pro Thr Phe Tyr Pro Leu Ser
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Pro Gly Gly Val Gly Gln Ile Thr Pro Pro Leu Gly Trp Gln Gly Gln
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217                 222                 227                 232

ctg tca gtc gac act tcc atg tcc agg ttt tcc cat cat atg att ccc      951
Leu Ser Val Asp Thr Ser Met Ser Arg Phe Ser His His Met Ile Pro
233                 238                 243                 248

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Gly Pro Pro Gly Pro His Thr Thr Gly Ile Pro His Pro Ala Ile Val
249                 254                 259                 264

aca cct cag gtc aaa cag gaa cat ccc cac act gac agt gac cta atg     1047
Thr Pro Gln Val Lys Gln Glu His Pro His Thr Asp Ser Asp Leu Met
265                 270                 275                 280

cac gtg aag cct cag cat gaa cag aga aag gag cag gag cca aaa aga     1095
His Val Lys Pro Gln His Glu Gln Arg Lys Glu Gln Glu Pro Lys Arg
281                 286                 291                 296

cct cac att aag aag cct ctg aat gct ttt atg tta tac atg aaa gaa     1143
Pro His Ile Lys Lys Pro Leu Asn Ala Phe Met Leu Tyr Met Lys Glu
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atg aga gcg aat gtc gtt gct gag tgt act cta aaa gaa agt gca gct     1191
Met Arg Ala Asn Val Val Ala Glu Cys Thr Leu Lys Glu Ser Ala Ala
313                 318                 323                 328

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Ile Asn Gln Ile Leu Gly Arg Arg Trp His Ala Leu Ser Arg Glu Glu
329                 334                 339                 344
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Gln Ala Lys Tyr Tyr Glu Leu Ala Arg Lys Glu Arg Gln Leu His Met
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cag ctt tat cca ggc tgg tct gca aga gac aat tat ggt aag aaa aag     1335
Gln Leu Tyr Pro Gly Trp Ser Ala Arg Asp Asn Tyr Gly Lys Lys Lys
361                 366                 371                 376

aag agg aag aga gag aaa cta cag gaa tct gca tca ggt aca ggt cca     1383
Lys Arg Lys Arg Glu Lys Leu Gln Glu Ser Ala Ser Gly Thr Gly Pro
377                 382                 387                 392

aga atg aca gct gcc tac atc tga aacatggtgg aaaacgaagc tcattcccaa    1437
Arg Met Thr Ala Ala Tyr Ile  *
393                 398

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